

GenCore version 5.1.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: February 23, 2005, 11:12:04 ; Search time 27 Seconds
(without alignments)
1967.098 Million cell updates/sec

Title: US-09-910-208B-1
Perfect score: 482
Sequence: 1 atgactaagctggaagatca.....acatagatatccacaagag 276

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp
-Q/cn2_1/USFTO_spool_p/HADDAD-09-910208/runat_23022005_101806_14731/app_query.fasta_1.
-DB=PIR_79 -QFMT=fiastan -SUFFIX=rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=HADDAD-09-910208 @CGN 1.1 63 @runat_23022005_101806_14731 -NCPu=6
-ICPU=3 -NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSBBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PIR 79.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	371	77.0	91	2 A55406	calgranulin c - pi
2	319	66.2	92	2 JC4712	S-100 calcium-bind
3	236.5	49.1	122	1 A42628	calgranulin B - bo
4	211.5	43.9	114	1 B31848	calgranulin B [val
5	190.5	39.5	113	1 JN0686	calgranulin B - ra
6	187	38.8	95	2 S24146	S-100 protein p -
7	184	38.2	92	2 A26557	S-100 protein beta
8	181	37.6	92	2 A48015	S-100 protein beta
9	180	37.3	91	1 BCHUIB	S-100 protein beta
10	176	36.5	91	1 BCBOIB	calgranulin A - mo
11	170	35.3	89	1 I56163	calgranulin A - ra
12	170	35.3	89	1 JN0685	calgranulin A - ra
13	169	35.1	95	1 S35985	S-100 protein alph
14	164.5	34.1	113	1 S68242	calgranulin B - mo

15	164	34.0	94	1 BCBOIA	S-100 protein alph
16	163	33.8	94	1 BCHUIA	S-100 protein alph
17	160	33.2	93	1 BCHUCF	calgranulin A [val
18	160	33.2	101	2 S06207	calvasculin - mouse
19	157	32.6	101	2 S01759	calvasculin - rat
20	155	32.2	100	2 A53217	placental calcium-
21	155	32.2	591	2 A45135	profilaggrin - hum
22	153	31.7	101	2 A48219	calvasculin - huma
23	152.5	31.6	79	1 KLPGI	calcium-binding pr
24	148.5	30.8	79	1 JN0246	calcium-binding pr
25	146	30.3	306	2 A48118	major epidermal ca
26	145.5	30.2	79	1 KLBOI	calcium-binding pr
27	139.5	28.9	97	1 JH0663	calpacin I light
28	139.5	28.9	97	2 A28489	calpacin I light
29	136.5	28.3	95	2 A31373	calpacin I light
30	136	28.2	90	1 BCHUY	calcylin - human
31	135	28.0	90	1 S27011	calcylin - rabbit
32	135	28.0	102	1 JQ1300	calgizarin - rabb
33	134.5	27.9	95	1 LUPG10	calpacin I light
34	134.5	27.9	97	2 JC1139	calpacin I light
35	134.5	27.9	97	2 B28489	calpacin I light
36	134.5	27.9	1130	2 T30251	repetin - mouse
37	133	27.6	1407	1 S28589	trichohyalin - rab
38	132.5	27.5	79	1 KLRTI	calcium-binding pr
39	131	27.2	89	2 A54314	calcylin - mouse
40	128	26.6	90	2 B28363	calgizarin - rat
41	128	26.6	105	1 I37080	S-100 calcium-bind
42	127	26.3	98	2 A41988	trichohyalin - she
43	127	26.3	1549	1 A40691	S-100 calcium-bind
44	126.5	26.2	98	2 JC5064	S-100 protein, lun
45	126	26.1	97	2 A30129	

ALIGNMENTS

RESULT 1

A55406
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 09-Jul-2004
C:Accession: A55406
R:Id:Angelic, E.C.; Schleicher, C.H.; Santome, J.A.
A:Title: Primary structure and binding properties of calgranulin C, a novel S100-like c
A:Reference number: A55406; MUID:95050708; PMID:7961855
A:Accession: A55406
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-91
A:Cross-references: UNIPROT:P80310
C:Superfamily: S-100 protein; calmodulin repeat homology
C:Keywords: calcium binding; EF hand
F:48-80/Domain: calmodulin repeat homology <EF2>

Alignment Scores:

Pred. No.: 1.14e-33 Length: 91
Score: 371.00 Matches: 74
Percent Similarity: 91.21% Conservative: 9
Best local Similarity: 81.32% Mismatches: 8
Query Match: 76.97% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-1 (1-276) x A55406 (1-91)

QY	4	ACTAAGCTGGAAGATCACCTGGAGGGAATCATCAACATCTTCCACCGACTCCGTCGG	63
DB	1	ThrLysLeuGluAspHisLeuGluGlyIleIleAsnIlePheHisGlnTyrSerValArg	20
QY	64	GTGGGGCATTTTCAGACCCCTCAACAGCGTGAAGCAGCTGATCATCAAGGAACTT	123
DB	21	LeuGlyHisTyrAspThrLeuIleLysArgGluLeuLysGlnLeuThrLysGluLeu	40
QY	124	CCCAAAACCCCTCCAGAACCAACCAAGATCAACCTTACCATTTGACAAAATATATTCACAGACCTG	183

Db 41 LeuProAsnPhenLeuLysLysGlnLysLysAsnGluAlaAlaLeuMetGlu 60
178 GACCTGGATCCGCAAAACAGCGAGCGTCAGCTTGAGGAATTCGTAGCTCTGGTGTC 237
Db 61 AspLeuAspThrAsnValAspLysGlnLeuSerPheGluGluPheIleMetLeuValAla 80
Qy 238 AGGGTGCTGAAACAGCCACATAGATATCCAC 270
Db 81 ArgLeuThrValAlaSerHisGluGluMetHis 91
RESULT 4
B31848
calgranulin B [validated] - human
N:Alternate names: calcium-binding protein MRP-14; cystic fibrosis-associated antigen (C
(MRP-14); MIF-related 14K protein; S-100 calcium-binding protein A9 (S100A9)
C:Species: Homo sapiens (man)
C:Date: 21-May-1990 #sequence_revision 23-May-1997 #text_change 09-Jul-2004
C:Accession: B31848; S00667; A33819; B60911; B61082; D54327
R:Agassee, E.; Clerc, R.G.
Mol. Cell. Biol. 8, 2402-2410, 1988
A:Title: Cloning and expression of two human genes encoding calcium-binding proteins the
A:Reference number: A93102; MUID:88302148; PMID:3405210
A:Accession: B31848
A:Molecule type: DNA
A:Residues: 1-114 <IAG>
A:Cross-references: UNIPROT:P06702; GB:M21064; NID:G188689; PIDN:AAA36326.1; PID:G386958
R:Odink, K.; Cerletti, N.; Brueggem, J.; Clerc, R.G.; Tarceay, L.; Zwadlo, G.; Gerhards,
Nature 330, 80-82, 1987
A:Title: Two calcium-binding proteins in infiltrate macrophages of rheumatoid arthritis.
A:Reference number: S00667; MUID:88039099; PMID:3313057
A:Accession: S00667
A:Molecule type: mRNA
A:Residues: 1-114 <ODI>
A:Cross-references: EMBL:X06233; NID:G34770; PIDN:CAA29579.1; PID:G34771
A:Note: parts of this sequence were confirmed by protein sequencing
R:Muro, S.; Collart, F.R.; Huberman, E.
J. Biol. Chem. 264, 8356-8360, 1989
A:Title: A protein containing the cystic fibrosis antigen is an inhibitor of protein kin
A:Reference number: A33819; MUID:89255276; PMID:2656677
A:Accession: A33819
A:Molecule type: mRNA
A:Residues: 1-114 <GUR>
A:Cross-references: GB:M26311; NID:G862619; PIDN:AAA68480.1; PID:G516621
A:Note: part of this sequence was confirmed by protein sequencing; the amino end of the
R:Andersson, K.B.; Sletten, K.; Berntzen, H.B.; Bale, I.; Brandtzaeg, P.; Jellum, E.; Fa
Scand. J. Immunol. 28, 241-245, 1988
A:Title: The leucocyte LI protein: identity with the cystic fibrosis antigen and the cal
A:Reference number: A60911; MUID:88321575; PMID:3413449
A:Accession: B60911
A:Molecule type: protein
A:Residues: 39-42, 'X', 44-50:64-77, 'X', 79:84, 'X', 86-90, 'X', 92-94, 'X', 96-98 <AND>
R:Trobe, T.; Murakami, K.; Tomita, M.; Nozawa, R.
Chem. Pharm. Bull. 37, 1576-1580, 1989
A:Title: Amino acid sequences of 6088 antigens induced in HL-60 cells by 1,25-dihydroxyv
A:Reference number: A61082; MUID:89376638; PMID:2776242
A:Accession: B61082
A:Molecule type: protein
A:Residues: 5-77;80-90, 'A', 92-114 <TOB>
A:Note: the blocked amino end of the mature protein is identified as 2-Thr; residue 91-H
R:Madson, P.; Rasmussen, H.H.; Leffers, H.; Honore, B.; Dejgaard, K.; Olsen, E.; Kiil, J
E.
Invest. Dermatol. 97, 701-712, 1991
A:Title: Molecular cloning, occurrence, and expression of a novel partially secreted pro
A:Reference number: A54327; MUID:92043866; PMID:1940442
A:Accession: D54327
A:Molecule type: protein
A:Residues: 11-19;26-38;94-105, 'X', 107 <MAD>
A:Note: in several peptide samples no PTH was detected for 95-His but in one peptide PTH
C:Comment: This protein appears to be expressed only in cells of myeloid origin actively
C:Genetics:
A:Gene: GDB:S100A9; 60B8AG; CAGB; CFAG; LIAG; MAC387; MIF; MRP14; NIF; P14

A:Cross-references: GDB:120570; OMIM:123886
A:Map position: 1q21-1q21
A:Introns: 50/3
C:Note: the first intron occurs before the initiator codon
C:Complex: heterodimer and higher complexes with calgranulin A (see PIR:BCHUCF)
C:Superfamily: S-100 protein; calmodulin repeat homology
C:Keywords: blocked amino end; calcium binding; EF hand; heterodimer; inflammation; pho
F:2-114/Product: calgranulin B #status experimental <MAT>
F:10-44/Domain: calmodulin repeat homology <EF1>
F:54-86/Domain: calmodulin repeat homology <EF2>
F:2/Modified site: blocked amino end (Thr) (in mature form) (probably acetylated) #stat
F:113/Binding site: phosphate (Thr) (covalent) #status predicted
Alignment Scores:
Pred. No.: 1.34e-15 Length: 114
Score: 211.50 Matches: 41
Percent Similarity: 71.74% Conservative: 25
Best Local Similarity: 44.57% Mismatches: 25
Query Match: 43.88% Indels: 1
DB: 1 Gaps: 1
US-09-910-208B-1 (1-276) x B31848 (1-114)
Qy 1 ATGACTAAGCTGGAAGATCACCTGGAGGAATCATCAACATCTTCACCAGTACTCCGTT 60
Db 5 MetSerGlnLeuGluArgAsnIleGluThrIleAsnThrPheHisGlnTyrSerVal 24
Qy 61 CGGGTGGGGCCATTTTCACACCCCTCAACAGCGTGAAGCTGAGTGAACGACGTGATCACAAAGGAA 120
Db 25 LysLeuGlyHisProAspThrLeuAsnGlnGlyGluPheLysGluLeuValArgLysAsp 44
Qy 121 CTTCCCAAAACCCCTC---CAGAACACCAAGATCAACCTTACCATTGACAAAATATTTCCAA 177
Db 45 LeuGlnAsnPhenLeuLysLysGluAsnLysAsnGluLysValIleGluHisIleMetGlu 64
Qy 178 GACCTGGATCCGCAAAACAGCGAGCGTCAGCTTGAGGAATTCGTAGCTCTGGTGTC 237
Db 65 AspLeuAspThrAsnValAspLysGlnLeuSerPheGluGluPheIleMetLeuValAla 84
Qy 238 AGGGTGCTGAAACAGCCACATAGATATCCACAA 273
Db 85 ArgLeuThrTrpAlaSerHisGluLysMetHisGlu 96
RESULT 5
JN0686
calgranulin B - rat
N:Alternate names: calcium-binding protein MRP-14; macrophage migration inhibitory fact
C:Species: Rattus norvegicus (Norway rat)
C:Date: 03-May-1994 #sequence_revision 23-May-1997 #text_change 09-Jul-2004
C:Accession: JN0686
R:Imamichi, T.; Uchida, I.; Wahl, S.M.; McCartney-Francis, N.
Biochem. Biophys. Res. Commun. 194, 819-825, 1993
A:Title: Expression and cloning of migration inhibitory factor-related protein (MRP)8 a
A:Reference number: JN0685; MUID:93343942; PMID:8343166
A:Accession: JN0686
A:Molecule type: mRNA
A:Residues: 1-113 <IMA>
A:Cross-references: UNIPROT:P50116; GB:L18948; NID:G488156; PIDN:AAA18214.1; PID:G48815
C:Genetics:
A:Gene: MRP14
C:Complex: heterodimer and higher complexes with calgranulin A
C:Superfamily: S-100 protein; calmodulin repeat homology
C:Keywords: acetylated amino end; calcium binding; EF hand; heterodimer; inflammation; i
F:2-113/Product: calgranulin B #status predicted <MAT>
F:11-45/Domain: calmodulin repeat homology <EF1>
F:55-87/Domain: calmodulin repeat homology <EF2>
F:2/Modified site: acetylated amino end (Ala) (in mature form) #status predicted
F:80-91/Disulfide bonds: #status predicted
Alignment Scores:
Pred. No.: 3.18e-13 Length: 113
Score: 190.50 Matches: 36
Percent Similarity: 67.03% Conservative: 25


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Db      41 LeuSerHisPheLeuGluGluLeuIleGluGluGluValValAspLysValMetGluThr 60
      181 CTGGATCGCCATAAAGACGAGCCGTCAGCTTTTGAGGAATTCGTAGTCTCGTGTGCCAGG 240
      61 LeuAspGluAspGlyAspGlyGluCysaspPheGlnGluPheMetAlaPheValSerMet 80
      241 GTGCTGAACACGCCAC 258
      81 ValThrAlaCysHis 86

RESULT 8
A48015
S-100 protein beta chain - mouse
C:Species: Mus musculus (house mouse)
C>Date: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 09-Jul-2004
C:Accession: A48015
R:Jiang, H.; Shah, S.; Hilt, D.C.
J. Biol. Chem. 268, 20502-20511, 1993
A:Title: Organization, sequence, and expression of the murine S100beta gene. Transcription
A:Reference number: A48015; MUID:93388628; PMID:8376406
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-92, <JIA>
A:Cross-references: UNIPROT:P50114; GB:I22144; NID:9404768; PIDN:AAA03075.1; PID:9404768
C:Genetics:
A:Introns: 46/3
C:Superfamily: S-100 protein; calmodulin repeat homology
C:Keywords: acetylated amino end; calcium binding; EF hand
F:2-92/Product: S-100 protein beta chain #status predicted <MAT>
F:6-40/Domain: calmodulin repeat homology <EPI>
F:49-81/Domain: calmodulin repeat homology <EP2>
F:2/Modified site: acetylated amino end (Ser) (in mature form) #status predicted
F:19,22,24,27,32/Binding site: calcium (Gly, Glu, Asp, Lys, Glu) #status predicted
F:162,64,66,68,70,73/Binding site: calcium (Asp, Asp, Glu, Asp, Glu) #status predicted

Alignment Scores:
Pred. No.:      3 63e-12      Length:      92
Score:          181.00      Matches:      36
Percent Similarity: 59.30%      Conservative: 15
Best Local Similarity: 41.86%      Mismatches: 35
Query Match:      37.55%      Indels:      0
DB:              2          Gaps:      0

US-09-910-208B-1 (1-276) x A48015 (1-92)

QY      1 ATGACTAAGCTGGAAGATCACCTGGAGGGAATCATCAACATCTTCCACCAGTACTCCGTT 60
      1 MetSerGluLeuGluLysAlaMetValAlaLeuIleAspValPheHisGlnTyrSerGly 20
      61 CGGTGGGGCATTTCACACCTTCAACAGCGTGAAGTGAACGACCTGATCATCAAGGAA 120
      21 ArgGluGlyAspLysHisLysLeuLysLysSerGluLeuLysGluLeuIleAsnAsnGlu 40
      121 CTTCCCAAAACCTCCAGAACACCAACATCAACCTACCATTCGACAAATATTTCCAAGAC 180
      41 LeuSerHisPheLeuGluGluLeuLysGluGluGluValValAspLysValMetGluThr 60
      181 CTGGATCGCCATAAAGACGAGCCGTCAGCTTTTGAGGAATTCGTAGTCTCGTGTGCCAGG 240
      61 LeuAspGluAspGlyAspGlyGluCysaspPheGlnGluPheMetAlaPheValAlaMet 80
      241 GTGCTGAACACGCCAC 258
      81 ValThrAlaCysHis 86

RESULT 9
BCHUIB
S-100 protein beta chain [validated] - human
N:Alternate names: neural S-100 calcium-binding protein beta
C:Species: Homo sapiens (man)
C>Date: 04-Dec-1986 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004

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C:Accession: A38364; A92972; A03076
R:Allore, R.J.; Friend, W.C.; O'Hanlon, D.; Neilson, K.M.; Bauman, R.; Dunn, R.J.; Marko
J. Biol. Chem. 265, 15537-15543, 1990
A:Title: Cloning and expression of the human S100beta gene.
A:Reference number: A38364; MUID:90368757; PMID:2394738
A:Accession: A38364
A:Molecule type: DNA
A:Residues: 1-92 <ALL>
A:Cross-references: UNIPROT:P04271; GB:J05600; GB:M59486; NID:9337726; GB:M59487; NID:93
R:Jensen, R.; Marehak, D.R.; Anderson, C.; Lukas, T.J.; Watterson, D.M.
J. Neurochem. 45, 700-705, 1985
A:Title: Characterization of human brain S100 protein fraction: amino acid sequence of
A:Reference number: A92972; MUID:85291729; PMID:4031854
A:Accession: A92972
A:Molecule type: protein
A:Residues: 2-92 <JEN>
R:Baudier, J.; Glaeser, N.; Haglid, K.; Gerard, D.
Biochim. Biophys. Acta 790, 164-173, 1984
A:Title: Purification, characterization and ion binding properties of human brain S100b
A:Reference number: A90653; MUID:85023393; PMID:6487634
A:Contents: annotation; metal ion-binding properties
C:Comment: This protein binds p53, tubulin and many other proteins at physiological con-
C:Comment: S-100 is an intracellular protein that binds calcium. It binds zinc more tigh-
different affinities exist for both ions on each monomer. Physiological concentrations
ning sites.
C:Comment: This protein is expressed predominantly in brain tissue by astroglial cells.
C:Comment: The homodimer contains disulfide bonds, but the bond pattern has not been dete-
C:Genetics:
A:Gene: GDB:S100B
A:Cross-references: GDB:120360; OMIM:176990
A:Map position: 21q22.3-21q22.3
A:Introns: 46/3
A:Note: the first intron occurs before the initiator codon
C:Complex: homodimer; heterodimer with S-100 protein alpha chain (see PIR:BCHUIA)
C:Superfamily: S-100 protein; calmodulin repeat homology
C:Keywords: blocked amino end; brain; calcium binding; EF hand; heterodimer; homodimer;
F:2-92/Product: S-100 protein beta chain #status experimental <MAT>
F:6-40/Domain: calmodulin repeat homology <EPI>
F:49-81/Domain: calmodulin repeat homology <EP2>
F:2/Modified site: blocked amino end (Ser) (in mature form) (probably acetylated) #stat
F:19,22,24,27,32/Binding site: calcium (Ser, Glu, Asp, Lys, Glu) #status predicted
F:162,64,66,68,73/Binding site: calcium (Asp, Asp, Glu, Glu) #status predicted

Alignment Scores:
Pred. No.:      4 7e-12      Length:      92
Score:          180.00      Matches:      36
Percent Similarity: 59.30%      Conservative: 15
Best Local Similarity: 41.86%      Mismatches: 35
Query Match:      37.34%      Indels:      0
DB:              1          Gaps:      0

US-09-910-208B-1 (1-276) x BCHUIB (1-92)

QY      1 ATGACTAAGCTGGAAGATCACCTGGAGGGAATCATCAACATCTTCCACCAGTACTCCGTT 60
      1 MetSerGluLeuGluLysAlaMetValAlaLeuIleAspValPheHisGlnTyrSerGly 20
      61 CGGTGGGGCATTTCGACACCTTCAACAGCGTGAAGTGAACGACCTGATCATCAAGGAA 120
      21 ArgGluGlyAspLysHisLysLeuLysLysSerGluLeuLysGluLeuIleAsnAsnGlu 40
      121 CTTCCCAAAACCTCCAGAACACCAACATCAACCTACCATTCGACAAATATTTCCAAGAC 180
      41 LeuSerHisPheLeuGluGluLeuLysGluGluGluValValAspLysValMetGluThr 60
      181 CTGGATCGCCATAAAGACGAGCCGTCAGCTTTTGAGGAATTCGTAGTCTCGTGTGCCAGG 240
      61 LeuAspAsnAspGlyAspGlyGluCysaspPheGlnGluPheMetAlaPheValAlaMet 80
      241 GTGCTGAACACGCCAC 258
      81 ValThrAlaCysHis 86

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QY 244 CTGAAACAGCCACATAGATATCCAAAGAG 276

Db 79 GlyValAlaSerHisLysAspSerHisLysGlu 89

RESULT 12

JN0685
calgranulin A - rat
N:Alternate names: calcium-binding protein MRP-8; macrophage migration inhibitory factor
C:Species: Rattus norvegicus (Norway rat)
C>Date: 03-May-1994 #sequence_revision 23-May-1997 #text_change 09-Jul-2004
C:Accession: JN0685
R:Imamichi, T.; Uchida, I.; Wahl, S.M.; McCartney-Francis, N.
Biochem. Biophys. Res. Commun. 194, 819-825, 1993
A:Title: Expression and cloning of migration inhibitory factor-related protein (MRP)8 and
A:Reference number: JN0685; MUID:93343942; PMID:8343166
A:Accession: JN0685
A:Molecule type: mRNA
A:Residues: 1-89 <RNA>
A:Cross-references: UNIPROT:P50115; GB:L18891; NID:G349548; PIDN:AAA1637.1; PID:G349549
A:Experimental source: strains LEW/N and F344/N
C:Comment: This protein has a role in susceptibility to SCW-induced chronic disease.
C:Genetics:

A:Gene: MRP8
C:Complex: homodimer; heterodimer and higher complexes with calgranulin B
C:Superfamily: S-100 protein; calmodulin repeat homology
C:Keywords: calcium binding; cytokine; EF hand; heterodimer; homodimer; inflammation
F:7-41/Domain: calmodulin repeat homology <EF1>
F:46-78/Domain: calmodulin repeat homology <EF2>

Alignment Scores:

Pred. No.:	6.33e-11	Length:	89
Score:	170.00	Matches:	34
Percent Similarity:	60.44%	Conservative:	21
Best Local Similarity:	37.36%	Mismatches:	32
Query Match:	35.27%	Indels:	4
DB:	1	Gaps:	1

US-09-910-208B-1 (1-276) x JN0685 (1-89)

QY 4 ACTAGCTGGAAGATCACCTGGAGGAATCATCAACATCTTCACAGTACTCCGTTCCG 63

Db 3 ThrGluLeuGluLysAlaLeuSerAsnValIleGluValTyrHisAsnTyrSerGlyIle 22

QY 64 GTGGGGCAATTCGACACACCTCCACAGCGTGAAGCAGCTGATCATCAAGAGAACTT 123

Db 23 LysGlyAsnHisAlaLeuTyrArgAspAspPheArgLysMetValThrThrGluCys 42

QY 124 CCCAAACCTCCAGAACCCAAAGATCAACCTTACCATTCGACAAATATTCACAGACCTG 183

Db 43 ProGlnPheValGlnAsn-----LysAsnThrGluSerLeuPheLysGluLeu 58

QY 184 GATCCGATAAAGACGCGCTGACCTTTGAGGATTCGTAGTCTGTGTCAGGGTG 243

Db 59 AspValAsnSerAspAsnAlaIleAsnPheGluGluPheLeuAlaLeuValIleArgVal 78

QY 244 CTGAAACAGCCACATAGATATCCAAAGAG 276

Db 79 GlyValAlaAlaHisLysAspSerHisLysGlu 89

RESULT 13

S35985
S-100 protein alpha chain - weatherfish
C:Species: Misgurnus fossilis (weatherfish)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: S35985
R:Ivanenkov, V.V.; Gerke, V.; Minin, A.A.; Plessmann, U.; Weber, K.
Mech. Dev. 42, 151-158, 1993
A:Title: Transduction of Ca(2+) signals upon fertilization of eggs; identification of an
A:Reference number: S35985; MUID:94031845; PMID:8217841
A:Accession: S35985
A:Molecule type: protein
A:Residues: 1-95 <IVA>
A:Cross-references: UNIPROT:Q7LZT1

C:Superfamily: S-100 protein; calmodulin repeat homology
C:Keywords: calcium binding; EF hand
F:49-81/Domain: calmodulin repeat homology <EF2>

Alignment Scores:

Pred. No.:	8.32e-11	Length:	95
Score:	169.00	Matches:	35
Percent Similarity:	64.56%	Conservative:	16
Best Local Similarity:	44.30%	Mismatches:	28
Query Match:	35.06%	Indels:	0
DB:	1	Gaps:	0

US-09-910-208B-1 (1-276) x S35985 (1-95)

QY 1 ATGACTAGCTGAAGATCACCTGGAGGAATCATCAACATCTTCACAGTACTCCGTT 60

Db 1 ValSerGlnLeuGluSerAlaMetGluSerLeuIleLysValPheHisThrTyrSerSer 20

QY 61 CGGTTGGGCAATTCGACACACCTCCACAGCGTGAAGCAGCTGATCATCAAGAGAA 120

Db 21 LysGluGlyAspLysTyrLysLeuSerLysAlaGluLeuLysSerLeuGlnGlyGlu 40

QY 121 CTTCCAAAACCTCCAGAACACCAAGATCAACCTACCATTCACAAAATATTCACAGAC 180

Db 41 LeuAsnAspPheLeuSerAlaSerLysAspProMetValValGluLysIleMetSerAsp 60

QY 181 CTGGATCGCGATAAAGACGCGCTGACGCTTTGAGGATTCGTAGTCTGTGTGCC 237

Db 61 LeuAspGluAsnGlnAspGlyValValAspPheGlnGluPheValValLeuValAla 79

RESULT 14

S68242

calgranulin B - mouse

N:Alternate names: calcium-binding protein MRP-14; macrophage migration inhibitory factor

C:Species: Mus musculus (house mouse)

C>Date: 06-Sep-1996 #sequence_revision 23-May-1997 #text_change 09-Jul-2004

C:Accession: S68242; S68272

R:Lagasse, E.; Weissman, I.L.

submitted to the EMBL Data Library, February 1992

A:Description: Mouse MRP8 and MRP14, two intracellular calcium-binding proteins associated

A:Reference number: S68242

A:Accession: S68242

A:Molecule type: mRNA

A:Residues: 1-113 <LAG>

A:Cross-references: UNIPROT:P31725; EMBL:W83219; NID:G199807; PIDN:AAB07228.1; PID:G199

R:Raftery, M.J.; Harrison, C.A.; Alewood, P.; Jones, A.; Geczy, C.L.

Biochem. J. 316, 285-293, 1996

A:Title: Isolation of the murine S100 protein MRP14 (14 kDa migration-inhibitory-factor

ding.

A:Reference number: S68272; MUID:96235204; PMID:8645219

A:Accession: S68272

A:Molecule type: protein

A:Residues: 2-10;95-109 <RAF>

A>Note: 107-His is identified as 3'-methylhistidine; the authors' source for the referen

ylhistidine

C:Genetics:

A:Gene: MRP14

C:Complex: heterodimer and higher complexes with calgranulin A

C:Superfamily: S-100 protein; calmodulin repeat homology

C:Keywords: acetylated amino end; calcium binding; EF hand; heterodimer; inflammation; i

F:2-113/Product: calgranulin B #status predicted <MAT>

F:11-45/Domain: calmodulin repeat homology <EF1>

F:55-87/Domain: calmodulin repeat homology <EF2>

F:2/Modified site: acetylated amino end (Ala) (in mature form) #status experimental

F:80-91/Disulfide bonds: #status experimental

F:103,105,107/Binding site: zinc (His) #status predicted

F:107/Modified site: 3'-methylhistidine (His) #status experimental

Alignment Scores:

Pred. No.:	2.78e-10	Length:	113
Score:	164.50	Matches:	31
Percent Similarity:	67.03%	Conservative:	30
Best Local Similarity:	34.07%	Mismatches:	29

Query Match: 34.13% Indels: 1 1
DB: 1 Gaps: 1

US-09-910-208B-1 (1-276) x S68242 (1-113)

QY 4 ACTAAGCTGGAAGATCACCTTGAGGGGNAATCATCAACATCTTCCACCAGTACTCCGTTCCG 63
Db SerGlnMetGluArgSerIleThrTrilleAaspThrPheHisGlnTySerArgLys 26
QY 64 GTGGGGCATTTGCACACCCCTCAACAAGCGTGAGCTGAAGCAGCTGATCAACAAGGAAC 123
Db GluGlyHisProAspThrLeuSerLysGluPheArgGlnMetValGluAlaGlnLeu 46
QY 124 CCCAAAACCCCTCCAGACACACAAA--GATCAACCTACCATTCACAAAATATTCCAGAC 180
Db AlaThrPheMetLysLysGluLysArgAsnGluAlaLeuIleAsnAspIleMetGluAsp 66
QY 181 CTGATGCCGATTAAGACGGAGCGCTCAGCTTTGAGGAATTCGTAGTCCTGGTGCAGG 240
Db LeuAspThrAsnGlnAspAsnGlnLeuSerPheGluGluCysMetMetLeuMetAlaLys 86
QY 241 GTGCTGAACACGCCACACATAGATATCCACAAA 273
Db LeuIlePheAlaCysHisGluLysLeuHisGlu 97

RESULT 15

BCBO1A

S-100 protein alpha chain - bovine
C/Species: Bos primigenius taurus (cattle)
C/Date: 14-Nov-1993 #sequence, revision 06-Feb-1995 #text_change 09-Jul-2004
C/Accession: A24156; A91110; S54346; A03078
R/Kuwano, R.; Maeda, T.; Usui, H.; Araki, K.; Yamakuni, T.; Ohshima, Y.; Kurihara, T.; Kuribara, T.; T.
FEBS Lett. 202, 97-101, 1986
A/Title: Molecular cloning of cDNA of S100alpha subunit mRNA.
A/Reference number: A24156; MUID: 86248083; PMID: 3755105
A/Accession: A24156
A/Molecule type: mRNA
A/Residues: 1-94 <KUW>
A/Cross-references: UNIPROT: P02639
R/Isobe, T.; Okuyama, T.
Eur. J. Biochem. 116, 79-86, 1981
A/Title: The amino-acid sequence of the alpha subunit in bovine brain S-100 a protein.
A/Reference number: A91110; MUID: 81236562; PMID: 7250124
A/Accession: A91110
A/Molecule type: protein
A/Residues: 2-64, 'D', 66-94 <ISO>
R/Baudier, J.; Gerard, D.
Biochemistry 22, 3360-3369, 1983
A/Title: Ions binding to S100 proteins: structural changes induced by calcium and zinc
A/Reference number: A90471; MUID: 84000339; PMID: 6615778
A/Contents: annotation; metal ion-binding properties
R/Okazaki, K.; Obata, N.H.; Inoue, S.; Hidaka, H.
Biochem. J. 306, 551-555, 1995
A/Title: S100-beta is a target protein of neurocalcin delta, an abundant isoform in glia
A/Reference number: S54343; MUID: 95194333; PMID: 7887910
A/Accession: S54346
A/Molecule type: protein
A/Residues: 24-33 <OKA>
C/Comment: The S-100 protein is composed of two related polypeptide chains, alpha and beta.
brain proteins, S-100 is also found in a variety of other tissues.
C/Comment: S-100 is an intracellular protein that weakly binds calcium. It binds zinc
es, with different affinities, exist for both ions on each monomer. Physiological concen
alcium-binding sites.
C/Superfamily: S-100 protein; calmodulin repeat homology
F/2-94/Product: S-100 protein alpha chain #status predicted <MAT>
F/7-41/Domain: calmodulin repeat homology <EF1>
F/50-82/Domain: calmodulin repeat homology <EF2>
F/2/Modified site: blocked amino end (Gly) (in mature form) (probably acetylated) #statu
F/20,23,25,28,33/Binding site: calcium (Ser, Glu, Asp, Lys, Glu) #status predicted
F/63,65,67,69,74/Binding site: calcium (Asp, Asn, Asp, Glu, Glu) #status predicted

Alignment Scores:

GenCore version 5.1.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: February 23, 2005, 11:11:14 ; Search time 116 Seconds
(without alignments)

2436.791 Million cell updates/sec

Title: US-09-910-208B-1

Perfect score: 482

Sequence: 1 atgactaagctggaagatca.....acatagatatccacaagag 276

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp
-O=/cn2_1/USPTO spoop_p/HADDAD-09-910208/runat_23022005_101805_14722/app_query.fasta_1.
-DB=UniProt_03 -QFMT=fastan -SUFFIX=rup -MINMATCH=0.1 -LOOPECL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000
-USER=HADDAD-09-910208 @CGN 1.1 244 @runat_23022005_101805_14722 -NCPU=6
-ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT_DSBLCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : UniProt 03:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	465	96.5	91	1 S112_BOVIN	P79105 bos taurus
2	371	77.0	91	1 S112_PIG	P80310 sus scrofa
3	349	72.4	70	2 Q9TR16	Q9TR16 bos taurus
4	314	65.1	91	1 S112_HUMAN	P80511 homo sapien
5	274	56.8	81	1 S112_RABIT	O77791 oryctolagus
6	238.5	49.5	122	1 S109_BOVIN	P28783 bos taurus
7	211.5	43.9	114	1 S109_HUMAN	P06702 homo sapien
8	210.5	43.7	118	1 S109_RABIT	P50117 oryctolagus
9	210	43.6	119	2 Q6PRV2	Q6PRV2 cornutus co
10	202	41.9	119	1 M126_CHICK	Q72V44 gallus gall
11	195	40.5	100	2 Q72V44	Q72V44 brachydanio
12	190.5	39.5	111	2 Q761U7	Q761U7 rattus norv
13	190.5	39.5	112	1 S109_RAT	P50116 rattus norv
14	187	38.8	95	1 S10P_HUMAN	P25815 homo sapien
15	185	38.4	92	2 Q925T3	Q925T3 cricetus
16	184	38.2	101	2 Q93395	Q93395 salvelinus

17	182	37.8	99	2 Q8AYJ2	Q8AYJ2 squalus aca
18	180	37.3	92	2 Q6YNR6	Q6YNR6 oryctolagus
19	179	37.1	91	1 S10B_RAT	P04631 rattus norv
20	177	36.7	92	1 S10I_1CTPU	Q91061 ictalurus p
21	176	36.5	91	1 S10B_BOVIN	P02638 bos taurus
22	176	36.5	91	1 S10B_MOUSE	P50114 mus musculu
23	175	36.3	91	1 S10B_HUMAN	P04271 homo sapien
24	175	36.3	92	2 Q9PSF6	Q9PSF6 ictalurus p
25	174	36.1	88	1 S108_RAT	P50115 rattus norv
26	170	35.3	88	1 S108_MOUSE	P27005 mus musculu
27	170	35.3	95	2 Q6DGT8	Q6DGT8 brachydanio
28	169	35.1	95	1 S10A_MUSFO	Q71511 misgurnus f
29	168	34.9	2850	1 HORN_HUMAN	Q86Y23 homo sapien
30	167	34.6	93	1 S10A_RAT	P35467 rattus norv
31	164.5	34.1	112	1 S109_MOUSE	P31725 mus musculu
32	164	34.0	93	1 S10A_BOVIN	P26339 bos taurus
33	163	33.8	93	1 S10A_HUMAN	P23297 homo sapien
34	163	33.8	98	1 S10Z_HUMAN	Q8W98 homo sapien
35	162	33.6	79	2 Q9JL08	Q9J108 mus musculu
36	161	33.4	94	2 Q9D3M4	Q9D3M4 mus musculu
37	161	33.4	94	2 Q91V77	Q91V77 m mus muscu
38	161	33.4	148	2 Q8BLX1	Q8BLX1 mus musculu
39	161	33.4	2496	1 HORN_MOUSE	Q8VHD8 mus musculu
40	160	33.2	93	1 S108_HUMAN	P05109 h calgranul
41	160	33.2	93	1 S10A_MOUSE	P56565 mus musculu
42	160	33.2	95	2 Q6XG62	Q6XG62 brachydanio
43	160	33.2	101	1 S104_MOUSE	P07091 mus musculu
44	157	32.6	101	1 S104_RAT	P05942 rattus norv
45	155	32.2	100	1 S104_BOVIN	P33466 bos taurus

ALIGNMENTS

RESULT 1

S112_BOVIN	STANDARD;	PRT;	91 AA.
ID S112_BOVIN			
AC P79105;			
DT 01-NOV-1997 (Rel. 35, Created)			
DT 01-NOV-1997 (Rel. 35, Last sequence update)			
DT 05-JUL-2004 (Rel. 44, Last annotation update)			
DE Calgranulin C (CAGC) (Calcium-binding protein in amniotic fluid 1)			
DE (CAAF1) (RAGE binding protein).			
GN Name=S100A12; Synonyms=CAAF1;			
OS Bos taurus (Bovine).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
OC Bovinae; Bos.			
OX NCBI_TaxID=9913;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC TISSUE=Oesophagus;			
RX MEDLINE=96298783; PubMed=8718672;			
RA Hitomi J., Yamaguchi K., Kikuchi Y., Kimura T., Maruyama K.,			
RA Nagasaki K.;			
RT "A novel calcium-binding protein in amniotic fluid, CAAF1: its			
RT molecular cloning and tissue distribution.";			
RL J. Cell Sci. 109:805-815(1996).			
RN [2]			
RP SEQUENCE FROM N.A.			
RC TISSUE=Lung;			
RX MEDLINE=99325504; PubMed=10399917; DOI=10.1016/S0092-8674(00)80801-6;			
RA Hofmann M.A., Drury S., Fu C., Qu W., Taguchi A., Lu Y., Avila C.,			
RA Kambhampati N., Blierhaus A., Nawroth P., Neurath M.P., Slattery T.,			
RA Beach D., McClary J., Nagashima M., Worsner J., Stern D., Schmidt A.M.;			
RT "RAGE mediates a novel proinflammatory axis: a central cell surface			
RT receptor for S100/calgranulin polypeptides.";			
RL Cell 97:889-901(1999).			
CC -!- SIMILARITY: Belongs to the S-100 family.			
CC -!- SIMILARITY: Contains 2 EF-hand calcium-binding domains.			
CC This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -			
CC the European Bioinformatics Institute. There are no restrictions on its			

CC use by non-profit institutions as long as its content is in no way
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 CC or send an email to license@isb-sib.ch).

CC -----
 CC EMBL; D49548; BAA08496.1; -
 CC EMBL; AF011757; AAB65423.1; -
 CC HSP; P80511; IGOM.
 CC InterPro; IPR001751; CaBP_S100.
 CC InterPro; IPR002048; EF-hand.
 CC InterPro; IPR010983; EF_Hand_Like.
 CC Pfam; PF00036; ehand; 1.
 CC Pfam; PF01023; S_100; 1.
 CC ProDom; PD003407; CaBP_S100; 1.
 CC PROSITE; PS00018; EF_HAND; 1.
 CC PROSITE; PS00303; S100_CaBP; 1.
 CC Calcium-binding; Metal-binding; Zinc.
 CC INIT MET 0 By similarity.
 CC CA_BIND 18 31 EF-hand 1; low affinity (By similarity).
 CC CA_BIND 61 72 EF-hand 2; high affinity (By similarity).
 CC SEQUENCE 91 AA; 10554 MW; 66FBC3C1B0354482 CRC64;

Alignment Scores:
 Pred. No.: 1.76e-41 Length: 91
 Score: 465.00 Matches: 91
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 96.47% Indels: 0
 DB: 1 Gaps: 0

US-09-910-208B-1 (1-276) x S112_BOVIN (1-91)

Qy 4 ACTAGCTGGAAGATCACTGGAGGGAATCATCAATCTTCCACCACTACCGTTGGG 63
 Db 1 ThrLysLeuGluAspHisLeuGluGlyIleleAsnIlePheHisGlnTyrSerValArg 20
 Qy 64 GTGGGGCATTTCCACACCTCAACAGCGTGAGCTGAAGCAGCTGATCACAAGAACTT 123
 Db 21 ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40
 Qy 124 CCCAAACCTCCAGAACCAACCAAGATCAACTACCATTTGACAAATATTTCCAGACCTG 183
 Db 41 ProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAspLeu 60
 Qy 184 GATCGCGATAAGAGCGGCGCTGAGCTTTCAGGAATTCGTAGTCTCGTGTCCAGGGTG 243
 Db 61 AspAlaAspLysAspGlyAlaValSerPheGluGluPheValValSerArgVal 80
 Qy 244 CTGAAAACAGCCCATAGATATCCACAAAGAG 276
 Db 81 LeuLysThrAlaHisAspIleHisLysGlu 91

RESULT 2
 S112_PIG : STANDARD; PRT; 91 AA.
 ID Q9TR16 : PRELIMINARY; PRT; 70 AA.
 AC Q9TR16;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Calgranulin C (CAGC).
 GN Name=S100A12;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Granulocyte;
 RX MEDLINE=95050708; PubMed=7961855;
 RA Dell'Angelica E.C., Schleicher C.H., Santome J.A.;
 RT "Primary structure and binding properties of calgranulin C, a novel
 RL S100-like calcium-binding protein from pig granulocytes.";
 RL J. Biol. Chem. 269:28929-28936(1994).

CC -!- TISSUE SPECIFICITY: Found essentially in granulocytes with small
 CC amounts found in lymphocytes.
 CC -!- MISCELLANEOUS: In the absence of zinc binds one calcium ion per
 CC molecule, in the presence of zinc binds two calcium ions per
 CC molecule.
 CC -!- SIMILARITY: Belongs to the S-100 family.
 CC -!- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
 CC PIR; A55406; A55406.
 CC HSP; P80511; 1B8A.
 CC InterPro; IPR001751; CaBP_S100.
 CC InterPro; IPR002048; EF-hand.
 CC InterPro; IPR010983; EF_Hand_Like.
 CC Pfam; PF00036; ehand; 1.
 CC Pfam; PF01023; S_100; 1.
 CC ProDom; PD003407; CaBP_S100; 1.
 CC PROSITE; PS00018; EF_HAND; FALSE_NEG.
 CC PROSITE; PS00303; S100_CaBP; 1.
 CC Calcium-binding; Direct protein sequencing; Metal-binding; Zinc.
 CC KW CA_BIND 18 31 EF-hand 1; low affinity (By similarity).
 CC FT CA_BIND 61 72 EF-hand 2; high affinity (By similarity).
 CC SEQUENCE 91 AA; 10614 MW; B4204461432D7FCE CRC64;

Alignment Scores:
 Pred. No.: 2.78e-31 Length: 91
 Score: 371.00 Matches: 74
 Percent Similarity: 91.21% Conservative: 9
 Best Local Similarity: 81.32% Mismatches: 8
 Query Match: 76.97% Indels: 0
 DB: 1 Gaps: 0

US-09-910-208B-1 (1-276) x S112_PIG (1-91)

Qy 4 ACTAGCTGGAAGATCACTGGAGGGAATCATCAATCTTCCACCACTACCGTTGGG 63
 Db 1 ThrLysLeuGluAspHisLeuGluGlyIleleAsnIlePheHisGlnTyrSerValArg 20
 Qy 64 GTGGGGCATTTCCACACCTCAACAGCGTGAGCTGAAGCAGCTGATCACAAGAACTT 123
 Db 21 LeuGlyHisTyrAspThrLeuIleLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40
 Qy 124 CCCAAACCTCCAGAACCAACCAAGATCAACTACCATTTGACAAATATTTCCAGACCTG 183
 Db 41 ProAsnThrLeuLysAsnThrLysAspGlnGlyThrIleAspLysIlePheGlnAsnLeu 60
 Qy 184 GATCGCGATAAGAGCGGCGCTGAGCTTTCAGGAATTCGTAGTCTCGTGTCCAGGGTG 243
 Db 61 AspAlaAsnGlnAspGluGlnValSerPheLysGluPheValValLeuValThrAspVal 80
 Qy 244 CTGAAAACAGCCCATAGATATCCACAAAGAG 276
 Db 81 LeuIleThrAlaHisAspAsnIleHisLysGlu 91

RESULT 3
 Q9TR16 : PRELIMINARY; PRT; 70 AA.
 ID Q9TR16;
 AC Q9TR16;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE CORNEA-associated antigen, CO-AG-CALGRANULIN C homolog.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=96181454; PubMed=8603881;
 RT Liu S.H., Gottsch J.D.;
 RA "Amino acid sequence of an immunogenic corneal stromal protein.";
 RL Invest. Ophthalmol. Vis. Sci. 37:944-948(1996).
 CC -!- SIMILARITY: Belongs to the S-100 family.
 CC HSP; P80511; 1B8A.

DR GO: 0005509; F:calcium ion binding; IEA.
 DR InterPro; IPR001751; CaBP_S100.
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR010983; EF_Hand_like.
 DR Pfam; PF01033; S100; 1_Hand_like.
 DR ProDom; PD003407; CaBP_S100; 1.
 SQ SEQUENCE 70 AA; 8134 MW; 7D52BEA97A4D53A5 CRC64;

Alignment Scores:
 Pred. No.: 6,66e-29 Length: 70
 Score: 349.00 Matches: 68
 Percent Similarity: 97.14% Conservative: 0
 Best Local Similarity: 97.14% Mismatches: 2
 Query Match: 72.41% Indels: 0
 DB: 2 Gaps: 0

US-09-910-208B-1 (1-276) x Q9TR16 (1-70)

QY 4 ACTAGCTGAGAGATCACTCGAGGGAATCATCAACATTTCCACAGTACTCCGTCGG 63
 Db 1 ThrLysLeuGluAspHisLeuGluGlyIleAAsnIlePheHisGlnTyrSerValArg 20
 QY 64 GTGGGCAATTCGACACCTCAACAGCTGAGCTGAAGCACTGATCAAGAAGACTT 123
 Db 21 ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40
 QY 124 CCAGAAACCTCCAGAACACCAAGATCAACCTACCATTCAGAAATATTCACAGACCTG 183
 Db 41 ProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAspLeu 60
 QY 184 GATGCGGATAAAGACGAGCGCTCAGCTT 213
 Db 61 AspAlaAspLysLysGlyAlaValValPhe 70

RESULT 4

ID S112_HUMAN STANDARD; PRT; 91 AA.
 AC P08511; P83219;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Calgranulin C (CAGC) (CGRP) (Neutrophil S100 protein) (Calcium-binding
 DE protein in amniotic fluid 1) (CAAF1) (p6) [Contains: Calcitermin].
 GN Name=S100A12;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97138564; PubMed=8985590; DOI=10.1016/S0143-4160(96)90087-1;
 RA Wicki R., Marenholz I., Mischke D., Schaefer B.W., Heizmann C.W.;
 RT "Characterization of the human S100A12 (calgranulin C, p6, CAAF1,
 RT CGRP) gene, a new member of the S100 gene cluster on chromosome
 RT 1q21.";
 RL Cell Calcium 20:459-464 (1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96192053; PubMed=8619860; DOI=10.1006/bbrc.1996.0600;
 RA Yamamura T., Hitomi J., Nagasaki K., Suzuki M., Takahashi E.,
 RA Saito S., Tsukada T., Yamaguchi K.;
 RT "Human CAAF1 gene -- molecular cloning, gene structure, and chromosome
 RT mapping.";
 RL Biochem. Biophys. Res. Commun. 221:356-360 (1996).
 RN [3]
 RP SEQUENCE.
 RX MEDLINE=96192069; PubMed=8619876; DOI=10.1006/bbrc.1996.0616;
 RA Marti T., Ertmann K.D., Gallin M.Y.;
 RT "Host-parasite interaction in human onchocerciasis: identification and
 RT sequence analysis of a novel human calgranulin.";
 RL Biochem. Biophys. Res. Commun. 221:454-458 (1996).
 RN [4]
 RP SEQUENCE.

RC TISSUE=Neutrophils;
 RX MEDLINE=96332419; PubMed=8769108; DOI=10.1006/bbrc.1996.1144;
 RA Ilg E.C., Troxler H., Buerigesser D.M., Kuster T., Markert M.,
 RA Guignard F., Hunziker P., Birchler N., Heizmann C.W.;
 RT "Amino acid sequence determination of human S100A12 (p6, calgranulin
 RT C, CGRP, CAAF1) by tandem mass spectrometry.";
 RL Biochem. Biophys. Res. Commun. 225:146-150 (1996).
 RN [5]
 RP SEQUENCE OF 1-20.
 RX MEDLINE=95351965; PubMed=7626002;
 RA Guignard F., Mael J., Markert M.;
 RT "Identification and characterization of a novel human neutrophil
 RT protein related to the S100 family.";
 RL Biochem. J. 309:395-401 (1995).
 RN [6]
 RP SEQUENCE OF 77-91, ANTIMICROBIAL ACTIVITY, AND MASS SPECTROMETRY.
 RX MEDLINE=95351965; PubMed=7626002;
 RA Guignard F., Mael J., Markert M.;
 RT "Identification and characterization of a novel human neutrophil
 RT protein related to the S100 family.";
 RL Biochem. J. 309:395-401 (1995).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (1.95 ANGSTROMS).
 RX MEDLINE=21065388; PubMed=11134923; DOI=10.1107/S090744490001458X;
 RA Moroz O.V., Antson A.A., Murshudov G.N., Maitland N.J., Dodson G.G.,
 RA Wilson K.S., Skibshoj I., Lukanidin E.M., Bronstein I.B.;
 RT "The three-dimensional structure of human S100A12.";
 RL Acta Crystallogr. D 57:20-29 (2001).
 CC -!- FUNCTION: Calcitermin possesses antifungal activity against
 CC C. albicans and is also active against E.coli and P.aeruginosa but
 CC not L.monocytogenes and S.aureus.
 CC -!- SUBUNIT: Homodimer.
 CC -!- TISSUE SPECIFICITY: Monocytes and lymphocytes.
 CC -!- MASS SPECTROMETRY: MW=10444; METHOD=Electrospray; RANGE=1-91;
 CC NOTE=Ref.6.
 CC -!- MASS SPECTROMETRY: MW=1688.9; METHOD=MALDI; RANGE=77-91;
 CC NOTE=Ref.6.
 CC -!- SIMILARITY: Belongs to the S-100 family.
 CC -!- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
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 DR EMBL; X97859; CAA66453.1; -.
 DR EMBL; X98288; CAA66934.1; -.
 DR EMBL; X98289; CAA66934.1; JOINED.
 DR EMBL; X98290; CAA66934.1; JOINED.
 DR EMBL; X98289; CAB94792.1; -.
 DR EMBL; X98290; CAB94792.1; JOINED.
 DR EMBL; D49549; BAA08497.1; -.
 DR EMBL; D83654; BAA12036.1; -.
 DR EMBL; D83657; BAA12030.1; -.
 DR PIR; JC4712; JC4712.
 DR PDB; 1E8A; X-ray; A/B=1-91.
 DR PDB; 1GQM; X-ray; A/B/C/D/E/F/G/H/I/J/K/L=1-91.
 DR PDB; 1ODB; X-ray; A/B/C/D/E/F=1-91.
 DR Genew; HGNC:10489; S100A12.
 DR MIM; 603112; -.
 DR GO; GO:0005829; C:cytosol; TAS.
 DR GO; GO:0005626; C:insoluble fraction; TAS.
 DR GO; GO:0005509; F:calcium ion binding; TAS.
 DR GO; GO:0006954; P:inflammatory response; TAS.
 DR InterPro; IPR001751; CaBP_S100.
 DR InterPro; IPR002048; EF_Hand.
 DR InterPro; IPR010983; EF_Hand_like.
 DR Pfam; PF00036; ehand; 1.
 DR Pfam; PF01023; S_100; 1.

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DR PRODom; PD003407; CaBP_S100; 1.
DR PROSITE; PS00018; EF HAND; FALSE_NEG.
DR PROSITE; PS00303; S100_CABP; 1.
KW 3D-structure; Antibiotic; Calcium-binding; Direct protein sequencing;
KW Fungicide; Metal-binding; Zinc.
FT INIT MET 0
FT PEPTIDE 77 91 Calctermin.
FT CA_BIND 18 31 EF-hand 1; low affinity (By similarity).
FT CA_BIND 61 72 EF-hand 2; high affinity (By similarity).
FT HELIX 2 18
FT TURN 19 19
FT TURN 24 25
FT STRAND 26 27
FT HELIX 29 39
FT TURN 41 43
FT TURN 45 48
FT HELIX 50 60
FT TURN 62 63
FT STRAND 68 69
FT HELIX 70 85
SQ SEQUENCE 91 AA; 10444 MW; 325685EA8695F6B7 CRC64;

Alignment Scores:
Pred. No.: 4.26e-25 Length: 91
Score: 314.00 Matches: 60
Percent Similarity: 80.22% Conservative: 13
Best Local Similarity: 65.92% Mismatches: 18
Query Match: 65.15% Indels: 0
DB: 1 Gaps: 0

US-09-910-208B-1 (1-276) x S112_HUMAN (1-91)
QY 4 ACTAGCTGGAGATCAGCTGGAGGATCATCAATCTTCCACAGTACTCCGTTCCG 63
Db 1 ThrLysLeuGluGluHisLeuGluGluGluValAenIlePheHisGlnTy-SerValArg 20
QY 64 GTGGGGCATTTCCGACACCTCAACAGCGCTGAGCTGAAGCAGCTGATCACAAGAACTT 123
Db 21 LysGlyHisPheAspThrLysSerLysGlyGluLeuLysGlnLeuThrLysGluLeu 40
QY 124 CCCAAACCTCCAGAACACCAAGATCACTACCTATGCAAAATATTCAGACCTG 183
Db 41 AlaAenThrIleLysAenIleLysAspLysAlaValIleAspGluIlePheGlnGlyLeu 60
QY 184 GATCCGATGAAGACGGACCGCTGAGCTTGGAGGATTCGATGCTGCTCCAGGGTG 243
Db 61 AspAlaAenGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIleAla 80
QY 244 CTGAACACAGCCCATAGATATCCACAAAGAG 276
Db 81 LeuLysAlaAlaHisTyrHisThrHisLysGlu 91

RESULT 5
S112_RABIT
ID S112_RABIT | STANDARD; PRT; 81 AA.
AC O77791.
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Calgranulin C (CAGC) (Fragment).
GN Name=S100A12;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=New Zealand white; TISSUE=Neutrophils;
RX MEDLINE=96355278; PubMed=8702688; DOI=10.1074/jbc.271.33.19802;
RA Yang Z., Devere M.J., Gardiner E.E., Devenish R.J., Handley C.J.,
RA Underwood J.R., Robinson H.C.;
RT "Rabbit polymorphonuclear neutrophils form 35S-labeled S-sulfo-
calgranulin C when incubated with inorganic [35S]sulfate.";
J. Biol. Chem. 271:19802-19809(1996).
-!- SIMILARITY: Belongs to the S-100 family.
-!- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
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EMBL; AF091848; AAC61770.1; -.
HSSP; P80511; 1B8A.
InterPro; IPR001751; CaBP_S100.
InterPro; IPR002048; EF-hand.
InterPro; IPR010983; EF_Hand_like.
Pfam; PF00036; ehand; 1.
Pfam; PF01023; S100; 1.
ProDom; PD003407; CaBP_S100; 1.
PROSITE; PS00018; EF HAND; 1.
PROSITE; PS00303; S100_CABP; 1.
KW Calcium-binding; Direct protein sequencing.
FT NON TER 1
FT CA_BIND 8 21 EF-hand 1; low affinity (By similarity).
FT CA_BIND 51 62 EF-hand 2; high affinity (By similarity).
SQ SEQUENCE 81 AA; 9401 MW; 95E67A209180CB66 CRC64;

Alignment Scores:
Pred. No.: 9.26e-21 Length: 81
Score: 274.00 Matches: 53
Percent Similarity: 81.48% Conservative: 13
Best Local Similarity: 65.43% Mismatches: 15
Query Match: 56.85% Indels: 0
DB: 1 Gaps: 0

US-09-910-208B-1 (1-276) x S112_RABIT (1-81)
QY 34 ATCAACATCTTCCACAGTACTCCGTTCCGTTGGGGCATTTCCGACACCTCAACAGCGT 93
Db 1 IleAsnIlePheHisGlnTySerValArgThrGlyHisTyAspThrLysSerLysCys 20
QY 94 GAGCTGAAGCAGCTGATCACAAGAACTTCCCAAAACCTCCAGAACACCAAGATCAA 153
Db 21 GluLeuLysLysLeuIleThrThrGluLeuValAsnThrIleLysAsnThrLysAspGln 40
QY 154 CCTACCATTTGACAAAATATTCAGACCTGATCCGATTAAGACGGAGCGCTCAGCTTT 213
Db 41 AlaThrValAspArgIlePheArgAspLeuAspGluAspGlyAspHisGlnValAspPhe 60
QY 214 GAGGAATTCGTAGTCTCGGTGCTCCAGGTGCTGAAAACAGCCCATAGATATCCACAA 273
Db 61 LysGluPheLeuSerLeuLeuAlaSerValLeuValThrAlaHisGluAsnIleHisLys 80
QY 274 GAG 276
Db 81 Glu 81

RESULT 6
S109_BOVIN
ID S109_BOVIN | STANDARD; PRT; 122 AA.
AC P28783;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Calgranulin B (Neutrophil cytosolic 23 kDa protein) (P23) (BEE22)
DE (Fragment).
GN Name=S100A9;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
```



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RN  SEQUENCE.
RP  TISSUE=Oesophageal epithelium;
RX  MEDLINE=93280230; PubMed=8505358;
RA  Tang T.K., Hong T.-M., Lin C.-Y., Lai M.-L., Liu C.H.L., Lo H.-J.,
RA  Wang M.-E., Chen L.B., Chen W.-T., Ip W., Lin D.C., Lin J.J.-C.,
RA  Lin S., Sun T.-T., Wang E., Wang J.L., Wu R., Wu C.-W., Chien S.;
RA  "Nuclear proteins of the bovine esophageal epithelium. I. Monoclonal
RT  antibody W2 specifically reacts with condensed nuclei of
RT  differentiated superficial cells.";
RL  J. Cell Sci. 104:237-247(1993).
RN  [2]
RP  SEQUENCE OF 4-56.
RP  TISSUE=Neutrophils;
RX  MEDLINE=92304974; PubMed=1610833;
RA  Dianoux A.-C., Stasia M.-J., Garin J., Gagnon J., Vignais P.V.;
RA  "The 23-kilodalton protein, a substrate of protein kinase C, in bovine
RT  neutrophil cytosol is a member of the S100 family.";
RL  Biochemistry 31:5898-5905(1992).
CC  -! SUBUNIT: Disulfide linked heterodimer of a 7/11 kDa and a 22/23
CC  kDa subunits.
CC  -! SUBCELLULAR LOCATION: Cytoplasmic; loosely associated to the
CC  cytoskeleton
CC  -! TISSUE SPECIFICITY: Found essentially in phagocytic cells.
CC  -! PTM: Phosphorylated by protein kinase C.
CC  -! SIMILARITY: Belongs to the S-100 family.
CC  -! SIMILARITY: Contains 2 EF-hand calcium-binding domains.
DR  HSP; P06704; IIRJ.
DR  InterPro; IPR001751; CaBP_S100.
DR  InterPro; IPR002048; EF_Hand.
DR  InterPro; IPR010983; EF_Hand_Like.
DR  Pfam; PF00036; ehand; 1.
DR  Pfam; PF01023; S100; 1.
DR  ProDom; PD003407; CaBP_S100; 1.
DR  PROSITE; PS00018; EF_HAND; PARTIAL.
DR  PROSITE; PS00303; S100_CaBP; 1.
KW  Calcium-binding; Direct protein sequencing; Phosphorylation.
FT  NON_TER 1
FT  CA_BIND 19 32 EF-hand 1; low affinity (Potential).
FT  CA_BIND 63 74 EF-hand 2; high affinity (Potential).
SQ  SEQUENCE 122 AA; 13673 MW; F3C8C48806BECCD CRC64;

Alignment Scores:
Pred. No.:      6,79e-17      Length:      122
Score:          238.50        Matches:      45
Percent Similarity: 75.82%    Conservative: 24
Best Local Similarity: 49.45%  Mismatches:   21
Query Match:     49.48%      Indels:       1
DB:              1           Gaps:         1

US-09-910-208B-1 (1-276) x S109_BOVIN (1-122)
QY  1 ATGACTAGCTGAAGTCACTCTGGGGAATCATCAATCTTCACAGTACTCCGTT 60
Db  1 MetSerGlnMetGluSerSerileGluThrIleAsnIlePheHisGlnTyrSerVal 20
QY  61 CGGTTGGGGCATTTGACACCTCTCAACAGCGTGACTGAAGCGTGTATCAAAAGGAA 120
Db  21 ArgLeuGluGlyHisTyrAspThrLeulleGlnLysGluPheLysGlnLeuValGlnLysGlu 40
QY  121 CTTCCCAAAACCCCTC---CAGAACACCAAGATCACTACCATTTGACAAAATATTCCAA 177
Db  41 LeuProAsnPheLeuLysLysGlnLysLysAsnGluAlaAlaIleAsnGluIleMetGlu 60
QY  178 GACCTGGATGCCGATAAAGCGAGCGTCGACGTTTGAGGAATTCGTAGCTCTGGTGTCT 237
Db  61 AspLeuAspThrAsnValAspLysGlnLysGlnLeuSerPheGluGluPheIleMetLeuValAla 80
QY  238 AGGGTCTGAAACACGCCACATAGATATCCAC 270
Db  81 ArgLeuThrValAlaSerHisGluGluMetHis 91

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RESULT 7

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S109 HUMAN
ID  S109 HUMAN STANDARD; PRT; 114 AA.
AC  P06702; Q9NYMO; Q9UCJ1;
DT  01-JAN-1988 (Rel. 06, Created)
DT  01-JAN-1988 (Rel. 06, Last sequence update)
DT  25-OCT-2004 (Rel. 45, Last annotation update)
DE  Calgranulin B (Migration inhibitory factor-related protein 14) (MRP-
DE  14) (P14) (Leukocyte LI complex heavy chain) (S100 calcium-binding
DE  protein A9) (Calprotectin LIH subunit).
GN  Name=S100A9; Synonyms=CAGB, MRP14;
OS  Homo sapiens (Human)
OC  Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=89039099; PubMed=3313057; DOI=10.1038/330080a0;
RA  Odink K., Cerletti N., Bruggen J., Clerc R.G., Tarsay L., Zwaldo G.,
RA  Gerhards G., Schlegel R., Sorg C.;
RT  "Two calcium-binding proteins in infiltrate macrophages of rheumatoid
RT  arthritis.";
RL  Nature 330:80-82(1987).
RN  [2]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=88302148; PubMed=3405210;
RA  Lagasse E., Clerc R.G.;
RT  "Cloning and expression of two human genes encoding calcium-binding
RT  proteins that are regulated during myeloid differentiation.";
RL  Mol. Cell. Biol. 8:2402-2410(1988).
RN  [3]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=89255276; PubMed=2656677;
RA  Murao S., Collart F.R., Huberman E.;
RT  "A protein containing the cystic fibrosis antigen is an inhibitor of
RT  protein kinases.";
RL  J. Biol. Chem. 264:8356-8360(1989).
RN  [4]
RP  SEQUENCE FROM N.A., AND VARIANT ARG-20.
RA  Wang M., Xu X., Cai Y., Xu H., Han Y., Xu Z., Wu M.;
RT  "Human gene for migration inhibitory factor-related protein 14
RT  (MRP14), variant allele.";
RL  Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN  [5]
RP  SEQUENCE FROM N.A.
TX  TISSUE=Lung;
RX  MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA  Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA  Klausner R.D., Collins F.S., Wagner L., Shenmen C.W., Schuler G.D.,
RA  Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA  Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA  Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA  Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA  Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA  Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullan S.J.,
RA  Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA  Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA  Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA  Fahey J., Hellon E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
RA  Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA  Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA  Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA  Butterfield Y.S., Krzywinski M.I., Skalska U., Smalish D.E.,
RA  Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT  "Generation and initial analysis of more than 15,000 full-length human
RT  and mouse cDNA sequences.";
RL  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN  [6]
RP  SEQUENCE OF 84-114, AND PHOSPHORYLATION SITE THR-113.
RX  MEDLINE=90044075; PubMed=2478889; DOI=10.1038/342189a0;
RA  Edgeworth J., Freemont P., Hogg N.;
RT  "Ionomycin-regulated phosphorylation of the myeloid calcium-binding
RT  protein p14.";
RL  Nature 342:189-192(1989).

```

RN [7]
 RP SEQUENCE OF 11-19; 26-37 AND 94-107.
 RC TISSUE=Keratinocytes;
 RA MEDLINE=931162043; PubMed=1286667;
 RX Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E.,
 RA Vandekerckhove J.;
 RT "Microsequences of 145 proteins recorded in the two-dimensional gel
 RT protein database of normal human epidermal keratinocytes.";
 RL Electrophoresis 13:960-969(1992).
 RN [8]
 RP SEQUENCE OF 5-34.
 RX MEDLINE=93139333; PubMed=8423249;
 RA Miyasaki K.T., Bodeau A.L., Murthy A.R., Lehrer R.I.;
 RT "In vitro antimicrobial activity of the human neutrophil cytosolic S-
 RT 100 protein complex, calprotectin, against *Campytophaga sputigena*.";
 RL J. Dent. Res. 72:517-523(1993).
 CC -!- FUNCTION: Expressed by macrophages in acutely inflamed tissues
 CC and in chronic inflammations. Seem to be an inhibitor of protein
 CC kinases. Also expressed in epithelial cells constitutively or
 CC induced during dermatoses. May interact with components of the
 CC intermediate filaments in monocytes and epithelial cells.
 CC -!- MISCELLANEOUS: Has been shown to bind calcium.
 CC -!- SIMILARITY: Belongs to the S-100 family.
 CC -!- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
 CC
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 DR EMBL; X06233; CA229579.1; -;
 DR EMBL; M21064; AAA36326.1; -;
 DR EMBL; M26311; AAA68480.1; -;
 DR EMBL; AF237581; AAF62536.1; -;
 DR EMBL; AF237582; AAF62537.1; -;
 DR EMBL; A12029; CAA01002.1; -;
 DR EMBL; A12032; CAA01004.1; -;
 DR EMBL; BC047681; AAH47681.1; -;
 DR PIR; B31848; B31848.
 DR PDB; 1IRJ; X-ray; A/B/C/D/E/F/G/H-2-114.
 DR SWISS-2DPAGE; P06702; HUMAN.
 DR Aarhuus/Ghent-2DPAGE; 5007; IEF.
 DR Aarhuus/Ghent-2DPAGE; 6010; IEF.
 DR Aarhuus/Ghent-2DPAGE; 6017; IEF.
 DR Aarhuus/Ghent-2DPAGE; 7013; IEF.
 DR OGP; P06702; -;
 DR PMMA-2DPAGE; P06702; -;
 DR Genew; HGNC:10499; S100A9.
 DR MIM; 123886; -;
 DR GO; GO:0005509; F:calcium ion binding; TAS.
 DR GO; GO:0004871; F:signal transducer activity; TAS.
 DR GO; GO:0007267; P:cell-cell signaling; TAS.
 DR GO; GO:0006954; P:inflammatory response; TAS.
 DR InterPro; IPR001751; CAPP S100.
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR010983; EF_Hand_Like.
 DR Pfam; PF00036; ehand; 1.
 DR Pfam; PF01023; S100; 1.
 DR ProDom; PD003407; CAPP S100; 1.
 DR PROSITE; PS00018; EF HAND; 1.
 DR PROSITE; PS00303; S100 CAPP; 1.
 KW 3D-structure; Calcium-binding; Direct protein sequencing; Macrophage;
 KW Phosphorylation; Polymorphism.
 FT CA BIND 23 36 EF-hand 1; low affinity (Potential).
 FT EF BIND 67 78 EF-hand 2; high affinity (Potential).
 FT MOD_RES 113 113 Phosphothreonine.
 FT VARIANT 20 20 H -> R.
 FT /FTID=VAR_013008.
 FT S -> H (in Ref. 8).
 FT K -> F (in Ref. 8).
 FT CONFLICT 25 25
 FT

FT CONFLICT 28 28 H -> L (in Ref. 8).
 FT HELIX 7 23
 FT TURN 24 24
 FT TURN 29 30
 FT STRAND 32 32
 FT HELIX 34 44
 FT TURN 46 51
 FT HELIX 52 54
 FT TURN 56 66
 FT TURN 68 69
 FT STRAND 74 74
 FT HELIX 76 80
 FT HELIX 81 85
 SQ SEQUENCE 114 AA; 13242 MW; C3BE19729E14C078 CRC64;
 Alignment Scores:
 Pred. No.: 5.75e-14 Length: 114
 Score: 211.50 Matches: 41
 Percent Similarity: 71.74% Conservative: 25
 Best Local Similarity: 44.57% Mismatches: 25
 Query Match: 43.88% Indels: 1
 DB: 1 Gaps: 1
 US-09-910-208B-1 (1-276) x S109_HUMAN (1-114)
 QY 1 ATGACTAAGCTGGAAGATCACTGGAGGAATCATCAACATCTTCCACGACTCTCCGTT 60
 DB 5 MetSerGlnLeuGluArgAsnIleGluThrIleLeuAsnThrPheHisGlnTySerVal 24
 QY 61 CGGTGGGGCATTTTCAGACCCCTCAACAGCGTGAAGTGAAGAGCTGATCACAAGGAA 120
 DB 25 LysLeuGlyHisProAspThrLeuAsnGlnGlyGluPheLysGluLeuValArgLysAsp 44
 QY 121 CTTCCTCAAAACCTCTC---CAGAACACCAAGATCACTACCATTCACAAATATTCCAA 177
 DB 45 LeuGlnAsnPheLeuLysLysGluAsnLysAsnGluLysValIleGluHisIleMetGlu 64
 QY 178 GACCTGGATGCGGATTAAGACGGAGCGCTCAGCTTTGAGGAATTCGTAGTCTCTGTGTCC 237
 DB 65 AspleuAspThrAsnAlaAspLysGlnLeuSerPheGluGluPheIleMetLeuMetala 84
 QY 238 AGGTGTGTAACACAGCCCATAGATATCCACAA 273
 DB 85 ArgLeuThrTrpAlaSerHisGluLysMetHisGlu 96
 RESULT 8
 S109_RABIT
 ID S109_RABIT STANDARD; PRT; 118 AA.
 AC P50117;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Calgranulin B (Migration inhibitory factor-related protein 14) (MRP-
 DE 14) (Fragment).
 GN Name=S100A9; Synonyms=MRP-14;
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=New Zealand white; TISSUE=Neutrophils;
 RX MEDLINE=96355278; PubMed=8702688; DOI=10.1074/jbc.271.33.19802;
 RA Yang Z., de Veer M.J., Gardiner E.E., Devenish R.J., Handley C.J.,
 RA Underwood J.R., Robinson H.C.;
 RT "Rabbit polymorphonuclear neutrophils form 35S-labeled S-sulfo-
 RT calgranulin C when incubated with inorganic [35S] sulfate.";
 RL J. Biol. Chem. 271:19802-19809(1996).
 RN [2]
 RP SEQUENCE OF 45-82 FROM N.A.
 RC STRAIN=New Zealand white;
 RX MEDLINE=94198229; PubMed=8148323;
 RA Mori S., Goto K., Goto F., Mutakami K., Ohkawara S., Yoshinaga M.;

RT "Dynamic changes in mRNA expression of neutrophils during the course
 RL of acute inflammation in rabbits."
 RL Int. Immunol. 6:149-156(1994).
 CC -!- SIMILARITY: Belongs to the S-100 family.
 CC -!- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
 CC -----
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 CC -----

DR EMBL; AF091849; AAC61771.1; -.
 DR EMBL; D17404; BAA04227.1; -.
 DR PIR; I46861; I46861.
 DR HSP; P06702; IIR9.
 DR InterPro; IPR001751; CaBP_S100.
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR010983; EF_Hand_like.
 DR Pfam; PF00036; ehand; 1.
 DR Pfam; PF01023; S_100; 1.
 DR ProDom; PD003407; CaBP_S100; 1.
 DR PROSITE; PS00018; EF_HAND; 1.
 DR PROSITE; PS00303; S100_CaBP; 1.
 DR Calcium-binding; Repeat.
 KW NON_TER 1
 FT CA_BIND 9 22 EF-hand 1; low affinity (Potential).
 FT CA_BIND 53 64 EF-hand 2; high affinity (Potential).
 FT DOMAIN 103 118 2 X 8 AA tandem repeats of G-H-G-H-G-H-S-
 FT H.
 FT REPEAT 103 110 1.
 FT REPEAT 111 118 2.
 FT REPEAT 111 118 2.
 SQ SEQUENCE 118 AA; 13292 MW; 7496118E21AD5C41 CRC64;

Alignment Scores:
 Pred. No.: 7.4e-14 Length: 118
 Score: 210.50 Matches: 41
 Percent Similarity: 75.61% Conservative: 21
 Best Local Similarity: 50.08% Mismatches: 19
 Query Match: 43.67% Indels: 1
 DB: 1 Gaps: 1

US-09-910-208B-1 (1-276) x S109_RABIT (1-118)

QY 31 ATCACTCAACATCTTCACAGTACTCCGTTCCGGTGGGCGCATTCGACACCTCAACAG 90
 Db 1 IIEIEASNILEPHEHISGLNTRYSERVALRGVALGYPROARGASPSERLEUSERGLN 20
 QY 91 CQTGAGCTGAAGCAGCTGATCAACAGGAACCTCCCAACCCCTC---CAGAACACCAA 147
 Db 21 LysGluPheLeuValGlnLysGluLeuHisAsnPheLeuLysGluAlaArg 40
 QY 148 GATCAACCTACCATCAAAAATATTCAGAGCTGCGGATGCGGATAAGACGAGCGGTC 207
 Db 41 AspGluLysAlaIleAsnAspIleMetGluAspLeuAspThrAsnGlnAspLysGlnLeu 60
 QY 208 ACCTTTGAGGAATTCGTAGTCTCTGTTCCAGGGTCTGAAACAGCCACATAGATATC 267
 Db 61 SerPheGluGluPheValIleLeuMetAlaArgLeuValHisAlaSerHisGluGluMet 80
 QY 268 CACAAA 273
 Db 81 HisLys 82

RESULT 9

Q6PRV2 PRELIMINARY; PRT; 119 AA.

ID Q6PRV2

AC Q6PRV2; (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE MRP protein.
 GN Name=MRP;
 OS Coturnix coturnix japonica (Japanese quail).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauaria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Coturnix.
 NCBI_TaxID=93934;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hartl M., Bister K.;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: Belongs to the S-100 family.
 DR EMBL; AY583752; AAT01286.1; -.
 DR HSP; P04631; I84C.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR InterPro; IPR001751; CaBP_S100.
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR010983; EF_Hand_like.
 DR Pfam; PF00036; ehand; 1.
 DR Pfam; PF01023; S_100; 1.
 DR ProDom; PD003407; CaBP_S100; 1.
 DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
 DR PROSITE; PS00303; S100_CaBP; 1.
 SQ SEQUENCE 119 AA; 14012 MW; 00DFB09902DC5CFB CRC64;

Alignment Scores:
 Pred. No.: 8.39e-14 Length: 119
 Score: 210.00 Matches: 42
 Percent Similarity: 71.11% Conservative: 22
 Best Local Similarity: 46.67% Mismatches: 26
 Query Match: 43.57% Indels: 0
 DB: 2 Gaps: 0

US-09-910-208B-1 (1-276) x Q6PRV2 (1-119)

QY 1 ATGACTAAGCTGGAAGATCACCTGGAGGAATCATCAATCTTCACAGTACTCCGTT 60
 Db 11 LeuSerGluLeuGluLysAlaMetAspThrIleAspValPheHisGlnTrySerArg 30
 QY 61 CGGTGGGGCATTTTCGACACCTCAACAGCTGAGCTGAAGCAGCTGATCAACAGGAA 120
 Db 31 ArgGluGluAspAsnAspThrLeuThrLysLysGluLeuLysLeuLeuLeuLeuGln 50
 QY 121 CTTCCAAAACCTCCAGAACACCAAGATCAACCTACCATGACAAAATATTTCAAGAC 180
 Db 51 LeuAlaAsnTryLeuLysHisValLysAsnGlnValSerIleAspGlnIlePheLysAsp 70
 QY 181 CTGGATGCGGATAAAGACGAGCCCTCAGCTTTGAGGAATTCGTAGTCTCTGTGTCCAGG 240
 Db 71 LeuAspGlyAsnLysAspGlnGlnLeuSerPheGlyGluValMetLeuLeuIleLeuArg 90
 QY 241 GTGCTGAAAACAGCCACATAGATATCCAC 270
 Db 91 ValIleIleAlaThrHisGluHisLeuHis 100

RESULT 10

M126 CHICK

ID M126_CHICK STANDARD; PRT; 119 AA.

AC P28318;

DT 01-DEC-1992 (Rel. 24, Created)

DT 01-DEC-1992 (Rel. 24, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Protein MRP-126.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauaria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

NCBI_TaxID=9031;

RN [1]

RP SEQUENCE FROM N.A.

STRAIN=White leghorn; TISSUE=Bone marrow;

RX MEDLINE=92195690; PubMed=1549365;

RA Nakano T., Graf T.;


```

Q761U7
ID Q761U7 PRELIMINARY; PRT; 111 AA.
AC Q761U7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Myeloid-related protein-14 (Fragment).
GN Name=MRP14;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=Lewis/N; TISSUE=Peritoneal cavity;
RX MEDLINE=93343942; PubMed=8343166;
RA Imanishi T., Uchida I., Wahl S.M., McCartney-Francis N.;
RT "Expression and cloning of migration inhibitory factor-related protein
(RMP)8 and MRP14 in arthritis-susceptible rats";
RL Biochem. Biophys. Res. Commun. 194:819-825(1993).
RN [2]
SEQUENCE OF 1-56; 61-64 AND 71-112, MASS SPECTROMETRY, ACETYLATION,
AND METHYLATION.
RP TISSUE=Spleen;
RX MEDLINE=98249881; PubMed=9570842; DOI=10.1006/abio.1997.2601;
RA Raftery M.J., Geazy C.L.;
RT "Identification of posttranslational modifications and cDNA sequencing
errors in the rat S100 proteins MRP8 and 14 using electrospray
ionization mass spectrometry.";
RL Anal. Biochem. 258:285-292(1998).
CC -!- MASS SPECTROMETRY: MW=13069; MW_ERR=2; METHOD=Electrospray;
CC RANGE=1-112; NOTE=Ref.2.
CC -!- SIMILARITY: Belongs to the S-100 family.
CC -!- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
CC
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CC
DR EMBL; L18948; AAA18214.1; -.
DR PIR; JN0686; JN0686.
DR HSSP; P06702; 1IR7.
DR RGD; 620267; S100a9.
DR InterPro; IPR001751; CapP_S100.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR010983; EF_Hand_like.
DR Pfam; PF00036; ehand; 1.
DR ProDom; PD003407; CapP_S100; 1.
DR PROSITE; PS00018; EF_HAND; FALSE_NEG.
DR PROSITE; PS00303; S100_CBP; 1.
DR PROSITE; PS00303; S100_CBP; 1.
DR ACetylation; Calcium-binding; Direct protein sequencing; Methylation.
FT INIT MET 0
FT MOD_RES 1 1 N-acetylalanine.
FT CA_BIND 106 106 Pros-methylhistidine.
FT CA_BIND 23 36 EF-hand 1; low affinity (Potential).
FT CA_BIND 67 78 EF-hand 2; high affinity (Potential).
FT CONFLICT 105 105 S -> R (in Ref. 1).
SQ SEQUENCE 112 AA; 13014 MW; 381EEB291175D068 CRC64;

Alignment Scores:
Pred. No.: 1,098-11 Length: 111
Score: 190.50 Matches: 36
Percent Similarity: 67.03% Conservative: 25
Best Local Similarity: 39.56% Mismatches: 29
Query Match: 39.52% Indels: 1
DB: 2 Gaps: 1

US-09-910-208B-1 (1-276) x Q761U7 (1-111)
QY 4 ACTAAGCTGGAAGATCACCTGGAGGGAATCATCAATCTCCACGACTCTCCGTCGG 63
Db 5 SerGlnLeuGluArgSerIleSerThrIleLeuAsnValPheHisGlnTyrSerArgLys 24
QY 64 GTGGGGCATTTGCGACCCCTCAACAGCGTGAAGCTGAGCTGATCACAAGGAATT 123
Db 25 TyrGlyHisProAspThrLeuAsnLysAlaGluPheLysGluMetValAsnLysAspLeu 44
QY 124 CCAAAACCTCCAGACACCAAA---GATCAACCTACCATTCACAAATATTCACAGAC 180
Db 45 ProAsnPheLeuArgGlnLysArgAsnGluLeuLeuArgAspIleMetGluAsp 64
QY 181 CTGGATCGCGATAAAGACGAGCCCTGAGCTTTGAGGAATCTAGTCTGCTGTCAGG 240
Db 65 LeuAspThrAsnGlnAspAsnGlnLeuSerPheGluGluCysMetMetLeuMetGlyLys 84
QY 241 GTGTGAACACGCCCATAGATATCCAAA 273
Db 85 LeuIlePheAlaCysHisGluLysLeuHisGlu 95

RESULT 13
S109_RAT
ID S109_RAT STANDARD; PRT; 112 AA.
AC P50116;
DT 01-OCT-1996 (Rel. 34, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Calgranulin B (Migration inhibitory factor-related protein 14) (MRP-
14) (p14).
GN Name=S100a9; Synonyms=Mrp14;

```

```

OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=Lewis/N; TISSUE=Peritoneal cavity;
RX MEDLINE=93343942; PubMed=8343166;
RA Imanishi T., Uchida I., Wahl S.M., McCartney-Francis N.;
RT "Expression and cloning of migration inhibitory factor-related protein
(RMP)8 and MRP14 in arthritis-susceptible rats";
RL Biochem. Biophys. Res. Commun. 194:819-825(1993).
RN [2]
SEQUENCE OF 1-56; 61-64 AND 71-112, MASS SPECTROMETRY, ACETYLATION,
AND METHYLATION.
RP TISSUE=Spleen;
RX MEDLINE=98249881; PubMed=9570842; DOI=10.1006/abio.1997.2601;
RA Raftery M.J., Geazy C.L.;
RT "Identification of posttranslational modifications and cDNA sequencing
errors in the rat S100 proteins MRP8 and 14 using electrospray
ionization mass spectrometry.";
RL Anal. Biochem. 258:285-292(1998).
CC -!- MASS SPECTROMETRY: MW=13069; MW_ERR=2; METHOD=Electrospray;
CC RANGE=1-112; NOTE=Ref.2.
CC -!- SIMILARITY: Belongs to the S-100 family.
CC -!- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
CC
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or send an email to license@sib-sib.ch).
CC
DR EMBL; L18948; AAA18214.1; -.
DR PIR; JN0686; JN0686.
DR HSSP; P06702; 1IR7.
DR RGD; 620267; S100a9.
DR InterPro; IPR001751; CapP_S100.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR010983; EF_Hand_like.
DR Pfam; PF00036; ehand; 1.
DR ProDom; PD003407; CapP_S100; 1.
DR PROSITE; PS00018; EF_HAND; FALSE_NEG.
DR PROSITE; PS00303; S100_CBP; 1.
DR ACetylation; Calcium-binding; Direct protein sequencing; Methylation.
FT INIT MET 0
FT MOD_RES 1 1 N-acetylalanine.
FT CA_BIND 106 106 Pros-methylhistidine.
FT CA_BIND 23 36 EF-hand 1; low affinity (Potential).
FT CA_BIND 67 78 EF-hand 2; high affinity (Potential).
FT CONFLICT 105 105 S -> R (in Ref. 1).
SQ SEQUENCE 112 AA; 13014 MW; 381EEB291175D068 CRC64;

Alignment Scores:
Pred. No.: 1,098-11 Length: 112
Score: 190.50 Matches: 36
Percent Similarity: 67.03% Conservative: 25
Best Local Similarity: 39.56% Mismatches: 29
Query Match: 39.52% Indels: 1
DB: 1 Gaps: 1

US-09-910-208B-1 (1-276) x S109_RAT (1-112)
QY 4 ACTAAGCTGGAAGATCACCTGGAGGGAATCATCAATCTCCACGACTCTCCGTCGG 63
Db 6 SerGlnLeuGluArgSerIleSerThrIleLeuAsnValPheHisGlnTyrSerArgLys 25
QY 64 GTGGGGCATTTGCGACCCCTCAACAGCGTGAAGCTGAGCTGATCACAAGGAATT 123
Db 26 TyrGlyHisProAspThrLeuAsnLysAlaGluPheLysGluMetValAsnLysAspLeu 45

```

QY 124 CCAAAACCCCTCCAGAACACCAAA--GATCAACCTACCATTCGACAAATATTCACAGAC 180
 Db 46 ProhenPheLeuLysArgGluLysArgGlnGluLeuLeuArgAspLeuMetGluLys 65
 QY 181 CTGGATCGCGATAAAGACGCGCTCAGCTTTGAGGAATTCGTAGTCTCTGTCGTCAGG 240
 Db 66 LeuAspThrAenGlnAspAenGlnLeuSerPheGluGluCysMetMetLeuMetGlyLys 85
 QY 241 GTGCTGAAACAGCCCATAGATATCCAAAA 273
 Db 86 LeuilePheAlaCysHisGluLysLeuHisGlu 96

RESULT 14
 ID_HUMAN STANDARD; PRT; 95 AA.
 AC P25815;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE S-100P protein.
 GN Name=S100P; Synonyms=S100E;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=92339442; PubMed=1633809;
 RA Becker T., Gerke V., Kube E., Weber K.;
 RT "S100P, a novel Ca(2+)-binding protein from human placenta. cDNA
 RT cloning, recombinant protein expression and Ca2+ binding properties.";
 RL Eur. J. Biochem. 207:541-547(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Jin G., Wang S., Chen J.;
 RT "Cloning, expression and characterization of a novel human calcium-
 RT binding S100 gene";
 RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Tohiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullihy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [4]
 RP SEQUENCE OF 1-91.
 RC TISSUE=Placenta;
 RX MEDLINE=92171935; PubMed=1540168;
 RA Emoto Y., Kobayashi R., Akatsuka H., Hidaka H.;
 RT "Purification and characterization of a new member of the S-100
 RT protein family from human placenta";
 RL Biochem. Biophys. Res. Commun. 182:1246-1253(1992).
 RN [5]

RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 RX PubMed=12507480; DOI=10.1016/S0022-2836(02)01278-0;
 RA Zhang H., Wang G., Ding Y., Wang Z., Barraclough R., Rudland P.S.,
 RA Fernig D.G., Rao Z.;
 RT "The crystal structure at 2A resolution of the Ca2+ -binding protein
 RT S100P";
 RL J. Mol. Biol. 325:785-794(2003).
 CC -!- SUBUNIT: Homodimer. Interacts with S100Z.
 CC -!- MISCELLANEOUS: This protein binds two calcium ions.
 CC -!- SIMILARITY: Belongs to the S-100 family.
 CC -!- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
 CC -----
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 CC -----
 DR EMBL; X65614; CAA46566.1; --
 DR EMBL; AF539739; AA041114.1; --
 DR EMBL; BC006819; AA06819.1; --
 DR PIR; S24146; S24146.
 DR PDB; 1J55; X-ray; A=1-95.
 DR Genew; HGNC:10504; S100P.
 DR H-InvDB; HIX0004067; --
 DR MIM; 600614; --
 DR GO; GO:0005509; F:calcium ion binding; TAS.
 DR GO; GO:0005515; F:protein binding; TAS.
 DR InterPro; IPR001751; CaBP_S100.
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR010983; EF_Hand_like.
 DR Pfam; PF00036; ehand; I.
 DR Pfam; PF01023; S_100; I.
 DR PRODOM; PD003407; CaBP_S100; I.
 DR PROSITE; PS00018; EF_HAND; FALSE_NEG.
 DR PROSITE; PS00303; S100_CaBP; 1.
 KW 3D-structure; Calcium-binding; Direct protein sequencing; Placenta.
 FT CA_BIND 19 32 EF-hand 1; low affinity.
 FT CA_BIND 62 73 EF-hand 2; high affinity.
 FT CA_BIND 32 32 E -> T (in Ref. 4).
 FT CONFLICT 44 44 F -> E (in Ref. 4).
 FT HELIX 3 18
 FT TURN 19 20
 FT TURN 25 26
 FT STRAND 27 28
 FT HELIX 30 40
 FT TURN 42 43
 FT HELIX 53 61
 FT STRAND 69 70
 FT TURN 71 92
 FT HELIX 93 93
 SQ SEQUENCE 95 AA; 10400 MW; 786E6E3F3EACC6C1 CRC64;

Alignment Scores:

Pred. No.: 2,58e-11 Length: 95
 Score: 187.00 Matches: 39
 Percent Similarity: 62.79% Conservative: 15
 Best Local Similarity: 45.35% Mismatches: 32
 Query Match: 38.80% Indels: 0
 DB: 1 Gaps: 0

US-09-910-208B-1 (1-276) x S100P_HUMAN (1-95)

QY 1 ATGACTAGCTGGAAGATCACCTGGAGGGAATCATCAATCTTCCACGACTCCGTT 60
 Db 1 MetThrGluLeuGluThrAlaMetGlyMetIleAspAlaPheSerArgTyrSerGly 20
 QY 61 CGGGTGGGGCATTTCCGACACCCCTCAACAAAGCGGTGAGCTGAAGCAGCTGATCACAAGGAA 120
 Db 21 SerGluGlySerThrThrGlnThrThrLysGlyGluLeuLysValLeuMetGluLysGlu 40

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OM nucleic - protein search, using frame_plus_n2p model

Run on: February 23, 2005, 11:08:19 ; Search time 113.5 Seconds
(without alignments)
1880.984 Million cell updates/sec

Title: US-09-910-208B-1
Perfect score: 482
Sequence: 1 atgactaagctggaagatca.....acatagatatccacaagaag 276

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 4211384

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ n2p.model -DEV=xlp
-O=/cgn2_1/USPTO.spool_p/HADAD-09-910208/runat_23022005_101805_14715/app_query.fasta_1.
-DB=A_Geneseq_16Dec04 -QFMT=fastan -SUFFIX=rag -MINWATCH=0.1 -DOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=Blosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=HADAD-09-910208 @cgn 1.1 224 @runat_23022005_101805_14715 -NCPU=6
-ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THRAIDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A_Geneseq_16Dec04:.*
1: Geneseq1980s:.*
2: Geneseq1990s:.*
3: Geneseq2000s:.*
4: Geneseq2001s:.*
5: Geneseq2002s:.*
6: Geneseq2003as:.*
7: Geneseq2003bs:.*
8: Geneseq2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	470	97.5	92	AAW03563	Calcium b
2	460	95.4	90	AAy90765	AAy90765 Bovine CA
3	460	95.4	90	AAy90764	AAy90764 Bovine co
4	371	77.0	91	AAW01826	AAW01826 Component
5	371	77.0	91	AAW93819	AAW93819 Angiotrop
6	319	66.2	92	AAW03564	AAW03564 Calcium b
7	319	66.2	92	AAW24137	AAW24137 Human che
8	319	66.2	92	AAW45542	AAW45542 Human S10
9	319	66.2	92	AAW31911	AAW31911 Amino aci
10	319	66.2	92	AAW31907	AAW31907 Amino aci

11	319	66.2	92	4	AAW31908	Aab31908 Amino aci
12	319	66.2	92	7	ADA93649	Ada93649 Human cal
13	319	66.2	92	8	ADN04192	ADN04192 Antipsori
14	319	66.2	92	8	ADO19540	ADO19540 Human PRO
15	319	66.2	92	8	ADR14333	ADR14333 Human NF-
16	319	66.2	92	8	ADP23921	ADP23921 PRO polyP
17	319	66.2	92	8	ADP23921	ADP23921 PRO polyP
18	319	66.2	92	8	ADP23921	ADP23921 PRO polyP
19	293	60.8	95	4	ABG27582	ABG27582 Novel hum
20	293	47.7	50	3	AAy90763	AAy90763 Human EN-
21	211.5	43.9	114	2	AAW17062	AAW17062 Human mul
22	211.5	43.9	114	2	AAW60178	AAW60178 Human cal
23	211.5	43.9	114	2	AAy48615	AAy48615 Human bre
24	211.5	43.9	114	3	AAy87637	AAy87637 Human cal
25	211.5	43.9	114	3	AAW45539	AAW45539 Human S10
26	211.5	43.9	114	4	ABB44613	ABB44613 Human wou
27	211.5	43.9	114	4	AAW31905	AAW31905 Amino aci
28	211.5	43.9	114	6	ABB82712	ABB82712 Human MRP
29	211.5	43.9	114	7	ADB17567	ADB17567 Human mye
30	211.5	43.9	114	7	ADE57110	ADE57110 Human Pro
31	211.5	43.9	114	7	ADE34548	ADE34548 Human mig
32	211.5	43.9	114	7	ADF09358	ADF09358 Human cal
33	211.5	43.9	114	8	ADL83164	ADL83164 Human PRO
34	211.5	43.9	114	8	ADN03968	ADN03968 Antipsori
35	211.5	43.9	114	8	ADQ30562	ADQ30562 Pancreas
36	211.5	43.9	114	8	ADR14329	ADR14329 Human NF-
37	211.5	43.9	114	8	ABM80144	ABM80144 Tumour-as
38	211.5	43.9	114	8	ADP23562	ADP23562 PRO polyP
39	211.5	43.9	114	8	ADS74315	ADS74315 PRO polyP
40	211.5	43.9	152	4	AAW39994	AAW39994 Human pol
41	201	41.7	115	4	AAW31930	AAW31930 Amino aci
42	193	40.0	46	4	ABB43183	ABB43183 Peptide #
43	193	40.0	46	4	AAW37021	AAW37021 Peptide #
44	193	40.0	46	4	ABB26281	ABB26281 Protein #
45	193	40.0	46	4	AAW76914	AAW76914 Human bon

ALIGNMENTS

RESULT 1
AAW03563
ID AAW03563 standard; protein; 92 AA.
XX

AC AAW03563;
XX
DT 01-MAY-1997 (first entry)
XX
DE Calcium binding protein CAAFI.
XX
KW Calcium binding protein; bovine; amniotic fluid; S100 protein family;
KW intracellular signal transduction; squamous epithelial cell; neutrophil;
KW macrophage; cancer; cancerous lesion; inflammation; neoplasia; cervix;
KW squamous cell carcinoma; skin; oesophagus; CAAFI; lung; blood disease.
XX
OS Bos taurus.
XX
PN EP731166-A2.
XX
PD 11-SEP-1996.
XX
PF 04-DEC-1995; 95EP-00119045.
XX
PR 06-MAR-1995; 95JP-00045564.
XX
PR 06-MAR-1995; 95JP-00070468.
XX
(TOFU) TONEN CORP.
(HITO/) HITOMI J.
XX
PI Hitomi J, Yamaguchi K, Yamamura T, Kimura T;
XX
DR WPI; 1996-403989/41.
XX
DR N-PSDB; AAT39345.

PT New human or bovine calcium binding protein and related nucleic acid - is
 XX a marker for inflammation, neoplasia, skin and blood diseases.
 PS Claim 1; Page 21; 36pp; English.

XX This sequence represents the CAAF1 calcium-binding protein isolated from
 CC bovine amniotic fluid. CAAF1 belongs to the S100 protein family, which
 CC includes calyculin, MRP8, and MRP14. Intracellular calcium ion
 CC concentration is one of the key factors for intracellular signal
 CC transduction. The calcium signals are transduced by various calcium-
 CC binding proteins, such as the protein encoded by this sequence. CAAF1 is
 CC normally expressed in squamous epithelial cells, neutrophils and
 CC macrophages, but atypical epithelial cells are negative for CAAF1 and
 CC overexpression is observed in several types of cancer cells and
 CC neutrophils/macrophages infiltrating cancerous lesions. Detection of
 CC CAAF1 (using antibodies in usual immunoassays) can be used to diagnose
 CC (or monitor) inflammation, neoplasia (particularly squamous cell
 CC carcinoma of the skin, oesophagus, lung and cervix), and skin and blood
 CC diseases

XX Sequence 92 AA;

Alignment Scores:

Pred. No.: 2,99e-49 Length: 92
 Score: 470.00 Matches: 92
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 97.51% Indels: 0
 DB: 2 Gaps: 0

US-09-910-208B-1 (1-276) x AAW03563 (1-92)

QY 1 ATGACTAAGCTGGAGATCACCTGGAGGGAATCATCAACATCTTCCACGACTCCGTT 60
 Db |||||||
 QY 61 CGGGTGGGGCATTTTCACACACCTTCAACAGCGTGAAGCGTCAAGCGCTGATCACAAGGAA 120
 Db |||||||
 QY 21 ArgValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuLeuThrLysGlu 40
 Db |||||||
 QY 121 CTTCCAAACCTCCAGACACCAAGATCACTACCATTTGACAAATATTTCCAGAC 180
 Db |||||||
 QY 41 LeuProLysThrLeuGlnAsnThrLysAspGlnProThrLysAspLysLeuPheGlnAsp 60
 Db |||||||
 QY 181 CTGGATGCGGATAAAGACGGAGCGCTGAGCTTTGAGGAATTCGTAGTCTCTGTGTCAGG 240
 Db |||||||
 QY 61 LeuAspAlaAspLysAspGlyAlaValSerPheGluGluPheValValLeuValSerArg 80
 Db |||||||
 QY 241 GTGCTGAAACAGCCCATAGATATCCACAAAGAG 276
 Db |||||||
 QY 81 ValLeuLysThrAlaHisIleAspIleHisLysGlu 92
 Db |||||||

RESULT 2

AAAY90765
 ID AAAY90765 standard; protein; 90 AA.

XX AC AAAY90765;

XX DT 18-AUG-2000 (first entry)

XX DE Bovine CAAF1 acid sequence SEQ ID NO:4.

XX KW Bovine: EN-RAGE; extracellular novel RAGE binding protein;
 KW receptor for advanced glycation endproduct; inflammation; inhibition;
 KW antiinflammatory; immunoglobulin; cell surface molecule; septic shock;
 KW systemic lupus erythematosus; inflammatory lupus nephritis; endotoxaemia;
 KW autoimmune disorder; inflammatory disorder.

OS Bos taurus.

XX PN WO200020621-A1.

XX PD 13-APR-2000.

XX 06-OCT-1999; 99WO-US023303.
 XX 06-OCT-1998; 98US-00167705.
 PR 05-MAR-1999; 99US-00263312.
 XX PA (UYCO) UNIV COLUMBIA NEW YORK.
 XX PI Schmidt AM, Stern D;
 XX DR WPI; 2000-303794/26.

XX New human EN-RAGE (extracellular novel receptor for advanced glycation
 XX end products) peptide, useful for identifying anti-inflammatory compounds
 XX that inhibit its interaction with RAGE.

XX Claim 2; Page 41; 132pp; English.

XX The present invention describes an isolated human EN-RAGE (extracellular
 CC novel receptor for advanced glycation end products) peptide (P1). The EN-
 CC RAGE peptide binds to RAGE which is a member of the immunoglobulin
 CC superfamily of cell-surface molecules. A compound capable of inhibiting
 CC the interaction of EN-RAGE with RAGE is useful for the suppression of
 CC inflammation resulting from systemic lupus erythematosus, inflammatory
 CC lupus nephritis, septic shock, endotoxaemia, or an autoimmune or
 CC inflammatory disorder in which the recruitment of EN-RAGE containing
 CC inflammatory cells occurs. The compound is also useful for the treatment
 CC of systemic lupus erythematosus, inflammatory lupus nephritis in a
 CC subject. The human EN-RAGE peptide is useful for identifying compounds
 CC that inhibit its interaction with RAGE. The present sequence represents
 CC the bovine CAAF1 which shows homology to the human EN-RAGE N-terminal
 CC amino acid sequence

XX Sequence 90 AA;

Alignment Scores:

Pred. No.: 5.2e-48 Length: 90
 Score: 460.00 Matches: 90
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 95.44% Indels: 0
 DB: 3 Gaps: 0

US-09-910-208B-1 (1-276) x AAAY90765 (1-90)

QY 4 ACTAAGCTGAAGATCACCTGGAGGGAATCATCAACATCTTCCACGACTCCGTTCCG 63
 Db |||||||
 QY 1 ThrLysLeuGluAspHisLeuGluGlyIleIleAsnIlePheHisGlnTySerValArg 20
 Db |||||||
 QY 64 GTGGGGCATTTTCGACACCTTCAACAGCGTGAAGCGTGAAGCGATGATCACAAGGAACTT 123
 Db |||||||
 QY 21 ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuLeuThrLysGluLeu 40
 Db |||||||
 QY 124 CCCAAACCTTCCAGAACACCAAGATCACTACCATTTGACAAATATTTCCAGACCTG 183
 Db |||||||
 QY 41 ProLysThrLeuGlnAsnThrLysAspGlnProThrLysAspLysIlePheGlnAspLeu 60
 Db |||||||
 QY 184 GATCCGATAAAGACGGAGCGCTGAGTTCGAGGAATTCGTAGTCTCTGTGTCAGGGTG 243
 Db |||||||
 QY 61 AspAlaAspLysAspGlyAlaValSerPheGluGluPheValValLeuValSerArgVal 80
 Db |||||||
 QY 244 CTGAAACAGCCCATAGATATCCACAA 273
 Db |||||||
 QY 81 LeuLysThrAlaHisIleAspIleHisLys 90
 Db |||||||

RESULT 3

AAAY90764
 ID AAAY90764 standard; protein; 90 AA.

XX AC AAAY90764;

XX DT 18-AUG-2000 (first entry)

XX PD

DE Bovine corneal antigen (B-COAG) acid sequence SEQ ID NO:3.
 XX
 KW Bovine; EN-RAGE; extracellular novel RAGE binding protein;
 KW receptor for advanced glycation endproduct; inflammation; inhibition;
 KW antiinflammatory; immunoglobulin; cell surface molecule; septic shock;
 KW systemic lupus erythematosus; inflammatory lupus nephritis; endotoxaemia;
 KW autoimmune disorder; inflammatory disorder.
 XX
 OS Bos taurus.
 XX
 XX WO200020621-A1.
 XX
 XX 13-APR-2000.
 XX
 XX 06-OCT-1999; 99WO-US023303.
 XX
 XX 06-OCT-1998; 98US-00167705.
 PR
 PR 05-MAR-1999; 99US-00263312.
 XX
 XX (UYCO) UNIV COLUMBIA NEW YORK.
 PA
 XX Schmidt AM, Stern D;
 XX
 XX WPI; 2000-303794/26.
 XX
 XX
 XX New human EN-RAGE (extracellular novel receptor for advanced glycation
 PT end products) peptide, useful for identifying anti-inflammatory compounds
 PT that inhibit its interaction with RAGE.
 XX
 XX PS Claim 2; Page 41; 132pp; English.
 XX
 XX The present invention describes an isolated human EN-RAGE (extracellular
 CC novel receptor for advanced glycation end products) peptide (p1). The EN-
 CC RAGE peptide binds to RAGE which is a member of the immunoglobulin
 CC superfamily of cell-surface molecules. A compound capable of inhibiting
 CC the interaction of EN-RAGE with RAGE is useful for the suppression of
 CC inflammation resulting from systemic lupus erythematosus, inflammatory
 CC lupus nephritis, septic shock, endotoxaemia, or an autoimmune or
 CC inflammatory disorder in which the recruitment of EN-RAGE containing
 CC inflammatory cells occurs. The compound is also useful for the treatment
 CC of systemic lupus erythematosus, inflammatory lupus nephritis in a
 CC subject. The human EN-RAGE peptide is useful for identifying compounds
 CC that inhibit its interaction with RAGE. The present sequence represents
 CC the bovine corneal antigen which shows homology to the human EN-RAGE N-
 CC terminal amino acid sequence
 XX
 XX SQ Sequence 90 AA;
 SQ
 Alignment Scores:
 Pred. No.: 5,2e-48 Length: 90
 Score: 460.00 Matches: 90
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 95.44% Indels: 0
 DB: 3 Gaps: 0
 US-09-910-208B-1 (1-276) x AAY90764 (1-90)
 QY 4 ACTAGCTGGAGATCACCCTGAGGGGAAATCATCAATCTTCCACAGTACTCCGTTGG 63
 Db 1 ThrLysLeuGluAspHisLeuGluGlyIleleAsnIlePheHisGlnTyrSerValArg 20
 QY 64 GTGGGGCATTTCGACACCCCTCAACAGCTGAGCTGAGCTGAAGCAGCTGATCAACAAGAACTT 123
 Db 21 ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40
 QY 124 CCAAAACCTCCAGAACCAACCAACCACTTACCATTCACAAATATTTCCAAGACCTG 183
 Db 41 ProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAspLeu 60
 QY 184 GATGCCGATAAAGACGGACCGCTGAGCTTTGAGGAATTCGTAGTCTGCTGTCAGGGTG 243
 Db 61 AspAlaAspLysAspGlyAlaValSerPheGluGluPheValValLeuValSerArgVal 80

QY 244 CTGAAACAGCCCATAGATATCCACAA 273
 Db 81 LeuLysThrAlaHisIleAspIleHisLys 90
 RESULT 4
 AAW01826
 ID AAW01826 standard; protein; 91 AA.
 XX
 XX AAW01826;
 XX
 XX 16-OCT-1997 (first entry)
 XX
 XX Component of bioactive metal RNA polypeptide.
 DE
 XX Bioactive; metal; RNA polypeptide; RNP; modulation; analysis;
 KW angiogenesis; vascular state; mammalian tissue; transfer; cell;
 KW genetic information; selective; alteration; nucleic acid content;
 KW leukocyte; pig; monocyto-CuRNP.
 XX
 XX Sus scrofa.
 XX
 XX DE19628895-A1.
 XX
 XX 23-JAN-1997.
 XX
 XX 17-JUL-1996; 96DE-01028895.
 XX
 XX 17-JUL-1995; 95DE-01025992.
 PR
 PR 18-AUG-1995; 95DE-01030500.
 XX
 XX (FRAU) FRAUNHOFER GBS FOERDERUNG ANGEWANDTEN.
 PA
 XX Wissler JH, Logemann E, Kieseewetter S, Heilmeyer LMG;
 PI
 XX WPI; 1997-088586/09.
 DR
 DR N-PSDB; AAT62569.
 XX
 XX Bioactive metal RNA polypeptide - useful for modulating angiogenesis,
 PT etc.
 XX
 XX Claim 1; Page 15; 16pp; German.
 PS
 XX A novel bioactive metal RNA polypeptide (RNP) has a RNA component
 CC including the sequence AAT62568 and a polypeptide component having the
 CC sequence AAW01826, which is encoded by AAT62569. The RNP, or anti-RNP
 CC immunoglobulins, can be used to modulate and/or analyse angiogenesis and
 CC the vascular state of mammalian tissue, transfer genetic information in
 CC cells and selectively alter the nucleic acid content of cells. Leukocytes
 CC from pig's blood were cultured in medium, and the supernatant treated
 CC with NH₄ sulphate at 35, 45 and 90% saturation to precipitate protein
 CC fractions. The residual supernatant was diluted to 45% NH₄ sulphate
 CC saturation and concentrated by ultrafiltration using a 0.5 kD membrane.
 CC The retentate was purified to give 8 mg of product described as monocyto-
 CC CuRNP
 XX
 XX SQ Sequence 91 AA;
 SQ
 Alignment Scores:
 Pred. No.: 6,12e-37 Length: 91
 Score: 371.00 Matches: 74
 Percent Similarity: 91.21% Conservative: 9
 Best Local Similarity: 81.32% Mismatches: 8
 Query Match: 76.97% Indels: 0
 DB: 2 Gaps: 0
 US-09-910-208B-1 (1-276) x AAW01826 (1-91)
 QY 4 ACTAGCTGGAGATCACCCTGAGGGGAAATCATCAATCTTCCACAGTACTCCGTTGG 63
 Db 1 ThrLysLeuGluAspHisLeuGluGlyIleleAsnIlePheHisGlnTyrSerValArg 20
 QY 64 GTGGGGCATTTCGACACCCCTCAACAGCTGAGCTGAGCTGAAGCAGCTGATCAACAAGAACTT 123

CC squamous epithelial cells, neutrophils and macrophages, but atypical
 CC epithelial cells are negative for CAAp1 and overexpression is observed in
 CC several types of cancer cells and neutrophils/macrophages infiltrating
 CC cancerous lesions. Detection of CAAp1 (using antibodies in usual
 CC immunosays) can be used to diagnose (or monitor) inflammation,
 CC neoplasia (particularly squamous cell carcinoma of the skin, oesophagus,
 CC lung and cervix), and skin and blood diseases

XX Sequence 92 AA;

Alignment Scores:
 Pred. No.: 1.8e-30 Length: 92
 Score: 319.00 Matches: 61
 Percent Similarity: 80.43% Conservative: 13
 Best Local Similarity: 66.30% Mismatches: 18
 Query Match: 66.18% Indels: 0
 DB: 2 Gaps: 0

US-09-910-208B-1 (1-276) x AAW03564 (1-92)

QY 1 ATGACTTAAGCTGGAAGATCACCTGGAGGGAATCATCAACATCTTCCACCACTACTCCGTT 60
 DB 1 MetThrLysLeuGluGluHisLeuGluGlyLeValAsnIlePheHisGlnIyrSerVal 20
 QY 61 CGGCTGGGCGCATTTCCGACACCTCAACAGCGCTGAGCTGAAGCAGCTGATCAACAAGGAA 120
 DB 21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGlu 40
 QY 121 CTTCCCAAAACCTCCAGAACACCAAGATCAACCTTACCTTGACAAATATTTCCAAGAC 180
 DB 41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60
 QY 181 CTGGATCGCGATAAAGACGGCCGTCAGCTTTGAGGAATTCGTAGTCTCTGTGTCAGG 240
 DB 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80
 QY 241 GTGCTGAAACACGCCACATAGATATCCACAAGAG 276
 DB 81 AlaLeuLysAlaAlaHisIyrHisThrHisLysGlu 92

RESULT 7

AAW24137
 ID AAW24137 standard; protein; 92 AA.

XX AAW24137;

XX 28-JAN-1998 (first entry)

DT Human chemotactic cytokine I.

DE chemotactic cytokine; tumour; autoimmune disease; antagonist; agonist.

KW Homo sapiens.

OS WO9723640-A1.

PN 03-JUL-1997.

XX 26-DEC-1995; 95WO-US016871.

XX 26-DEC-1995; 95WO-US016871.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ni J, Yu G, Alfonso P, Gentz R, Su JY;

XX WPI; 1997-351075/32.

XX N-PSDB; AAT85774.

XX DNA encoding chemotactic cytokine I - used to treat, e.g. tumours,

XX chronic infection, leukaemia, etc.

XX Claim 12; Page 48-49; 64pp; English.

XX

This is a human chemotactic cytokine I polypeptide. The encoding
 CC polynucleotide, along with a vector and a host cell can be used for the
 CC recombinant production of the chemotactic cytokine. Cytokine agonists and
 CC antagonists can be used for the treatment of a patient requiring a
 CC chemotactic cytokine I and for the treatment of a patient requiring the
 CC inhibition of a chemotactic cytokine I polypeptide, respectively. The
 CC chemotactic cytokine is used to treat tumours, chronic infection,
 CC leukaemia and T-cell mediated autoimmune diseases

XX Sequence 92 AA;

Alignment Scores:
 Pred. No.: 1.8e-30 Length: 92
 Score: 319.00 Matches: 61
 Percent Similarity: 80.43% Conservative: 13
 Best Local Similarity: 66.30% Mismatches: 18
 Query Match: 66.18% Indels: 0
 DB: 2 Gaps: 0

US-09-910-208B-1 (1-276) x AAW24137 (1-92)

QY 1 ATGACTTAAGCTGGAAGATCACCTGGAGGGAATCATCAACATCTTCCACCACTACTCCGTT 60
 DB 1 MetThrLysLeuGluGluHisLeuGluGlyLeValAsnIlePheHisGlnIyrSerVal 20
 QY 61 CGGCTGGGCGCATTTCCGACACCTCAACAGCGCTGAGCTGAAGCAGCTGATCAACAAGGAA 120
 DB 21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGlu 40
 QY 121 CTTCCCAAAACCTCCAGAACACCAAGATCAACCTTACCTTGACAAATATTTCCAAGAC 180
 DB 41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60
 QY 181 CTGGATCGCGATAAAGACGGCCGTCAGCTTTGAGGAATTCGTAGTCTCTGTGTCAGG 240
 DB 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80
 QY 241 GTGCTGAAACACGCCACATAGATATCCACAAGAG 276
 DB 81 AlaLeuLysAlaAlaHisIyrHisThrHisLysGlu 92

RESULT 8

AAW24137

ID AAW24137 standard; protein; 92 AA.

XX AAW24137;

XX 22-FEB-2001 (first entry)

DT Human S100A12 protein.

DE S100 protein; human; treatment; cardiomyopathy; cardiac insufficiency;
 KW calcium-binding protein; calcium homeostasis; cardiac muscle;
 KW pumping capacity; myocardial cell; systolic calcium ion release;
 KW sarcoplasmic reticulum; cardiac disease; hypertension; rhythm disorder;
 KW valve defect.

OS Homo sapiens.

PN DE19915485-A1.

XX 19-OCT-2000.

XX 07-APR-1999; 99DE-01015485.

XX 07-APR-1999; 99DE-01015485.

XX (KATU/) KATUS H A.

XX (REMP/) REMPPIS A.

XX Katus HA, Remppis A;

DR WPI; 2000-673510/66.
 DR N-PSDB; AAC81812.
 XX
 PT Composition containing S100 protein, corresponding nucleic acid or
 PT vector, useful for treating cardiomyopathy and cardiac insufficiency.
 XX
 PS Claim 35; Page 20; 36pp; German.
 XX
 CC This invention describes a novel composition for treating primary or
 CC secondary cardiomyopathy or cardiac insufficiency contains at least one
 CC S100 protein (I) or nucleic acid (II) encoding (I), or their mutants or
 CC fragments, or a gene transfer vector containing (II), optionally
 CC formulated with auxiliaries and/or carriers. (I) are calcium-binding
 CC proteins involved in calcium homeostasis, so their overexpression in
 CC cardiac muscle will improve pumping capacity (and overall capacity) of
 CC the heart. In cultured myocardial cells they increase the contraction and
 CC relaxation rates associated with increased systolic calcium ion release
 CC from the sarcoplasmic reticulum (SR) and calcium re-uptake by SR. (I) are
 CC used to treat cardiomyopathy (CMP) where inherited or caused by
 CC spontaneous mutations and ischemic CMP caused by arteriosclerosis,
 CC dilative CMP caused by toxic/infectious disease, cardiac disease caused
 CC by pulmonary and/or arterial hypertension, and structural disease caused
 CC by rhythm disorders or valve defects, generally any condition associated
 CC with reduced contractile force. Unlike calmodulin, which is expressed
 CC ubiquitously, (I) show tissue-specific expression and treat the
 CC underlying defect in the sarcoplasmic reticulum (SR) that causes cardiac
 CC disease
 XX

SQ Sequence 92 AA;

Alignment Scores:
 Pred. No.: 1.8e-30 Length: 92
 Score: 319.00 Matches: 61
 Percent Similarity: 80.43% Conservative: 13
 Best Local Similarity: 66.30% Mismatches: 18
 Query Match: 66.18% Indels: 0
 DB: 3 Gaps: 0

US-09-910-208B-1 (1-276) x AAB45542 (1-92)

QY 1 ATGACTAAGCTGGAGATCACCTGGAGGAATCATCAACATCTTCCACGACTCCGTT 60
 DB 1 MetThrLysLeuGluGluHisLeuGluGlyIleValAsnIlePheHisGlnTySerVal 20
 QY 61 CGGTGGGGCATTTTCGACACCTCAACAGCGTGAGCTGAAGCAGCTGATCACAAGAA 120
 DB 21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuThrLysGlu 40
 QY 121 CTTCCTCAAAACCTCCAGAACACCAAGATCAACCTACCATTTGACAAATATTTCAAGAC 180
 DB 41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60
 QY 181 CTGGATCCGATAAAGACGGCCGCTCAGCTTTTGAGGAATTCGTAGTCTCGTGTCCAGG 240
 DB 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80
 QY 241 GTGCTGAAAACAGCCCATAGATATCCAAAGAG 276
 DB 81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92

RESULT 9

AAB31911

ID AAB31911 standard; protein; 92 AA.

XX AC AAB31911;

XX 15-MAY-2001 (first entry)

XX Amino acid sequence of a human protein.

XX Human; perlecan; retinol-binding plasma protein; calgranulin B; vaccine;
 KW ganglioside GM2 activator; saposin B; degenerative disease; glial cell;
 KW neurological disease; auto-immune disease; multiple sclerosis; toxicity;

KW Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;
 KW rheumatoid polyarthritis; lupus erythematosus; gene therapy.
 XX
 OS Homo sapiens.
 XX WO200105422-A2.
 PN
 XX
 PD 25-JAN-2001.
 XX
 XX 17-JUL-2000; 2000WO-FR002057.
 PF
 XX 15-JUL-1999; 99FR-00009372.
 PR
 XX (INNR) BIOMERIEUX STELHYS.
 PA
 XX Rosekkin D, Kolbe H, Charles M, Malcus C, Santoro L, Perron H;
 FI WPI; 2001-159475/16.
 XX
 DR Detecting, preventing and treating degenerative, neurological and
 XX polypeptides or related nucleic acid or ligand.
 PT
 XX Claim 1; Page 168; 209pp; French.

The present sequence represents a human protein, which is used in the
 method of the invention. The specification describes a method which uses
 at least one polypeptide or polynucleotide sequence belonging to the
 perlecan, precursor of the retinol-binding plasma protein, precursor of
 the ganglioside GM2 activator, calgranulin B or saposin B protein
 families. The method is used for detecting, preventing or treating a
 degenerative, neurological and/or auto-immune disease. The
 polynucleotides and polypeptides are used for diagnosis, prognosis,
 prevention and treatment of multiple sclerosis (in its various forms and
 phases). They may also be useful in cases of e.g. Alzheimer's and
 Parkinson's diseases, amyotrophic lateral sclerosis, rheumatoid
 polyarthritis and lupus erythematosus, including use as vaccines and in
 gene therapy (expression of sense or antisense sequences). They can also
 be used to assess efficacy of potential therapeutic agents, particularly
 compounds that reduce or inhibit toxicity towards glial cells

SQ Sequence 92 AA;

Alignment Scores:
 Pred. No.: 1.8e-30 Length: 92
 Score: 319.00 Matches: 61
 Percent Similarity: 80.43% Conservative: 13
 Best Local Similarity: 66.30% Mismatches: 18
 Query Match: 66.18% Indels: 0
 DB: 4 Gaps: 0

US-09-910-208B-1 (1-276) x AAB31911 (1-92)

QY 1 ATGACTAAGCTGGAGATCACCTGGAGGAATCATCAACATCTTCCACGACTCCGTT 60
 DB 1 MetThrLysLeuGluGluHisLeuGluGlyIleValAsnIlePheHisGlnTySerVal 20
 QY 61 CGGTGGGGCATTTTCGACACCTCAACAGCGTGAGCTGAAGCAGCTGATCACAAGAA 120
 DB 21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuThrLysGlu 40
 QY 121 CTTCCTCAAAACCTCCAGAACACCAAGATCAACCTACCATTTGACAAATATTTCCAGAC 180
 DB 41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60
 QY 181 CTGGATCCGATAAAGACGGCCGCTCAGCTTTTGAGGAATTCGTAGTCTCGTGTCCAGG 240
 DB 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80
 QY 241 GTGCTGAAAACAGCCCATAGATATCCAAAGAG 276
 DB 81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92

RESULT 10	121	CTTCCAAACCCCTCCAGAACCAACGATCAACCTACCATTCACAAATATTTCCAGAC	180
AAB31907	41	LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly	60
XX			
AC			
XX			
XX			
DT	15-MAY-2001	(first entry)	
XX			
DE			
XX			
KW		Human; perlecan; retinol-binding plasma protein; calgranulin B; vaccine;	
KW		ganglioside GM2 activator; saposin B; degenerative disease; glial cell;	
KW		neurological disease; auto-immune disease; multiple sclerosis; toxicity;	
KW		Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;	
KW		rheumatoid polyarthritis; lupus erythematosus; gene therapy.	
XX			
OS		Homo sapiens.	
XX			
XX		WO200105422-A2.	
PN		25-JAN-2001.	
PD		17-JUL-2000; 2000WO-FR002057.	
XX		15-JUL-1999; 99PR-00009372.	
XX		(INNR) BIOMERIEUX STELHVS.	
PI		Roeklin D., Kolbe H., Charles M., Malcus C., Santoro L., Perron H;	
DR		WPI; 2001-159475/16.	
XX		Detecting, preventing and treating degenerative, neurological and	
PT		autoimmune diseases, particularly multiple sclerosis, using specified	
PT		polypeptides or related nucleic acid or ligand.	
XX		Claim 1; Page 166-167; 209pp; French.	
XX		The present sequence represents a human protein, which is used in the	
CC		method of the invention. The specification describes a method which uses	
CC		at least one polypeptide or polynucleotide sequence belonging to the	
CC		perlecan, precursor of the retinol-binding plasma protein, precursor of	
CC		the ganglioside GM2 activator, calgranulin B or saposin B protein	
CC		families. The method is used for detecting, preventing or treating a	
CC		degenerative, neurological and/or auto-immune disease. The	
CC		polynucleotides and polypeptides are used for diagnosis, prognosis,	
CC		prevention and treatment of multiple sclerosis (in its various forms and	
CC		phases). They may also be useful in cases of e.g. Alzheimer's and	
CC		Parkinson's diseases, amyotrophic lateral sclerosis, rheumatoid	
CC		polyarthritis and lupus erythematosus, including use as vaccines and in	
CC		gene therapy (expression of sense or antisense sequences). They can also	
CC		be used to assess efficacy of potential therapeutic agents, particularly	
CC		compounds that reduce or inhibit toxicity towards glial cells	
XX		Sequence 92 AA;	
SQ			
Alignment Scores:			
Pred. No.:	1.8e-30	Length:	92
Score:	319.00	Matches:	61
Percent Similarity:	80.43%	Conservative:	13
Best Local Similarity:	66.30%	Mismatches:	18
Query Match:	66.18%	Indels:	0
DB:	4	Gaps:	0
US-09-910-208b-1 (1-276) x AAB31907 (1-92)			
QY	1	ATGACTTAAGCTGGAATCACCTGGAGGGAATCATCAATCTTCCACAGTACTCCGTT	60
Db	1	MetThrLysLeuGluGluHisLeuGluGlyIleValAsnIlePheHisGlnTyrSerVal	20
QY	61	CGGTGGGGCATTTCCACACCTTCAACAGCGGTAGCTGAACGAGCTGATCAAGGAA	120
Db	21	ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGlu	40

Best Local Similarity: 66.30% Mismatches: 18
Query Match: 66.18% Indels: 0
DB: 4 Gaps: 0

US-09-910-208B-1 (1-276) x AAB31908 (1-92)

QY 1 ATGACTAAGCTGGAGATCACCTGGAGGAATCATCAACATCTTCCACAGTACTCCGTT 60
DB 1 MetThrylsLeuGluHisLeuGluGlyLeValAsnIlePheHisGlnTy-SerVal 20

QY 61 CGGTGGGGCATTTTCACACCTCAACAGCGTGAAGCTGAGCTGATCACAAGAA 120
DB 21 ArglysGlyHisPheAspThrLeuSerlysglyGluLeuLeuThrysglu 40

QY 121 CTCTCCAAAACCTCCAGAACACCAACATCAACCTACCTTGCAGAAATATTCACAGAC 180
DB 41 LeuAlaAsnThrIleYsAsnIleYsAspGlyValIleAspGluIlePheGlnGly 60

QY 181 CTGGATGCCGATAAAGACGGAGCCGTCAGCTTTGAGGAATTCGTAGTCTCGTCCAGG 240
DB 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80

QY 241 GTGCTGAAAACAGCCCATAGATATCCACAAAGAG 276
DB 81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92

RESULT 12
ADA93649
ID ADA93649 standard; protein; 92 AA.
AC ADA93649;
DT 20-NOV-2003 (first entry)
XX Human calgranulin C protein SEQ ID NO:2.
DE inflammatory disease; calgranulin C; antiinflammatory; gene therapy;
KW vasculitis; Kawasaki disease; cystic fibrosis;
KW chronic inflammatory disease; ulcerative colitis; Crohn's disease;
KW chronic bronchitis; inflammatory arthritis; psoriatic arthritis;
KW rheumatoid arthritis; seronegative arthritis;
KW systemic onset juvenile rheumatoid arthritis; SJORA; Still's disease;
KW acute inflammation; human.
OS Homo sapiens.
XX WO2003069341-A2.
XX 21-AUG-2003.
XX 17-FEB-2003; 2003WO-EP001575.
XX 15-FEB-2002; 2002US-00077600.
XX (SWIT-) SWITCH BIOTECH AG.
PA (SORG/) SORG C.
PA (ROTH/) ROTH J.
XX SORG C, Roth J;
XX WPI; 2003-671681/63.
DR N-PSDB; ADA93648.
XX Diagnosing, treating or preventing inflammatory diseases comprises
PT determining the amount and/or concentration of CALGRANULIN C polypeptide
PT and/or nucleic acids encoding the polypeptide present in a biological
PT sample.
XX Claim 7; Page 64; 64pp; English.
PS
XX The present invention describes a method for diagnosing inflammatory
CC diseases, which comprises determining the amount and/or concentration of
CC calgranulin C polypeptide and/or nucleic acids encoding the polypeptide

CC present in the biological sample. Also described are methods for treating
CC or preventing an inflammatory disease in a mammal, and medical treatment
CC of the mammal, where the treatment is based on the stage of the disease
CC to be treated or prevented. Calgranulin C has antiinflammatory activity
CC and can be used in gene therapy. The method is useful for diagnosing,
CC treating or preventing inflammatory diseases, e.g. vasculitis
CC (particularly Kawasaki disease), cystic fibrosis, chronic bronchitis,
CC diseases like ulcerative colitis or Crohn's disease, chronic bronchitis,
CC inflammatory arthritis (e.g. psoriatic arthritis, rheumatoid arthritis or
CC seronegative arthritis), systemic onset juvenile rheumatoid arthritis
CC (SJORA or Still's disease), acute inflammation above the background of a
CC chronic inflammation, an acquired infection on the background of an
CC inflammatory disease, or an exacerbation of an already present disease.
CC The method is also useful for diagnosing specific stages of inflammatory
CC diseases, for determining the risk of relapse, and for discriminating
CC between diseases with similar symptoms. The present sequence represents
CC human calgranulin C, which is used in the exemplification of the present
CC invention.
XX Sequence 92 AA;
SQ

Alignment Scores:
Pred. No.: 1.8e-30 Length: 92
Score: 319.00 Matches: 61
Percent Similarity: 80.43% Conservative: 13
Best Local Similarity: 66.30% Mismatches: 18
Query Match: 66.18% Indels: 0
DB: 7 Gaps: 0

US-09-910-208B-1 (1-276) x ADA93649 (1-92)

QY 1 ATGACTAAGCTGGAGATCACCTGGAGGAATCATCAACATCTTCCACAGTACTCCGTT 60
DB 1 MetThrylsLeuGluHisLeuGluGlyLeValAsnIlePheHisGlnTy-SerVal 20

QY 61 CGGTGGGGCATTTTCACACCTCAACAGCGTGAAGCTGAGCTGATCACAAGAA 120
DB 21 ArglysGlyHisPheAspThrLeuSerlysglyGluLeuLysGlnLeuThrysglu 40

QY 121 CTCTCCAAAACCTCCAGAACACCAACATCAACCTACCTTGCAGAAATATTCACAGAC 180
DB 41 LeuAlaAsnThrIleYsAsnIleYsAspGlyValIleAspGluIlePheGlnGly 60

QY 181 CTGGATGCCGATAAAGACGGAGCCGTCAGCTTTGAGGAATTCGTAGTCTCGTCCAGG 240
DB 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80

QY 241 GTGCTGAAAACAGCCCATAGATATCCACAAAGAG 276
DB 81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92

RESULT 13
ADN04192
ID ADN04192 standard; protein; 92 AA.
AC ADN04192;
XX 01-JUL-2004 (first entry)
XX Antipsoriatic protein sequence #291.
DE antipsoriatic; gene therapy; psoriasis; diagnosis.
KW Homo sapiens.
OS
XX WO2004028479-A2.
XX 08-APR-2004.
XX 25-SEP-2003; 2003WO-US030907.
XX 25-SEP-2002; 2002US-0414006P.
XX

PA (GETH) GENENTECH INC.
 XX Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;
 PI Wu TD;
 XX
 XX
 DR WPI: 2004-305105/28.
 DR N-PSDB; ADN04191.
 XX
 PT New PRO nucleic acid or polypeptide, useful for preparing a
 PT pharmaceutical composition for diagnosing or treating psoriasis in a
 PT mammal.
 XX
 XX
 PS Claim 9; SEQ ID NO 586; 3069pp; English.
 XX
 CC The invention relates to novel polynucleotide and polypeptides for
 CC treating psoriasis or a sequence having at least 80% identity to the
 CC above sequences. The nucleic acid is useful for preparing a composition
 CC for diagnosing or treating psoriasis in a mammal. This sequence
 CC corresponds to one of the polypeptides of the invention.
 XX
 SQ Sequence 92 AA;
 Alignment Scores:
 Pred. No.: 1.8e-30 Length: 92
 Score: 319.00 Matches: 61
 Percent Similarity: 80.43% Conservative: 13
 Best Local Similarity: 66.30% Mismatches: 18
 Query Match: 66.18% Indels: 0
 DB: 8 Gaps: 0
 US-09-910-208B-1 (1-276) x ADN04192 (1-92)
 QY 1 ATGACTAAGCTGGAAGATCACCTGGAGGGAATCATCAACATCTTCCACGACTCCGTT 60
 Db 1 MetThrLysLeuGluGluHisLeuGluGlyIleValAsnIlePheHisGlnTyrSerVal 20
 QY 61 CGGTGGGGCATTTTCGACACCTCAACAGCGTGTGAGCTGAACGAGCTGATCAAAAGAA 120
 Db 21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGlu 40
 QY 121 CTTCCAAAACCTCCAGACACCAAGATCAACCTACCATTCGACAAATATTTCCAAGAC 180
 Db 41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60
 QY 181 CTGGATGCCGATAAAGACGGAGCGGTGACGTTTGGAGGATTCGTAGTCTCGTGTCCAGG 240
 Db 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80
 QY 241 GTGCTGAAACAGCCCATAGATATCCAAAGAG 276
 Db 81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92
 RESULT 14
 AD019540
 ID AD019540 standard; protein; 92 AA.
 XX
 AC AD019540;
 XX
 XX
 DT 12-AUG-2004 (first entry)
 XX
 DE Human PRO polypeptide #235.
 XX
 KW Human; PRO; immune related disorder; systemic lupus erythematosus;
 KW rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis;
 KW systemic sclerosis; Sjogren's syndrome; vasculitis; sarcoidosis;
 KW autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis;
 KW diabetes mellitus; renal disease; demyelinating disease;
 KW central nervous system; peripheral nervous system;
 KW demyelinating polyneuropathy; Guillain-Barre syndrome;
 KW chronic inflammatory demyelinating polyneuropathy.
 XX
 OS Homo sapiens.
 XX

PN WO2004043361-A2.
 XX
 PD 27-MAY-2004.
 XX
 PF 06-NOV-2003; 2003WO-US035268.
 XX
 PR 08-NOV-2002; 2002US-0425235P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Fong S, Dennis K, Clark H, Chiu H, Schoenfeld J, Williams PM;
 PI Wood WI, Wu TD;
 XX
 DR WPI: 2004-420067/39.
 DR N-PSDB; ADO19539.
 XX
 PT Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO86388 useful for
 PT treating an immune related disorder such as systemic lupus erythematosus,
 PT rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or
 PT spondyloarthropathy.
 XX
 PS Claim 7; SEQ ID NO 470; 1731pp; English.
 XX
 CC The invention relates to human PRO polypeptides and the polynucleotides
 CC encoding them. The polypeptides and polynucleotides are useful for
 CC treating and diagnosing immune related disorders in mammals. The immune
 CC related disorders include systemic lupus erythematosus, rheumatoid
 CC arthritis, osteoarthritis, juvenile chronic arthritis, systemic
 CC sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune
 CC haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes
 CC mellitus, immune-mediated renal disease, demyelinating diseases of the
 CC central or peripheral nervous system, demyelinating polyneuropathy,
 CC Guillain-Barre syndrome and chronic inflammatory demyelinating
 CC polyneuropathy. This sequence represents a human PRO polypeptide of the
 CC invention.
 XX
 SQ Sequence 92 AA;
 Alignment Scores:
 Pred. No.: 1.8e-30 Length: 92
 Score: 319.00 Matches: 61
 Percent Similarity: 80.43% Conservative: 13
 Best Local Similarity: 66.30% Mismatches: 18
 Query Match: 66.18% Indels: 0
 DB: 8 Gaps: 0
 US-09-910-208B-1 (1-276) x ADO19540 (1-92)
 QY 1 ATGACTAAGCTGGAAGATCACCTGGAGGGAATCATCAACATCTTCCACGACTCCGTT 60
 Db 1 MetThrLysLeuGluGluHisLeuGluGlyIleValAsnIlePheHisGlnTyrSerVal 20
 QY 61 CGGTGGGGCATTTTCGACACCTCAACAGCGTGTGAGCTGAACGAGCTGATCAAAAGAA 120
 Db 21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGlu 40
 QY 121 CTTCCAAAACCTCCAGACACCAAGATCAACCTACCATTCGACAAATATTTCCAAGAC 180
 Db 41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60
 QY 181 CTGGATGCCGATAAAGACGGAGCGGTGACGTTTGGAGGATTCGTAGTCTCGTGTCCAGG 240
 Db 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80
 QY 241 GTGCTGAAACAGCCCATAGATATCCAAAGAG 276
 Db 81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92
 RESULT 15
 ADRI4333
 ID ADRI4333 standard; protein; 92 AA.
 XX
 AC ADRI4333;

XX 21-OCT-2004 (first entry)
XX Human NF-kappaB pathway-associated protein SeqID334.
XX
XX NF-kappaB pathway; antiinflammatory; cytostatic; hepatotropic; virucide;
XX antiarthritic; antirheumatic; gastrointestinal-Gen; antiasthmatic;
XX antiarteriosclerotic; immunomodulator; cerebroprotective; vasotropic;
KW immunosuppressive; vulnery; gene therapy; immune disorder;
KW inflammatory disorder; NF-kappaB regulation; cancer; aberrant apoptosis;
KW hepatic disorder; Hodgkin's lymphoma; haematopoietic tumour;
KW hyper-IgM syndrome; hypohidrotic ectodermal dysplasia;
KW X-linked anhidrotic ectodermal dysplasia; immunodeficiency;
KW viral infection; HIV-1; HTLV-1; hepatitis B; hepatitis C; EBV; influenza;
KW viral replication; host cell survival; evasion of immune response;
KW rheumatoid arthritis; inflammatory bowel disease; colitis; asthma;
KW atherosclerosis; cachexia; euthyroid sick syndrome; stroke; EAE;
KW autoimmune disorder; hyper immune activity;
KW aberrant acute phase response; hypercongenital condition; birth defect;
KW necrotic lesion; wound; organ transplant rejection;
KW aberrant signal transduction; proliferating disorder; cancer;
KW HIV propagation; human.
XX
XX Homo sapiens.
OS
XX WO2004065577-A2.
PN
XX
XX 05-AUG-2004.
PD
XX
XX 13-JAN-2004; 2004WO-US000798.
PF
XX
XX 14-JAN-2003; 2003US-0440068P.
PR
XX 12-MAY-2003; 2003US-0469757P.
PR
XX (BRIM) BRISTOL-MYERS SQUIBB CO.
PA
XX
XX Nadler SG, Neubauer MG, Feder JN, Carman J;
PI
XX
XX WPI; 2004-562168/54.
DR
XX N-PSDB; ADR14332.
DR
XX
XX New isolated polynucleotides and polypeptides associated with NF-kappaB
PT pathway, useful for diagnosing, treating, or preventing disorders or
PT diseases associated with NF-kappaB pathway.
PT
XX
XX Claim 6; SEQ ID NO 334; 237pp; English.
PS
XX

CC was obtained by the indexer from Genbank.
XX
XX Sequence 92 AA;
SQ
Alignment Scores:
Pred. No.: 1.8e-30 Length: 92
Score: 319.00 Matches: 61
Percent Similarity: 80.43% Conservative: 13
Best Local Similarity: 66.30% Mismatches: 18
Query Match: 66.18% Indels: 0
DB: 8 Gaps: 0
US-09-910-208B-1 (1-276) x ADR14333 (1-92)
Qy 1 ATGACTAAGCTGGAGATCACCTGAGGGAATCATCAACATCTTCCACGACTCTCCGTT 60
Db 1 MetThrLysLeuGluGluHisLeuGluGluGlyIleValAsnIlePheHisGlnTySerVal 20
Qy 61 CGGGTGGGGCAATTTTCGACACCCCTCAACAGCGTGAAGCAGCTGATGACAAAGGAA 120
Db 21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuThrLysGlu 40
Qy 121 CTTCCCAAAACCTCCAGACACCAACAGATCAACCTACCATTGACAAATATTCCAGAC 180
Db 41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60
Qy 181 CTGGATGCCGATAAAGAGCGGAGCGCTGAGCTTTGAGGAATTCGTAGTCTCGTGTCCAGG 240
Db 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80
Qy 241 GTGCTGAAACAGCCCATAGATATCCACAAAGAG 276
Db 81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92
Search completed: February 23, 2005, 11:18:50
Job time : 116.5 secs

GenCore version 5.1.6
: Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: February 23, 2005, 11:19:00 ; Search time 89 Seconds
(without alignments)
2029.630 Million cell updates/sec

Title: us-09-910-208b-1

Perfect score: 482

Sequence: 1 atgactaagctggaagatca.....acatgatattcaccaagag 276

Scoring table:

BL0SUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 1380268 seqs, 327241040 residues

Total number of hits satisfying chosen parameters: 2760536

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q/cgn2_1/USPTO_spool_p/HADDAD-09-910208/runat_23022005_101809_14837/app_query.fasta_1.
-DB=Published Applications AA -QWTF=fastan -SUFFIX=rapb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=bl0sum62
-TRANS=human40.cdi -LIST=45 -DOCLAL=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000
-USER-HADDAD-09-910208 @CIGN 1 199 @runat_23022005_101809_14837 -NCPU=6
-ICPU=3 -NO_MMAPP -LARGQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications AA:

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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
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5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
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7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
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10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Alignment Scores: 5.34e-45 Length: 90
Pred. No.: 90

Result No.	Score	Query Match	Length	DB ID	Description
1	460	95.4	90	9	US-09-826-589-3
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3	460	95.4	90	9	US-09-872-185B-11
4	460	95.4	90	9	US-09-872-185B-12
5	460	95.4	90	15	US-10-666-513-3
6	460	95.4	90	16	US-10-665-867-3
7	460	95.4	90	16	US-10-665-867-4
8	319	66.2	92	14	US-10-077-600-2
9	319	66.2	92	16	US-10-755-889-334
10	230	47.7	50	9	US-09-826-589-2
11	230	47.7	50	9	US-09-872-185B-9
12	230	47.7	50	15	US-10-666-513-2
13	230	47.7	50	16	US-10-665-867-2
14	211.5	43.9	114	9	US-09-214-272-4
15	211.5	43.9	114	14	US-10-134-841-4
16	211.5	43.9	114	14	US-10-308-279-32
17	211.5	43.9	114	15	US-10-116-275-225
18	211.5	43.9	114	15	US-10-131-410-146
19	211.5	43.9	114	15	US-10-434-599-159736
20	211.5	43.9	114	16	US-10-755-889-330
21	193	40.0	46	9	US-09-864-761-41579
22	190.5	39.5	112	14	US-10-205-219-161
23	190.5	39.5	113	10	US-09-492-026-7
24	187	38.8	95	9	US-09-919-172-102
25	187	38.8	95	9	US-09-981-353-98
26	187	38.8	113	15	US-10-276-774-2377
27	184	38.2	97	16	US-10-363-829-412
28	180	37.3	92	10	US-09-492-026-5
29	180	37.3	92	10	US-09-919-039-184
30	179	37.1	92	15	US-10-336-603A-102
31	173	35.9	91	14	US-10-106-698-6907
32	170	35.3	89	14	US-10-134-841-1
33	170	35.3	89	14	US-10-316-253-46
34	170	35.3	89	16	US-10-624-631-32
35	164.5	34.1	113	14	US-10-134-841-3
36	163	33.8	94	14	US-10-097-340-270
37	160	33.2	93	9	US-09-214-272-2
38	160	33.2	93	14	US-10-134-841-2
39	160	33.2	93	15	US-10-434-599-273325
40	160	33.2	93	16	US-10-624-631-31
41	160	33.2	93	16	US-10-755-889-328
42	160	33.2	101	9	US-09-393-433-2
43	160	33.2	101	9	US-09-781-509-2
44	160	33.2	101	14	US-10-289-643-2
45	160	33.2	119	13	US-10-087-192-1155

ALIGNMENTS

RESULT 1
US-09-826-589-3
; Sequence 3, Application US/09826589
; Patent No. US20020106726A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Stern, David
; TITLE OF INVENTION: EXTRACELLULAR NOVEL RAGE BINDING PROTEIN (EN-RAGE) AND USES THEREOF
; FILE REFERENCE: 0575/55873-B-PCT-US
; CURRENT APPLICATION NUMBER: US/09/826,589
; CURRENT FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Bovine
US-09-826-589-3

Score: 460.00 Matches: 90
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 95.44% Indels: 0
DB: 9 Gaps: 0

US-09-910-208B-1 (1-276) x US-09-826-589-3 (1-90)

QY 4 ACTAAGCTGGAGATCACCCTGGAGGAGTATCATCAATCTTCCACAGTACTCCGTTCCG 63
DB 1 ThrLysLeuGluAspHisLeuGluGlyIleLeuAsnIlePheHisGlnTyrSerValArg 20
QY 64 GTGGGGCATTTCCGACACCTCAACAAGCGTGAAGCTGAGCTGATCACAAGAACTT 123
DB 21 ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40
QY 124 CCCAAACCCCTCCAGAACACCAAGATCAACTACCATTTGACAAATATTTCCAGACCTG 183
DB 41 ProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAspLeu 60
QY 184 GATCCCGATAAGACGGCCGCTGACCTTGGAGGATTCGTAGTCTGCTCCAGGCTG 243
DB 61 AspAlaAspLysAspGlyAlaValSerPheGluGluPheValValLeuValSerArgVal 80
QY 244 CTGAACAGCCACATAGATATCCACAAA 273
DB 81 LeuLysThrAlaHisIleAspIleHisLys 90

RESULT 2

US-09-826-589-4

; Sequence 4, Application US/09826589

; Patent No. US20020106726A1

; GENERAL INFORMATION:

; APPLICANT: Schmidt, Ann Marie

; APPLICANT: Stern, David

; TITLE OF INVENTION: EXTRACELLULAR NOVEL RAGE BINDING PROTEIN (EN-RAGE) AND USES THERE

; FILE REFERENCE: 0575/5873-B-PCT-US

; CURRENT APPLICATION NUMBER: US/09/826,589

; CURRENT FILING DATE: 2001-04-05

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: Patent in version 3.1

; SEQ ID NO 4

; LENGTH: 90

; TYPE: PRT

; ORGANISM: Bovine

US-09-826-589-4

Alignment Scores:

Pred. No.: 5,34e-45 Length: 90
Score: 460.00 Matches: 90
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 95.44% Indels: 0
DB: 9 Gaps: 0

US-09-910-208B-1 (1-276) x US-09-826-589-4 (1-90)

QY 4 ACTAAGCTGGAGATCACCCTGGAGGAGTATCATCAATCTTCCACAGTACTCCGTTCCG 63
DB 1 ThrLysLeuGluAspHisLeuGluGlyIleLeuAsnIlePheHisGlnTyrSerValArg 20
QY 64 GTGGGGCATTTCCGACACCTCAACAAGCGTGAAGCTGAGCTGATCACAAGAACTT 123
DB 21 ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40
QY 124 CCCAAACCCCTCCAGAACACCAAGATCAACTACCATTTGACAAATATTTCCAGACCTG 183
DB 41 ProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAspLeu 60
QY 184 GATCCCGATAAGACGGCCGCTGACCTTGGAGGATTCGTAGTCTGCTCCAGGCTG 243
DB 61 AspAlaAspLysAspGlyAlaValSerPheGluGluPheValValLeuValSerArgVal 80

QY 244 CTGAACAGCCACATAGATATCCACAAA 273
DB 81 LeuLysThrAlaHisIleAspIleHisLys 90

RESULT 3

US-09-872-185B-11

; Sequence 11, Application US/09872185B

; Patent No. US20020122799A1

; GENERAL INFORMATION:

; APPLICANT: Stern, David M.

; APPLICANT: Herold, Kevan

; APPLICANT: Yan, Shi Du

; APPLICANT: Schmidt, Ann Marie

; APPLICANT: Lamster, Ira

; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATION

; FILE REFERENCE: 0575/64080

; CURRENT APPLICATION NUMBER: US/09/872,185B

; CURRENT FILING DATE: 2001-06-01

; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: Patent in version 3.1

; SEQ ID NO 11

; LENGTH: 90

; TYPE: PRT

; ORGANISM: Bovine

US-09-872-185B-11

Alignment Scores:
Pred. No.: 5,34e-45 Length: 90
Score: 460.00 Matches: 90
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 95.44% Indels: 0
DB: 9 Gaps: 0

US-09-910-208B-1 (1-276) x US-09-872-185B-11 (1-90)

QY 4 ACTAAGCTGGAGATCACCCTGGAGGAGTATCATCAATCTTCCACAGTACTCCGTTCCG 63
DB 1 ThrLysLeuGluAspHisLeuGluGlyIleLeuAsnIlePheHisGlnTyrSerValArg 20
QY 64 GTGGGGCATTTCCGACACCTCAACAAGCGTGAAGCTGAGCTGATCACAAGAACTT 123
DB 21 ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40
QY 124 CCCAAACCCCTCCAGAACACCAAGATCAACTACCATTTGACAAATATTTCCAGACCTG 183
DB 41 ProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAspLeu 60
QY 184 GATCCCGATAAGACGGCCGCTGACCTTTGAGGAATTCGTAGTCTGCTCCAGGCTG 243
DB 61 AspAlaAspLysAspGlyAlaValSerPheGluGluPheValValLeuValSerArgVal 80
QY 244 CTGAACAGCCACATAGATATCCACAAA 273
DB 81 LeuLysThrAlaHisIleAspIleHisLys 90

RESULT 4

US-09-872-185B-12

; Sequence 12, Application US/09872185B

; Patent No. US20020122799A1

; GENERAL INFORMATION:

; APPLICANT: Stern, David M.

; APPLICANT: Herold, Kevan

; APPLICANT: Yan, Shi Du

; APPLICANT: Schmidt, Ann Marie

; APPLICANT: Lamster, Ira

; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATION

; FILE REFERENCE: 0575/64080

; CURRENT APPLICATION NUMBER: US/09/872,185B

; CURRENT FILING DATE: 2001-06-01

; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: Patent in version 3.1

; SEQ ID NO 12

; LENGTH: 90
; TYPE: PRT
; ORGANISM: Bovine
US-09-872-185B-12

Alignment Scores:

Pred. No.: 5.34e-45 Length: 90
Score: 460.00 Matches: 90
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 95.44% Indels: 0
DB: 9 Gaps: 0

US-09-910-208B-1 (1-276) x US-09-872-185B-12 (1-90)

QY 4 ACTAAGCTGAAGATCACCTGGAGGAATCATCAACATCTTCCACCAGTACTCCGTTCCG 63
DB 1 ThrLysLeuGluAspHisLeuGluGlyIleAAsnIlePheHisGlnTyrSerValArg 20
QY 64 GTGGGCAATTTCGACACCCCTCAACAAGCGTGAAGCGAGCTGAAGCAGCTGATCAAAAGGAACCTT 123
DB 21 ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40
QY 124 CCDAAAACCTCCAGAACACCAAGATCAACCTACCTTCAACATTCGACAAATATTTCCAAAGACCTG 183
DB 41 ProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAspLeu 60
QY 184 GATCCGATAAAGACGAGCGCTCAGCTTTGAGGAATTCGTAGTCTCGTGTGCCAGGCTG 243
DB 61 AspAlaAspLysAspGlyAlaValSerPheGluGluPheValValLeuValSerArgVal 80
QY 244 CTGAAACAGCCACATAGATATCCACAAA 273
DB 81 LeuLysThrAlaHisIleAspIleHisLys 90

RESULT 5

US-10-666-513-3
; Sequence 3, Application US/10666513
; Publication No. US20040043412A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Ann Marie
; TITLE OF INVENTION: Extracellular No. US20040043412A1el RAGE Binding Protein (EN-RAGE)
; FILE REFERENCE: 0575/55873
; CURRENT APPLICATION NUMBER: US/10/666,513
; PRIOR FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/167,705B
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Human
US-10-666-513-3

Alignment Scores:

Pred. No.: 5.34e-45 Length: 90
Score: 460.00 Matches: 90
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 95.44% Indels: 0
DB: 15 Gaps: 0

US-09-910-208B-1 (1-276) x US-10-666-513-3 (1-90)

QY 4 ACTAAGCTGAAGATCACCTGGAGGAATCATCAACATCTTCCACCAGTACTCCGTTCCG 63
DB 1 ThrLysLeuGluAspHisLeuGluGlyIleAAsnIlePheHisGlnTyrSerValArg 20
QY 64 GTGGGCAATTTCGACACCCCTCAACAAGCGTGAAGCGAGCTGAAGCAGCTGATCAAAAGGAACCTT 123

DB 21 ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40
QY 124 CCCAAACCCCTCCAGAACACCAAGATCAACCTACCTTGCACAAAATATTTCCAAAGACCTG 183
DB 41 ProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAspLeu 60
QY 184 GATCCGATAAAGACGAGCGCTCAGCTTTGAGGAATTCGTAGTCTCGTGTGCCAGGCTG 243
DB 61 AspAlaAspLysAspGlyAlaValSerPheGluGluPheValValLeuValSerArgVal 80
QY 244 CTGAAACAGCCACATAGATATCCACAAA 273
DB 81 LeuLysThrAlaHisIleAspIleHisLys 90

RESULT 6

US-10-665-867-3
; Sequence 3, Application US/10665867
; Publication No. US20040121372A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Ann Marie
; TITLE OF INVENTION: EXTRACELLULAR NOVEL RAGE BINDING PROTEIN (EN-RAGE) AND USES THEREOF
; FILE REFERENCE: 0575/55873-B-PCT-US
; CURRENT APPLICATION NUMBER: US/10/665,867
; PRIOR FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US/09/826,589
; PRIOR FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 3
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Bovine
US-10-665-867-3

Alignment Scores:

Pred. No.: 5.34e-45 Length: 90
Score: 460.00 Matches: 90
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 95.44% Indels: 0
DB: 16 Gaps: 0

US-09-910-208B-1 (1-276) x US-10-665-867-3 (1-90)

QY 4 ACTAAGCTGAAGATCACCTGGAGGAATCATCAACATCTTCCACCAGTACTCCGTTCCG 63
DB 1 ThrLysLeuGluAspHisLeuGluGlyIleAAsnIlePheHisGlnTyrSerValArg 20
QY 64 GTGGGCAATTTCGACACCCCTCAACAAGCGTGAAGCGAGCTGAAGCAGCTGATCAAAAGGAACCTT 123
DB 21 ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40
QY 124 CCCAAACCCCTCCAGAACACCAAGATCAACCTACCTTGCACAAAATATTTCCAAAGACCTG 183
DB 41 ProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAspLeu 60
QY 184 GATCCGATAAAGACGAGCGCTCAGCTTTGAGGAATTCGTAGTCTCGTGTGCCAGGCTG 243
DB 61 AspAlaAspLysAspGlyAlaValSerPheGluGluPheValValLeuValSerArgVal 80
QY 244 CTGAAACAGCCACATAGATATCCACAAA 273
DB 81 LeuLysThrAlaHisIleAspIleHisLys 90

RESULT 7

US-10-665-867-4
; Sequence 4, Application US/10665867
; Publication No. US20040121372A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Ann Marie
; TITLE OF INVENTION: EXTRACELLULAR NOVEL RAGE BINDING PROTEIN (EN-RAGE) AND USES THEREOF

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; FILE REFERENCE: 0575/55873-B-PCT-US
; CURRENT APPLICATION NUMBER: US/10/665,867
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US/09/826,589
; PRIOR FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Bovine
US-10-665-867-4

Alignment Scores:
Pred. No.: 5,348-45 Length: 90
Score: 460.00 Matches: 90
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 95.44% Indels: 0
DB: 16 Gaps: 0

US-09-910-208B-1 (1-276) x US-10-665-867-4 (1-90)
QY 4 ACTAGCTGGAGATCACCTGGAGGAATCATCAACATCTTCCACAGTACTCCGTTCCG 63
Db 1 ThrLysLeuGluAspHisLeuGluGlyIleAsnIlePheHisGlnTyrSerValArg 20
QY 64 GTGGGGCATTTTCGACACCTCAACAGCGTGAAGCTGAGCGAGCTGATCACAAGGAAC 123
Db 21 ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40
QY 124 CCCAAACCTCCAGAACACCAACATCAACCTACCTTGCACAAATATTTCCAAAGAC 183
Db 41 ProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAspLeu 60
QY 184 GATGCCGATAAAGACGCGCTGAGCTTTGAGGAATTCGTAGTCTCTGTTCCAGGGTG 243
Db 61 AspAlaAspLysAspGlyAlaValSerPheGluGluPheValValLeuValSerArgVal 80
QY 244 CTGAAACAGCCCATAGATATCCACAA 273
Db 81 LeuLysThrAlaHisIleAspIleHisLys 90

RESULT 8
US-10-077-600-2
; Sequence 2, Application US/10077600
; Publication NO. US2003017513A1
; GENERAL INFORMATION:
; APPLICANT: Switch Biotech AG
; TITLE OF INVENTION: Method for diagnosis of inflammatory diseases using Calgranulin C
; CURRENT APPLICATION NUMBER: US/10/077,600
; CURRENT FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 92
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-077-600-2

Alignment Scores:
Pred. No.: 1,866-28 Length: 92
Score: 319.00 Matches: 61
Percent Similarity: 80.43% Conservatives: 13
Best Local Similarity: 66.30% Mismatches: 18
Query Match: 66.18% Indels: 0
DB: 14 Gaps: 0

US-09-910-208B-1 (1-276) x US-10-077-600-2 (1-92)
QY 1 ATGACTAGCTGGAGATCACCTGGAGGAATCATCAACATCTTCCACAGTACTCCGTT 60
Db 1 MetThrLysLeuGluGluHisLeuGluGlyIleAsnIlePheHisGlnTyrSerVal 20
QY 61 CCGGTGGGGCATTTTCGACACCTCAACAGCGTGAAGCTGAGCGAGCTGATCACAAGGA 120
Db 21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGlu 40
QY 121 CTTCCTGATAAAGACGCGCTGAGCTTTGAGGAATTCGTAGTCTCTGTTCCAGG 180
Db 41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60
QY 181 CTGGATCCGATAAAGACGCGCTGAGCTTTGAGGAATTCGTAGTCTCTGTTCCAGG 240
Db 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80
QY 241 GTGCTGAAAACAGCCCATAGATATCCAAAGAG 276
Db 81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92

RESULT 10
US-09-826-589-2
; FILE REFERENCE: 0575/55873-B-PCT-US
; CURRENT APPLICATION NUMBER: US/10/665,867
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US/09/826,589
; PRIOR FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Bovine
US-10-665-867-4

Alignment Scores:
Pred. No.: 5,348-45 Length: 90
Score: 460.00 Matches: 90
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 95.44% Indels: 0
DB: 16 Gaps: 0

US-09-910-208B-1 (1-276) x US-10-665-867-4 (1-90)
QY 4 ACTAGCTGGAGATCACCTGGAGGAATCATCAACATCTTCCACAGTACTCCGTTCCG 63
Db 1 ThrLysLeuGluAspHisLeuGluGlyIleAsnIlePheHisGlnTyrSerValArg 20
QY 64 GTGGGGCATTTTCGACACCTCAACAGCGTGAAGCTGAGCGAGCTGATCACAAGGAAC 123
Db 21 ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40
QY 124 CCCAAACCTCCAGAACACCAACATCAACCTACCTTGCACAAATATTTCCAAAGAC 183
Db 41 ProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAspLeu 60
QY 184 GATGCCGATAAAGACGCGCTGAGCTTTGAGGAATTCGTAGTCTCTGTTCCAGGGTG 243
Db 61 AspAlaAspLysAspGlyAlaValSerPheGluGluPheValValLeuValSerArgVal 80
QY 244 CTGAAACAGCCCATAGATATCCACAA 273
Db 81 LeuLysThrAlaHisIleAspIleHisLys 90

RESULT 8
US-10-077-600-2
; Sequence 2, Application US/10077600
; Publication NO. US2003017513A1
; GENERAL INFORMATION:
; APPLICANT: Switch Biotech AG
; TITLE OF INVENTION: Method for diagnosis of inflammatory diseases using Calgranulin C
; CURRENT APPLICATION NUMBER: US/10/077,600
; CURRENT FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 92
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-077-600-2

Alignment Scores:
Pred. No.: 1,866-28 Length: 92
Score: 319.00 Matches: 61
Percent Similarity: 80.43% Conservatives: 13
Best Local Similarity: 66.30% Mismatches: 18
Query Match: 66.18% Indels: 0
DB: 14 Gaps: 0

US-09-910-208B-1 (1-276) x US-10-077-600-2 (1-92)
QY 1 ATGACTAGCTGGAGATCACCTGGAGGAATCATCAACATCTTCCACAGTACTCCGTT 60
Db 1 MetThrLysLeuGluGluHisLeuGluGlyIleAsnIlePheHisGlnTyrSerVal 20
QY 61 CCGGTGGGGCATTTTCGACACCTCAACAGCGTGAAGCTGAGCGAGCTGATCACAAGGA 120
Db 21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGlu 40
QY 121 CTTCCTGATAAAGACGCGCTGAGCTTTGAGGAATTCGTAGTCTCTGTTCCAGG 180
Db 41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60
QY 181 CTGGATCCGATAAAGACGCGCTGAGCTTTGAGGAATTCGTAGTCTCTGTTCCAGG 240
Db 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80
QY 241 GTGCTGAAAACAGCCCATAGATATCCAAAGAG 276
Db 81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92

RESULT 10
US-09-826-589-2
; FILE REFERENCE: 0575/55873-B-PCT-US
; CURRENT APPLICATION NUMBER: US/10/665,867
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US/09/826,589
; PRIOR FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Bovine
US-10-665-867-4

Alignment Scores:
Pred. No.: 5,348-45 Length: 90
Score: 460.00 Matches: 90
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 95.44% Indels: 0
DB: 16 Gaps: 0

US-09-910-208B-1 (1-276) x US-10-665-867-4 (1-90)
QY 4 ACTAGCTGGAGATCACCTGGAGGAATCATCAACATCTTCCACAGTACTCCGTTCCG 63
Db 1 ThrLysLeuGluAspHisLeuGluGlyIleAsnIlePheHisGlnTyrSerValArg 20
QY 64 GTGGGGCATTTTCGACACCTCAACAGCGTGAAGCTGAGCGAGCTGATCACAAGGAAC 123
Db 21 ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40
QY 124 CCCAAACCTCCAGAACACCAACATCAACCTACCTTGCACAAATATTTCCAAAGAC 180
Db 41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60
QY 181 CTGGATCCGATAAAGACGCGCTGAGCTTTGAGGAATTCGTAGTCTCTGTTCCAGG 240
Db 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80
QY 241 GTGCTGAAAACAGCCCATAGATATCCAAAGAG 276
Db 81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92

RESULT 10
US-09-826-589-2
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; Sequence 2, Application US/09826589
; Patent No. US20020106726A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Ann Marie
; TITLE OF INVENTION: EXTRACELLULAR NOVEL RAGE BINDING PROTEIN (EN-RAGE) AND USES THERE
; FILE REFERENCE: 0575/5873-B-PCT-US
; CURRENT APPLICATION NUMBER: US/09/826,589
; CURRENT FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Human
; NAME/KEY: MISC FEATURE
; LOCATION: (47)..(47)
; OTHER INFORMATION: x=any amino acid
US-09-826-589-2

Alignment Scores:
Pred. No.: 4,45e-18 Length: 50
Score: 230.00 Matches: 46
Percent Similarity: 92.00% Conservatives: 0
Best Local Similarity: 92.00% Mismatches: 4
Query Match: 47.72% Indels: 0
DB: Gaps: 0

US-09-910-208B-1 (1-276) x US-09-826-589-2 (1-50)

QY 4 ACTAAGCTGGAAGATCACCTGGAGGGAATCATCAACATCTTCCACCAGTACTCCGTTCCG 63
Db 1 ThrLysLeuGluAspHisLeuGluGlyIlelleAsnIleGlyHisGlnTyrSerValArg 20
QY 64 GTGGGGCATTTTCGACACCCCTCAACAGCGTGAAGCTGATCATCAAGGAACCTT 123
Db 21 ValGlyHisPheAspThrLeuAsnLysTyrGluLeuLysGlnLeuGlyThrLysGluLeu 40
QY 124 CCCAAACCCCTCCAGAACACCAAGATCAA 153
Db 41 ProlYsThrLeuGlnAsn***LysAspGln 50

RESULT 11
US-09-872-185B-9
; Sequence 9, Application US/09872185B
; Patent No. US20020122799A1
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Herold, Kevin
; APPLICANT: Yan, Shi Du
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Lamster, Ira
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATION
; FILE REFERENCE: 0575/64080
; CURRENT APPLICATION NUMBER: US/09/872,185B
; CURRENT FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Bovine
; NAME/KEY: MISC FEATURE
; LOCATION: (47)..(47)
; OTHER INFORMATION: Where Xaa = unknown
US-09-872-185B-9

Alignment Scores:
Pred. No.: 4,45e-18 Length: 50
Score: 230.00 Matches: 46
Percent Similarity: 92.00% Conservatives: 0

Best Local Similarity: 92.00% Mismatches: 4
Query Match: 47.72% Indels: 0
DB: Gaps: 0

US-09-910-208B-1 (1-276) x US-09-872-185B-9 (1-50)

QY 4 ACTAAGCTGGAAGATCACCTGGAGGGAATCATCAACATCTTCCACCAGTACTCCGTTCCG 63
Db 1 ThrLysLeuGluAspHisLeuGluGlyIlelleAsnIleGlyHisGlnTyrSerValArg 20
QY 64 GTGGGGCATTTTCGACACCCCTCAACAGCGTGAAGCTGATCATCAAGGAACCTT 123
Db 21 ValGlyHisPheAspThrLeuAsnLysTyrGluLeuLysGlnLeuGlyThrLysGluLeu 40
QY 124 CCCAAACCCCTCCAGAACACCAAGATCAA 153
Db 41 ProlYsThrLeuGlnAsn***LysAspGln 50

RESULT 12
US-10-666-513-2
; Sequence 2, Application US/10666513
; Publication No. US20040043412A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Ann Marie
; TITLE OF INVENTION: Extracellular No. US20040043412A1el RAGE Binding Protein (EN-RAG
; TITLE OF INVENTION: Uses Thereof
; FILE REFERENCE: 0575/55873
; CURRENT APPLICATION NUMBER: US/10/666,513
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/167,705B
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Human
; NAME/KEY: UNSURE
; LOCATION: (47)
; OTHER INFORMATION: Xaa at this position is unknown
US-10-666-513-2

Alignment Scores:
Pred. No.: 4,45e-18 Length: 50
Score: 230.00 Matches: 45
Percent Similarity: 92.00% Conservatives: 0
Best Local Similarity: 92.00% Mismatches: 4
Query Match: 47.72% Indels: 0
DB: Gaps: 0

US-09-910-208B-1 (1-276) x US-10-666-513-2 (1-50)

QY 4 ACTAAGCTGGAAGATCACCTGGAGGGAATCATCAACATCTTCCACCAGTACTCCGTTCCG 63
Db 1 ThrLysLeuGluAspHisLeuGluGlyIlelleAsnIleGlyHisGlnTyrSerValArg 20
QY 64 GTGGGGCATTTTCGACACCCCTCAACAGCGTGAAGCTGATCATCAAGGAACCTT 123
Db 21 ValGlyHisPheAspThrLeuAsnLysTyrGluLeuLysGlnLeuGlyThrLysGluLeu 40
QY 124 CCCAAACCCCTCCAGAACACCAAGATCAA 153
Db 41 ProlYsThrLeuGlnAsn***LysAspGln 50

RESULT 13
US-10-665-867-2
; Sequence 2, Application US/10665867
; Publication No. US20040121372A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Stern, David

```
; TITLE OF INVENTION: EXTRACELLULAR NOVEL RAGE BINDING PROTEIN (EN-RAGE) AND USES THERE
; FILE REFERENCE: 0575/55873-B-PCT-US
; CURRENT APPLICATION NUMBER: US/10/665,867
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US/09/826,589
; PRIOR FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Human
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (47)..(47)
; OTHER INFORMATION: x=any amino acid
US-10-665-867-2

Alignment Scores:
Pred. No.: 4,45e-18 Length: 50
Score: 230.00 Matches: 46
Percent Similarity: 92.00% Conservative: 0
Best Local Similarity: 92.00% Mismatches: 4
Query Match: 47.72% Indels: 0
DB: 16 Gaps: 0

US-09-910-208B-1 (1-276) x US-10-665-867-2 (1-50)

QY 4 ACTAAGCTGGAGATCACTGGAGGGAATCATCAACATCTTCCACGATCTCCGTTCCG 63
Db 1 ThrLysLeuGluAspHisLeuGluGlyIleAsnIleGlyHisGlnTy-SerValArg 20
QY 64 GTGGGGCATTTTCGACACCTCAACAGCGTGAGCTGAGCGAGCTGATCACAAGGAAGCTT 123
Db 21 ValGlyHisPheAspThrLeuAsnLysTyrgluLeuLysGlnLeuGlyThrLysGluLeu 40
QY 124 CCCAAACCCCTCCAGAACACCAAGATCAAA 153
Db 41 ProlLysThrLeuGlnAsn**LysAspGln 50

RESULT 14
US-09-214-272-4
; Sequence 4, Application US/09214272
; Publication No. US20010007674A1
; GENERAL INFORMATION:
; APPLICANT: Siegenthaler, Georges
; TITLE OF INVENTION: Isolated Arachidonic Acid-Binding Heteromer and its Use in
; FILE REFERENCE: 016800-254
; CURRENT APPLICATION NUMBER: US/09/214,272
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: PCT/FR97/01164
; PRIOR FILING DATE: 1997-06-30
; PRIOR APPLICATION NUMBER: FR 96/08219
; PRIOR FILING DATE: 1996-07-02
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of MRP-14.
US-09-214-272-4

Alignment Scores:
Pred. No.: 8e-16 Length: 114
Score: 211.50 Matches: 41
Percent Similarity: 71.74% Conservative: 25
Best Local Similarity: 44.57% Mismatches: 25
Query Match: 43.88% Indels: 1
DB: 9 Gaps: 1

; TITLE OF INVENTION: MRP8/MRP14 heterodimer, or its
; TITLE OF INVENTION: individual components in combination, for treating and/or
; TITLE OF INVENTION: preventing skin diseases, wounds and/or wound-healing
; TITLE OF INVENTION: disturbances, having a reduced quantity of MRP8/MRP14
; TITLE OF INVENTION: heterodimers
; FILE REFERENCE: 50125/031002
; CURRENT APPLICATION NUMBER: US/10/134,841
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: US 60/322,925
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: DE 10121254.2
; PRIOR FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-134-841-4

Alignment Scores:
Pred. No.: 8e-16 Length: 114
Score: 211.50 Matches: 41
Percent Similarity: 71.74% Conservative: 25
Best Local Similarity: 44.57% Mismatches: 25
Query Match: 43.88% Indels: 1
DB: 14 Gaps: 1

US-09-910-208B-1 (1-276) x US-10-134-841-4 (1-114)

QY 1 ATGACTAAGCTGGAGATCACTGGAGGGAATCATCAACATCTTCCACGATCTCCGTT 60
Db 5 MetSerGlnLeuGluArgAsnIleGluThrIleAsnThrPheHisGlnTy-SerVal 24
QY 61 CGGTGGGGCATTTTCGACACCTCAACAGCGTGAGCTGAGCGAGCTGATCACAAGGAA 120
Db 25 LysLeuGlyHisProAspThrLeuAsnGlnGlyGluPheLysGluLeuValArgLysAsp 44
QY 121 CTTCCCAAAACCCCTC---CAGAACACCAAGATCAACCTACCATTTGACAAATATTC 177
Db 45 LeuGlnAsnPheLeuLysLysGluAsnLysValIleGluHisIleMetGlu 64
QY 178 GACCTGATCCGATAAAGCGGAGCGCTGAGCTTTCAGGAAATTCGATGCTGGTGCC 237
Db 65 AspLeuAspThrAsnAlaAspLysGlnLeuSerPheGluGluPheIleMetLeuMetAla 84
QY 238 AGGTGCTGAAACACAGCCCATAGATATCCACAAA 273
Db 85 ArgLeuThrTrpAlaSerHisGluLysMetHisGlu 96

RESULT 15
US-10-134-841-4
; Sequence 4, Application US/10134841
; Publication No. US20030003482A1
; GENERAL INFORMATION:
; APPLICANT: HALLIE, JORN-PETER
; TITLE OF INVENTION: MRP8/MRP14 heterodimer, or its
; TITLE OF INVENTION: individual components in combination, for treating and/or
; TITLE OF INVENTION: preventing skin diseases, wounds and/or wound-healing
; TITLE OF INVENTION: disturbances, having a reduced quantity of MRP8/MRP14
; TITLE OF INVENTION: heterodimers
; FILE REFERENCE: 50125/031002
; CURRENT APPLICATION NUMBER: US/10/134,841
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: US 60/322,925
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: DE 10121254.2
; PRIOR FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-134-841-4

Alignment Scores:
Pred. No.: 8e-16 Length: 114
Score: 211.50 Matches: 41
Percent Similarity: 71.74% Conservative: 25
Best Local Similarity: 44.57% Mismatches: 25
Query Match: 43.88% Indels: 1
DB: 14 Gaps: 1

US-09-910-208B-1 (1-276) x US-10-134-841-4 (1-114)

QY 1 ATGACTAAGCTGGAGATCACTGGAGGGAATCATCAACATCTTCCACGATCTCCGTT 60
Db 5 MetSerGlnLeuGluArgAsnIleGluThrIleAsnThrPheHisGlnTy-SerVal 24
QY 61 CGGTGGGGCATTTTCGACACCTCAACAGCGTGAGCTGAGCGAGCTGATCACAAGGAA 120
Db 25 LysLeuGlyHisProAspThrLeuAsnGlnGlyGluPheLysGluLeuValArgLysAsp 44
QY 121 CTTCCCAAAACCCCTC---CAGAACACCAAGATCAACCTACCATTTGACAAATATTC 177
Db 45 LeuGlnAsnPheLeuLysLysGluAsnLysValIleGluHisIleMetGlu 64
QY 178 GACCTGATCCGATAAAGCGGAGCGCTGAGCTTTCAGGAAATTCGATGCTGGTGCC 237
Db 65 AspLeuAspThrAsnAlaAspLysGlnLeuSerPheGluGluPheIleMetLeuMetAla 84
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Db 65 AspLeuAspThrAsnAlaAspLysGlnLeuSerPheGluGluPheIleMetLeuMetAla 84
QY 238 AGGGTGCTGAAACAGCCACATAGATATCCACAAA 273
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Db 85 ArgLeuThrTrpAlaSerHisGluLysMetHisGlu 96

Search completed: February 23, 2005, 11:39:22
Job time : 90 secs

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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: February 23, 2005, 11:12:49 ; Search time 29.5 Seconds

(without alignments)

1396.823 Million cell updates/sec

Title: US-09-910-208B-1

Perfect score: 482

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Ygapop 10.0, Ygapext 0.5

Fgapop 6.0, Fgapext 7.0

Delop 6.0, Delext 7.0

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 1027090

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=HADDAD-09-910208 @CGN 1.1 46 @runat_23022005_101806_14745 -NCPUs=6
-ICPU=3 -NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSBBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents AA:*
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2: /cgn2_6/prodata/1/iaa/5B_COMB.pep:*
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6: /cgn2_6/prodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	470	97.5	92	2	US-08-568-310D-19
2	470	97.5	92	3	US-09-270-455-19
3	460	95.4	90	4	US-09-263-312-3
4	460	95.4	90	4	US-09-826-589-3
5	460	95.4	90	4	US-09-826-589-4
6	371	77.0	91	3	US-08-794-000-2
7	371	77.0	91	4	US-09-646-651C-1
8	319	66.2	92	2	US-08-568-310D-20
9	319	66.2	92	3	US-09-270-455-20
10	266	55.2	51	2	US-08-568-310D-2
11	266	55.2	51	3	US-09-270-455-2
12	230	47.7	50	4	US-09-263-312-2

13	230	47.7	50	4	US-09-826-589-2	Sequence 2, Appli
14	211.5	43.9	114	1	US-08-385-241-3	Sequence 3, Appli
15	211.5	43.9	114	4	US-09-214-272-4	Sequence 4, Appli
16	211.5	43.9	114	4	US-09-806-382A-4	Sequence 4, Appli
17	204.5	42.4	109	1	US-07-987-272A-8	Sequence 8, Appli
18	190.5	39.5	113	2	US-08-918-727-7	Sequence 7, Appli
19	190.5	39.5	113	3	US-09-205-680A-7	Sequence 7, Appli
20	187	38.8	95	4	US-09-919-172-102	Sequence 102, App
21	187	38.8	95	4	US-09-976-594-467	Sequence 467, App
22	187	38.8	102	4	US-09-949-016-10557	Sequence 10557, A
23	184	38.2	92	2	US-09-051-589-1	Sequence 1, Appli
24	180	37.3	92	2	US-08-918-727-5	Sequence 5, Appli
25	180	37.3	92	3	US-09-205-680A-5	Sequence 5, Appli
26	180	37.3	92	4	US-09-919-039-184	Sequence 184, App
27	175	36.3	91	1	US-07-987-272A-11	Sequence 11, Appli
28	170	35.3	88	1	US-07-987-272A-1	Sequence 1, Appli
29	170	35.3	89	1	US-07-987-272A-14	Sequence 14, Appli
30	163	33.8	131	4	US-09-949-016-11241	Sequence 11241, A
31	160	33.2	31	2	US-08-568-310D-6	Sequence 6, Appli
32	160	33.2	31	3	US-09-270-455-6	Sequence 6, Appli
33	160	33.2	74	4	US-09-513-999C-5490	Sequence 5490, Ap
34	160	33.2	93	1	US-07-987-272A-7	Sequence 7, Appli
35	160	33.2	93	1	US-07-987-272A-16	Sequence 16, Appli
36	160	33.2	93	1	US-08-385-241-1	Sequence 1, Appli
37	160	33.2	93	4	US-09-214-272-2	Sequence 2, Appli
38	160	33.2	93	4	US-09-806-382A-3	Sequence 3, Appli
39	153	31.7	101	1	US-08-190-560-2	Sequence 2, Appli
40	153	31.7	101	1	US-08-469-277-2	Sequence 2, Appli
41	153	31.7	101	2	US-08-468-946-2	Sequence 2, Appli
42	153	31.7	101	2	US-08-468-942-2	Sequence 2, Appli
43	153	31.7	101	4	US-09-298-625-2	Sequence 2, Appli
44	145	30.1	75	1	US-07-987-272A-12	Sequence 12, Appli
45	144	29.9	76	1	US-07-987-272A-17	Sequence 17, Appli

ALIGNMENTS

RESULT 1
US-08-568-310D-19
; Sequence 19, Application US/08568310D
; Patent No. 5976832
; GENERAL INFORMATION:
; APPLICANT: HITOMI, JIRO
; APPLICANT: YAMAGUCHI, KEN
; APPLICANT: YAMAMURA, TOKUJIRO
; APPLICANT: KIMURA, TATSUJI
; TITLE OF INVENTION: NOVEL CALCIUM-BINDING PROTEINS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WYATT, GERBER, MELLER & O'ROURKE
; STREET: 99 PARK AVENUE
; STREET: 6th FLOOR
; CITY: NEW YORK CITY
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH, 720 Kb
; MEDIUM TYPE: STORAGE
; COMPUTER: IBM-PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS 6.2
; SOFTWARE: WORDPERFECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/568,310D
; FILING DATE: DECEMBER 6, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 7-70468 and 7-45564 (both Japan)
; FILING DATE: 3/6/95 and 3/6/95, respectively
; ATTORNEY/AGENT INFORMATION:
; NAME: KLEIN, MILTON
; REGISTRATION NUMBER: 27101
; REFERENCE/DOCKET NUMBER: 3316

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)953-3350
TELEFAX: (212)953-3352
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 92
TYPE: amino acid
STRANDEDNESS: linear
MOLECULE TYPE: cDNA
PUBLICATION INFORMATION:
RELEVANT RESIDUES IN SEQ ID NO: 19:
FROM 1 TO 92

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/568,310
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: KLEIN, MILTON
REGISTRATION NUMBER: 27101
REFERENCE/DOCKET NUMBER: 3316
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)953-3350
TELEFAX: (212)953-3352
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 92
TYPE: amino acid
STRANDEDNESS: linear
MOLECULE TYPE: cDNA
PUBLICATION INFORMATION:
RELEVANT RESIDUES IN SEQ ID NO: 19:
FROM 1 TO 92

US-08-568-310D-19
Alignment Scores:
Pred. No.: 3.95e-53 Length: 92
Score: 470.00 Matches: 92
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 97.51% Indels: 0
DB: 2 Gaps: 0

US-09-270-455-19
Alignment Scores:
Pred. No.: 3.95e-53 Length: 92
Score: 470.00 Matches: 92
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 97.51% Indels: 0
DB: 3 Gaps: 0

US-09-910-208B-1 (1-276) x US-08-568-310D-19 (1-92)
QY 1 ATGACTAAGCTGGAGATCACTGGAGGAATCATCAACATCTTCCACGACTCTCGTT 60
Db 1 MetThrLysLeuGluAspHisLeuGluGlyllelleAenillePheHisGlnrSerVal 20

QY 61 CGGTGGGGCATTTTCACACCCCTCAACAGCGTGGAGCTGAAGCAGCTGATCACAAGGAA 120
Db 21 ArgValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuLeuThrLysGlu 40

QY 121 CTTCCAAAACCTCCAGAACCAAGATCACTACCATTCGACAAATATTCACAGAC 180
Db 41 LeuProLysThrLeuGlnAsnThrLysAspGlnProThrLysAspLysPheGlnAsp 60

QY 181 CTGGATCGCGATAAGAGCGGCGCTCAGCTTTGAGGAATTCGTAGTCTCGTGCCAGG 240
Db 61 LeuAspAlaAspLysAspGlyAlaValSerPheGluGluPheValLeuValSerArg 80

QY 241 GTGCTGAAACAGCCCATAGATATCCAAAAGAG 276
Db 81 ValLeuLysThrAlaHisLeuAspLysGlu 92

RESULT 2
US-09-270-455-19
Sequence 19, Application US/09270455
Patent No. 6313267
GENERAL INFORMATION:
APPLICANT: HITOMI, JIRO
APPLICANT: YAMAGUCHI, KEN
APPLICANT: YAMAMURA, TOKUJI
APPLICANT: KIMURA, TATSUJI
TITLE OF INVENTION: NOVEL CALCIUM-BINDING PROTEINS
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: WYATT GERBER, MELLER & O'ROURKE
STREET: 99 PARK AVENUE
STREET: 6th FLOOR
CITY: NEW YORK CITY
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH, 720 Kb
MEDIUM TYPE: STORAGE
COMPUTER: IBM-PC COMPATIBLE
OPERATING SYSTEM: PC-DOS 6.2
SOFTWARE: WORDPERFECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/270,455
FILING DATE:

US-09-910-208B-1 (1-276) x US-09-270-455-19 (1-92)
QY 1 ATGACTAAGCTGGAGATCACTGGAGGAATCATCAACATCTTCCACGACTCTCGTT 60
Db 1 MetThrLysLeuGluAspHisLeuGluGlyllelleAenillePheHisGlnrSerVal 20

QY 61 CGGTGGGGCATTTTCACACCCCTCAACAGCGTGGAGCTGAAGCAGCTGATCACAAGGAA 120
Db 21 ArgValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuLeuThrLysGlu 40

QY 121 CTTCCAAAACCTCCAGAACCAAGATCACTACCATTCGACAAATATTCACAGAC 180
Db 41 LeuProLysThrLeuGlnAsnThrLysAspGlnProThrLysAspLysPheGlnAsp 60

QY 181 CTGGATCGCGATAAGAGCGGCGCTCAGCTTTGAGGAATTCGTAGTCTCGTGCCAGG 240
Db 61 LeuAspAlaAspLysAspGlyAlaValSerPheGluGluPheValLeuValSerArg 80

QY 241 GTGCTGAAACAGCCCATAGATATCCAAAAGAG 276
Db 81 ValLeuLysThrAlaHisLeuAspLysGlu 92

RESULT 3
US-09-263-312-3
Sequence 3, Application US/09263312
Patent No. 655340
GENERAL INFORMATION:
APPLICANT: Schmidt, Ann Marie
APPLICANT: Stern, David
TITLE OF INVENTION: Extracellular No. 655340el RAGE Binding Protein (EN-RAGE) and
TITLE OF INVENTION: Uses Thereof
FILE REFERENCE: 0575/55873-A
CURRENT APPLICATION NUMBER: US/09/263,312
CURRENT FILING DATE: 1999-03-05
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 90
TYPE: PRT
ORGANISM: Human
US-09-263-312-3
Alignment Scores:

US-09-263-312-3
Sequence 3, Application US/09263312
Patent No. 655340
GENERAL INFORMATION:
APPLICANT: Schmidt, Ann Marie
APPLICANT: Stern, David
TITLE OF INVENTION: Extracellular No. 655340el RAGE Binding Protein (EN-RAGE) and
TITLE OF INVENTION: Uses Thereof
FILE REFERENCE: 0575/55873-A
CURRENT APPLICATION NUMBER: US/09/263,312
CURRENT FILING DATE: 1999-03-05
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 90
TYPE: PRT
ORGANISM: Human
US-09-263-312-3
Alignment Scores:

Pred. No.: 8.06e-52 Length: 90
Score: 460.00 Matches: 90
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 95.44% Indels: 0
DB: 4 Gaps: 0

US-09-910-208B-1 (1-276) x US-09-263-312-3 (1-90)

QY 4 ACTAAGCTGAAGATCACCTGAGGGAATCATCAATCTCCACAGTACTCCGTTCCG 63
DB 1 ThrLysLeuGluAspHisLeuGluGlyIleAsnIlePheHisGlnTyrSerValArg 20
QY 64 GTGGGGCATTTTCGACACCTTCAACAGCGTGAAGCTGATCAACAAAGAACTT 123
DB 21 ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40
QY 124 CCCAAACCTTCAGAACACCAAGATCAACCTTACCAATTCAGAAATATTCACAGCTG 183
DB 41 ProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAspLeu 60
QY 184 GATCGCGATAAAGACGGAGCGCTGAGCTTTGAGGAATTCGTAGTCTCGTGTCCAGGGTG 243
DB 61 AspAlaAspLysAspGlyAlaValSerPheGluGluPheValValLeuValSerArgVal 80
QY 244 CTGAAACAGCCCATAGATATCCACAA 273
DB 81 LeuLysThrAlaHisIleAspIleHisLys 90

RESULT 4

US-09-826-589-3 ;
; Sequence 3, Application US/09826589
; Patent No. 6670136

GENERAL INFORMATION:

; APPLICANT: Schmidt, Ann Marie

; APPLICANT: Stern, David

; TITLE OF INVENTION: EXTRACELLULAR NOVEL RAGE BINDING PROTEIN (EN-RAGE) AND USES THERE

; FILE REFERENCE: 0575/55873-B-PCT-US

; CURRENT APPLICATION NUMBER: US/09/826,589

; CURRENT FILING DATE: 2001-04-05

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: Patent in version 3.1

; SEQ ID NO 3

; LENGTH: 90

; TYPE: PRT

; ORGANISM: Bovine

US-09-826-589-3

Alignment Scores:

Pred. No.: 8.06e-52 Length: 90
Score: 460.00 Matches: 90
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 95.44% Indels: 0
DB: 4 Gaps: 0

US-09-910-208B-1 (1-276) x US-09-826-589-3 (1-90)

QY 4 ACTAAGCTGAAGATCACCTGAGGGAATCATCAATCTCCACAGTACTCCGTTCCG 63
DB 1 ThrLysLeuGluAspHisLeuGluGlyIleAsnIlePheHisGlnTyrSerValArg 20
QY 64 GTGGGGCATTTTCGACACCTTCAACAGCGTGAAGCTGATCAACAAAGAACTT 123
DB 21 ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40
QY 124 CCCAAACCTTCAGAACACCAAGATCAACCTTACCAATTCAGAAATATTCACAGCTG 183
DB 41 ProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAspLeu 60
QY 184 GATCGCGATAAAGACGGAGCGCTGAGCTTTGAGGAATTCGTAGTCTCGTGTCCAGGGTG 243
DB 61 AspAlaAspLysAspGlyAlaValSerPheGluGluPheValValLeuValSerArgVal 80

QY 244 CTGAAACAGCCCATAGATATCCACAA 273
DB 81 LeuLysThrAlaHisIleAspIleHisLys 90

RESULT 5

US-09-826-589-4

; Sequence 4, Application US/09826589

; Patent No. 6670136

; GENERAL INFORMATION:

; APPLICANT: Schmidt, Ann Marie

; APPLICANT: Stern, David

; TITLE OF INVENTION: EXTRACELLULAR NOVEL RAGE BINDING PROTEIN (EN-RAGE) AND USES THERE

; FILE REFERENCE: 0575/55873-B-PCT-US

; CURRENT APPLICATION NUMBER: US/09/826,589

; CURRENT FILING DATE: 2001-04-05

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: Patent in version 3.1

; SEQ ID NO 4

; LENGTH: 90

; TYPE: PRT

; ORGANISM: Bovine

US-09-826-589-4

Alignment Scores:

Pred. No.: 8.06e-52 Length: 90
Score: 460.00 Matches: 90
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 95.44% Indels: 0
DB: 4 Gaps: 0

US-09-910-208B-1 (1-276) x US-09-826-589-4 (1-90)

QY 4 ACTAAGCTGAAGATCACCTGAGGGAATCATCAATCTCCACAGTACTCCGTTCCG 63
DB 1 ThrLysLeuGluAspHisLeuGluGlyIleAsnIlePheHisGlnTyrSerValArg 20
QY 64 GTGGGGCATTTTCGACACCTTCAACAGCGTGAAGCTGATCAACAAAGAACTT 123
DB 21 ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40
QY 124 CCCAAACCTTCAGAACACCAAGATCAACCTTACCAATTCAGAAATATTCACAGCTG 183
DB 41 ProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAspLeu 60
QY 184 GATCGCGATAAAGACGGAGCGCTGAGCTTTGAGGAATTCGTAGTCTCGTGTCCAGGGTG 243
DB 61 AspAlaAspLysAspGlyAlaValSerPheGluGluPheValValLeuValSerArgVal 80

RESULT 6

US-08-794-000-2

; Sequence 2, Application US/08794000

; Patent No. 6687123

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: Metal-Containing Ribonucleotide Polypeptides

; NUMBER OF SEQUENCES: 4

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/794,000

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/DE96/01337

; FILING DATE: 17-JUL-1996

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;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 195 25 992.0
; FILING DATE: 17-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 195 30 500.0
; FILING DATE: 18-AUG-1995
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 91 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-794-000-2

Alignment Scores:
Pred. No.: 4.02e-40 Length: 91
Score: 371.00 Matches: 74
Percent Similarity: 91.21% Conservative: 9
Best Local Similarity: 81.32% Mismatches: 8
Query Match: 76.97% Indels: 0
DB: 3 Gaps: 0

US-09-910-208B-1 (1-276) x US-08-794-000-2 (1-91)
Qy 4 ACTAGCTGGAGATCACCTGGAGGAGATCATCAACATCTTCCACAGTACTCGTTGG 63
Db 1 ThrLysLeuGluAspHisLeuGluGlylleleasnillePheHisGlnTyrSerValArg 20
Qy 64 GTGGGGCATTTCGACACCCCTCAACAGCGTGAGCTGAAGCAGCTGATCACAAGAACTT 123
Db 21 LeuGlyHisTyrAspThrLeuIleLysArgGluLeuLysGlnLeuLeuThrLysGluLeu 40
Qy 124 CCCAAACCTCCAGAACACCAAGATCAACCTACCATTCGACAAATATTCACAGACCTG 183
Db 41 ProAsnThrLeuLysAsnThrLysAspGlnGlyThrIleAspLysIlePheGlnAsnLeu 60
Qy 184 GATCCGATTAAGACGGAGCGCTCAGCTTTGAGGAATTCGTAGTCTCTGTCCTCAGGGTG 243
Db 61 AspAlaAsnGlnAspGluGlnValSerPheLysGluPheValValLeuValThrAspVal 80
Qy 244 CTGAAACAGCCCATAGATATCCACAAAGAG 276
Db 81 LeuIleThrAlaHisAspAsnIleHisLysGlu 91

RESULT 7
US-09-646-651C-1
; Sequence 1, Application US/09646651C
; Patent No. 6770455
; GENERAL INFORMATION:
; APPLICANT: Klesewetter, Stefan
; APPLICANT: Kuhn, Eckehard
; APPLICANT: Koch-Pelster, Brigitte
; APPLICANT: Brunner, Herwig
; TITLE OF INVENTION: METAL-CONTAINING RIBONUCLEOTIDE POLYPEPTIDES
; FILE REFERENCE: 206579
; CURRENT APPLICATION NUMBER: US/09/646,651C
; CURRENT FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: PCT/EP98/07722
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: DE 198 11 047.2
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..()
; OTHER INFORMATION: Angiotropin-related protein
; US-09-646-651C-1
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Alignment Scores:
Pred. No.: 4.02e-40 Length: 91
Score: 371.00 Matches: 74
Percent Similarity: 91.21% Conservative: 9
Best Local Similarity: 81.32% Mismatches: 8
Query Match: 76.97% Indels: 0
DB: 4 Gaps: 0

US-09-910-208B-1 (1-276) x US-09-646-651C-1 (1-91)
Qy 4 ACTAAGCTGGAAGATCACCTGGAGGAGATCATCAACATCTTCCACAGTACTCGTTGG 63
Db 1 ThrLysLeuGluAspHisLeuGluGlylleleasnillePheHisGlnTyrSerValArg 20
Qy 64 GTGGGGCATTTCGACACCCCTCAACAGCGTGAGCTGAAGCAGCTGATCACAAGAACTT 123
Db 21 LeuGlyHisTyrAspThrLeuIleLysArgGluLeuLysGlnLeuLeuThrLysGluLeu 40
Qy 124 CCCAAACCTCCAGAACACCAAGATCAACCTACCATTCGACAAATATTCACAGACCTG 183
Db 41 ProAsnThrLeuLysAsnThrLysAspGlnGlyThrIleAspLysIlePheGlnAsnLeu 60
Qy 184 GATCCGATTAAGACGGAGCGCTCAGCTTTGAGGAATTCGTAGTCTCTGTCCTCAGGGTG 243
Db 61 AspAlaAsnGlnAspGluGlnValSerPheLysGluPheValValLeuValThrAspVal 80
Qy 244 CTGAAACAGCCCATAGATATCCACAAAGAG 276
Db 81 LeuIleThrAlaHisAspAsnIleHisLysGlu 91

RESULT 8
US-08-568-310D-20
; Sequence 20, Application US/08568310D
; Patent No. 5976832
; GENERAL INFORMATION:
; APPLICANT: HITOMI, JIRO
; APPLICANT: YAMAGUCHI, KEN
; APPLICANT: YAMAMURA, TOKUJIRO
; APPLICANT: KIMURA, TATSUJI
; TITLE OF INVENTION: NOVEL CALCIUM-BINDING PROTEINS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WYATT GERBER, MELLER & O'ROURKE
; STREET: 99 PARK AVENUE
; CITY: NEW YORK CITY
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH, 720 Kb
; MEDIUM TYPE: STORAGE
; COMPUTER: IBM-PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS 6.2
; SOFTWARE: WORDPERFECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/568,310D
; FILING DATE: DECEMBER 6, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 7-70468 and 7-45564 (both Japan)
; FILING DATE: 3/6/95 and 3/6/95, respectively
; ATTORNEY/AGENT INFORMATION:
; NAME: KLEIN, MILTON
; REGISTRATION NUMBER: 27101
; REFERENCE/DOCKET NUMBER: 3316
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)953-3350
; TELEFAX: (212)953-3352
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 92
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/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ PUBLICATION INFORMATION:
/ RELEVANT RESIDUES IN SEQ ID NO: 20:
/ RELEVANT RESIDUES IN SEQ ID NO: FROM 1 TO 92
US-08-568-310D-20

Alignment Scores:
Pred. No.: 2,75e-33 Length: 92
Score: 319.00 Matches: 61
Percent Similarity: 80.43% Conservative: 13
Best Local Similarity: 66.30% Mismatches: 18
Query Match: 66.18% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-1 (1-276) x US-08-568-310D-20 (1-92)
QY 1 ATGACTAAGCTGGAAGATCACCTGGAGGGAATCATCAACATCTTCCACCAGTACTCCGTT 60
Db 1 MetThrLysLeuGluGluHisLeuGluGlyLeuValAsnIlePheHisGlnTyrSerVal 20
QY 61 CGGGTGGGGCATTTCGACACCTCAACAAAGCGTGAAGCAGCTGATCAAAAGGAA 120
Db 21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGlu 40
QY 121 CTTCCCAAAACCTCCAGAACCAACCAAGATCAACCTACCATTCGACAAATATTTCCAAGAC 180
Db 41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60
QY 181 CTGGATCGCGATAAAGACGGAGCGTCAGCTTTGAGGAATTCGTAGTCTCGTGTGCCAGG 240
Db 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80
QY 241 GTGCTGAAACAGCCCATAGATATCCACAAAGAG 276
Db 81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92

RESULT 9
US-09-270-455-20
/ Sequence 20, Application US/09270455
/ Patent No. 6313267
/ GENERAL INFORMATION:
/ APPLICANT: HITOMI, JIRO
/ APPLICANT: YAMAGUCHI, KEN
/ APPLICANT: YAMAMURA, TOKUJIRO
/ APPLICANT: KIMURA, TATSUJI
/ TITLE OF INVENTION: NOVEL CALCIUM-BINDING PROTEINS
/ NUMBER OF SEQUENCES: 20
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: WYATT, GERBER, MELLER & O'ROURKE
/ STREET: 99 PARK AVENUE
/ STREET: 6th FLOOR
/ CITY: NEW YORK CITY
/ STATE: NEW YORK
/ COUNTRY: USA
/ ZIP: 10016
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: DISKETTE, 3.50 INCH, 720 KB
/ MEDIUM TYPE: STORAGE
/ COMPUTER: IBM-PC COMPATIBLE
/ OPERATING SYSTEM: PC-DOS 6.2
/ SOFTWARE: WORDPERFECT 6.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/270,455
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/568,310
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: KLEIN, MILTON

/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ PUBLICATION INFORMATION:
/ RELEVANT RESIDUES IN SEQ ID NO: 20:
/ RELEVANT RESIDUES IN SEQ ID NO: FROM 1 TO 92
US-08-568-310D-20

Alignment Scores:
Pred. No.: 2,75e-33 Length: 92
Score: 319.00 Matches: 61
Percent Similarity: 80.43% Conservative: 13
Best Local Similarity: 66.30% Mismatches: 18
Query Match: 66.18% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-1 (1-276) x US-08-568-310D-20 (1-92)
QY 1 ATGACTAAGCTGGAAGATCACCTGGAGGGAATCATCAACATCTTCCACCAGTACTCCGTT 60
Db 1 MetThrLysLeuGluGluHisLeuGluGlyLeuValAsnIlePheHisGlnTyrSerVal 20
QY 61 CGGGTGGGGCATTTCGACACCTCAACAAAGCGTGAAGCAGCTGATCAAAAGGAA 120
Db 21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGlu 40
QY 121 CTTCCCAAAACCTCCAGAACCAACCAAGATCAACCTACCATTCGACAAATATTTCCAAGAC 180
Db 41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60
QY 181 CTGGATCGCGATAAAGACGGAGCGTCAGCTTTGAGGAATTCGTAGTCTCGTGTGCCAGG 240
Db 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80
QY 241 GTGCTGAAACAGCCCATAGATATCCACAAAGAG 276
Db 81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92

RESULT 10
US-08-568-310D-2
/ Sequence 2, Application US/08568310D
/ Patent No. 5976832
/ GENERAL INFORMATION:
/ APPLICANT: HITOMI, JIRO
/ APPLICANT: YAMAGUCHI, KEN
/ APPLICANT: YAMAMURA, TOKUJIRO
/ APPLICANT: KIMURA, TATSUJI
/ TITLE OF INVENTION: NOVEL CALCIUM-BINDING PROTEINS
/ NUMBER OF SEQUENCES: 20
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: WYATT, GERBER, MELLER & O'ROURKE
/ STREET: 99 PARK AVENUE
/ STREET: 6th FLOOR
/ CITY: NEW YORK CITY
/ STATE: NEW YORK
/ COUNTRY: USA
/ ZIP: 10016
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: DISKETTE, 3.50 INCH, 720 KB
/ MEDIUM TYPE: STORAGE
/ COMPUTER: IBM-PC COMPATIBLE
/ OPERATING SYSTEM: PC-DOS 6.2
/ SOFTWARE: WORDPERFECT 6.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/568,310D
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/568,310
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: KLEIN, MILTON
```

;; FILING DATE: DECEMBER 6, 1995
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 7-70468 and 7-45564 (both Japan)
;; FILING DATE: 3/6/95 and 3/6/95, respectively
;; ATTORNEY/AGENT INFORMATION:
;; NAME: KLEIN, MILTON
;; REGISTRATION NUMBER: 27101
;; REFERENCE/DOCKET NUMBER: 3316
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212)953-3350
;; TELEFAX: (212)953-3352
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 51
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;; PUBLICATION INFORMATION:
;; RELEVANT RESIDUES IN SEQ ID NO: 2:
;; RELEVANT RESIDUES IN SEQ ID NO: FROM 1 TO 51
US-08-568-310D-2

Alignment Scores:
Pred. No.: 2.03e-26 Length: 51
Score: 266.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 55.19% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-1 (1-276) x US-08-568-310D-2 (1-51)
QY 4 ACTAAGCTGGAAGATCACCTGGAGGGAATCATCAATCTTCCACAGTACTCCGTTCCG 63
DB 1 ThrLysLeuGluAspHisLeuGluGlyIleIleAsnIlePheHisGlnTy-SerValArg 20
QY 64 GTGGGGCATTTCCGACACCTCAACAGCGTGAAGCTGATCACAAGGAACTT 123
DB 21 ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40
QY 124 CCCAAACCTCCAGAACACCAAGATCAACCT 156
DB 41 ProLysThrLeuGlnAsnThrLysAspGlnPro 51

RESULT 11
US-09-270-455-2
; Sequence 2, Application US/09270455
; Patent No. 6313267
; GENERAL INFORMATION:
; APPLICANT: HITOMI, JIRO
; APPLICANT: YAMAGUCHI, KEN
; APPLICANT: YAMAMURA, TOKUJIRO
; APPLICANT: KIMURA, TATSUJI
; TITLE OF INVENTION: NOVEL CALCIUM-BINDING PROTEINS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WYATT, GERBER, MELLER & O'ROURKE
; STREET: 99 PARK AVENUE
; STREET: 6th FLOOR
; CITY: NEW YORK CITY
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH, 720 KB
; MEDIUM TYPE: STORAGE
; COMPUTER: IBM-PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS 6.2
; SOFTWARE: WORDPERFECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/270,455
; FILING DATE:

;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/568,310
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: KLEIN, MILTON
;; REGISTRATION NUMBER: 27101
;; REFERENCE/DOCKET NUMBER: 3316
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212)953-3350
;; TELEFAX: (212)953-3352
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 51
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;; PUBLICATION INFORMATION:
;; RELEVANT RESIDUES IN SEQ ID NO: 2: FROM 1 TO 51
US-09-270-455-2

Alignment Scores:
Pred. No.: 2.03e-26 Length: 51
Score: 266.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 55.19% Indels: 0
DB: 3 Gaps: 0

US-09-910-208B-1 (1-276) x US-09-270-455-2 (1-51)
QY 4 ACTAAGCTGGAAGATCACCTGGAGGGAATCATCAATCTTCCACAGTACTCCGTTCCG 63
DB 1 ThrLysLeuGluAspHisLeuGluGlyIleIleAsnIlePheHisGlnTy-SerValArg 20
QY 64 GTGGGGCATTTCCGACACCTCAACAGCGTGAAGCTGATCACAAGGAACTT 123
DB 21 ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40
QY 124 CCCAAACCTCCAGAACACCAAGATCAACCT 156
DB 41 ProLysThrLeuGlnAsnThrLysAspGlnPro 51

RESULT 12
US-09-263-312-2
; Sequence 2, Application US/09263312
; Patent No. 655340
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Stern, David
; TITLE OF INVENTION: Extracellular No. 655340el RAGE Binding Protein (EN-RAGE) and
; TITLE OF INVENTION: Uses Thereof
; FILE REFERENCE: 0575/55873-A
; CURRENT APPLICATION NUMBER: US/09/263,312
; CURRENT FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Human
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (47)
; OTHER INFORMATION: Xaa at this position is unknown
US-09-263-312-2

Alignment Scores:
Pred. No.: 1.08e-21 Length: 50
Score: 230.00 Matches: 46
Percent Similarity: 92.00% Conservative: 0
Best Local Similarity: 92.00% Mismatches: 4
Query Match: 47.72% Indels: 0

; TITLE OF INVENTION: Cosmetics and Pharmaceuticals
; FILE REFERENCE: 016800-254
; CURRENT APPLICATION NUMBER: US/09/214,272
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: PCT/FR97/01164
; PRIOR FILING DATE: 1997-06-30
; PRIOR APPLICATION NUMBER: FR 96/08219
; PRIOR FILING DATE: 1996-07-02
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of MRP-14.
US-09-214-272-4

Alignment Scores:
Pred. No.: 3 98e-19 Length: 114
Score: 211.50 Matches: 41
Percent Similarity: 71.74% Conservative: 25
Best Local Similarity: 44.57% Mismatches: 25
Query Match: 43.88% Indels: 1
DB: 4 Gaps: 1

US-09-910-208B-1 (1-276) x US-09-214-272-4 (1-114)

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QY 1 ATGACTAAGCTGAAGATCACCTGGAGGGAATCATCAATCTTCCACAGTACTCCGTT 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 5 MetSerGlnLeuGluArgAsnIleGluThrIleAsnThrPheHisGlnTy-SerVal 24

QY 61 CGGGTGGGGCATTTGCACACCTCAACAGCGGTGAGCTGAACGACCTGATCACAAAGGAA 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 25 LysLeuGlyHisProAspThrLeuAsnGlnGlyGluPheLysGluLeuValArgLysAsp 44

QY 121 CTTCCTCAAAACCCCTC--CAGAAACACCAAGATCAACCTTACCATTCAGCAAAATATTCCAA 177
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 45 LeuGlnAsnPheLeuLysGluAsnLysAsnGluLysValIleGluHisIleMetGlu 64

QY 178 GACCTGGATGCCGATAAGACGCGTCAGCTTTGAGGAATTCGTAGTCTCGTGTGCC 237
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 65 AspLeuAspThrAsnAlaAspLysGlnLeuSerPheGluGluPheIleMetLeuMetAla 84

QY 238 AGGGTCTCAAAACAGCCCATAGATATCCACAA 273
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 85 ArgLeuThrTrpAlaSerHisGluLysMetHisGlu 96
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Search completed: February 23, 2005, 11:24:52
Job time : 30.5 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: February 23, 2005, 11:25:01 ; Search time 27 Seconds

(without alignments)

1967.098 Million cell updates/sec

Title: US-09-910-208B-1

Perfect score: 92

Sequence: 1 atgactaagctggaagatca.....acatagatatccacaaagag 276

Scoring table:

OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues

Word size: 1

Total number of hits satisfying chosen parameters: 565918

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Command line parameters:

-MODEL=frame+n2p.model -DEV=xlp
-O/cn2_1/USPTO spool_p/RHDDAD-09-910208/runat_23022005_101830_14965/app_query.fasta_1.
-DB=PIR79 -QFM=fastan -SUFFIX=oligo.rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi -LIST=500
-DOCALIGN=200 -THR SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=HADDAD-09-910208 @CGN 1.1.63 @runat_23022005_101830_14965 -NCPU=6
-ICPU=3 -NO MMAP -LARGQUERY -NEG_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	21.7	91	2 A55406	calgranulin c - pi
2	11	12.0	122	1 A42628	calgranulin B - bo
3	9	9.8	92	2 JC4712	S-100 calcium-bind
4	8	8.7	72	2 T12854	hypothetical prote
5	8	8.7	275	2 T22414	hypothetical prote
6	8	8.7	334	2 G71228	hypothetical prote
7	8	8.7	363	2 AF2375	hypothetical prote
8	8	8.7	725	2 A41258	a-agglutinin core
9	8	8.7	819	2 T19351	hypothetical prote
10	7	7.6	41	2 B41655	sucrose catabolism
11	7	7.6	57	2 AH2906	conserved hypothet
12	7	7.6	78	2 T03670	reverse transcript
13	7	7.6	81	2 T03707	reverse transcript
14	7	7.6	81	2 T06548	RNA-directed DNA p

reverse transcript
RNA-directed DNA p
retrovirus-related
reverse transcript
parvalbumin beta
hypothetical prote
hypothetical prote
export protein xps
hypothetical prote
pol polyprotein -
hypothetical prote
insulin receptor -
adenylate kinase
hypothetical prote
hypothetical prote
CDP-diglyceride cyti
CDP-diglyceride sy
CDP-diglyceride fu
1-acylglycerol-3-p
1-acyl-sn-glycerol
1-acylglycerol-3-p
1-acylglycerol-3-p
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
mucin - rat
transcription regu
hypothetical prote
fructose 1-phospha
hypothetical prote
N5-(carboxyethyl)o
potassium channel
conserved hypothet
probable sugar ABC
hypothetical prote
ABC transporter, A
probable membrane
probable UDP-glucos
protein FlAJ16.8
hypothetical prote
MID2 protein - yea
hypothetical prote
polyamine transport
hypothetical prote
hypothetical prote
fimbrial assembly
FlA08.16 protein -
OXAL protein precu
probable integral
probable cell surf
maltose/maltodextr
hypothetical prote
probable alpha/bet
probable MFS trans
hypothetical prote
hypothetical prote
4-hydroxybutyrate
probable membrane
periplasmic sorbit
4-hydroxybutyrate
hypothetical prote
probable signaling
sucrose porin scry
sucrose porin scry
probable exonuclea
PTS system, (possi
hypothetical prote
ASM4 protein - yea
laccase (EC 1.10.3
related to COP1-in

88	7	7.6	533	2	S62371	laccase (EC 1.10.3	c 161	6	6.5	88	2	147759	retrovirus-related
89	7	7.6	547	2	S35047	mucin JUL7 - human	c 162	6	6.5	88	2	D47759	retrovirus-related
90	7	7.6	543	2	A48442	membrane transport	c 163	6	6.5	88	2	B47760	retrovirus-related
91	7	7.6	548	2	T49948	hypothetical prote	c 164	6	6.5	88	2	D90957	hypothetical prote
92	7	7.6	556	2	T16790	hypothetical prote	c 165	6	6.5	88	2	D56084	interleukin-beta
93	7	7.6	560	2	A82220	hypothetical prote	c 166	6	6.5	88	2	H83933	hypothetical prote
94	7	7.6	602	2	S58336	probable membrane	c 167	6	6.5	89	2	E47758	retrovirus-related
95	7	7.6	610	2	S35049	mucin JERS7 - huma	c 168	6	6.5	90	2	G72240	hypothetical prote
96	7	7.6	616	2	A81973	serine/threonine k	c 169	6	6.5	91	2	T07178	hypothetical prote
97	7	7.6	635	2	T00011	ccal protein - rat	c 170	6	6.5	93	2	B41609	hlaA protein - Cry
98	7	7.6	641	2	E96612	probable transcrip	c 171	6	6.5	95	1	S35985	S-100 protein alph
99	7	7.6	647	2	S26386	transcription fact	c 172	6	6.5	95	2	G84548	hypothetical prote
100	7	7.6	675	2	S74399	sensory transducti	c 173	6	6.5	95	2	T18004	hypothetical prote
101	7	7.6	687	2	A40711	RNA polymerase II	c 174	6	6.5	97	2	JC7322	deafness dystonia
102	7	7.6	703	2	T48019	hypothetical prote	c 175	6	6.5	100	2	F69133	ribosomal protein
103	7	7.6	729	2	T5028	probable glycosyl	c 176	6	6.5	100	2	C71012	hypothetical prote
104	7	7.6	775	2	A83936	stage V sporulatio	c 177	6	6.5	100	2	T49857	hypothetical prote
105	7	7.6	776	1	S44047	glucocorticoid rec	c 178	6	6.5	101	2	D69395	H+-transporting AT
106	7	7.6	794	2	F85040	hypothetical prote	c 179	6	6.5	101	2	F82797	hypothetical prote
107	7	7.6	796	2	T21460	hypothetical prote	c 180	6	6.5	103	2	T03148	hypothetical prote
108	7	7.6	845	2	T52518	related to cytosin	c 181	6	6.5	105	1	W7ML18	E7 protein - human
109	7	7.6	849	2	S37350	luxN protein - Vib	c 182	6	6.5	105	2	G95911	probable ferredoxi
110	7	7.6	859	2	S51646	inscuteable protei	c 183	6	6.5	106	1	QBP4	orf-106 protein -
111	7	7.6	877	2	S49783	probable membrane	c 184	6	6.5	106	2	B41830	DNA replication pr
112	7	7.6	902	1	S54495	probable carrier p	c 185	6	6.5	106	2	AD1063	hypothetical P4 ph
113	7	7.6	982	2	T13653	hypothetical prote	c 186	6	6.5	107	2	A72456	hypothetical prote
114	7	7.6	1023	2	E71376	conserved hypotet	c 187	6	6.5	108	1	KVMS49	Ig kappa chain V r
115	7	7.6	1098	2	T50364	hypothetical prote	c 188	6	6.5	108	2	AF1935	hypothetical prote
116	7	7.6	1123	2	AB0125	exodeoxyribonuclea	c 189	6	6.5	109	2	C97824	SOS ribosomal prot
117	7	7.6	1129	2	T19779	hypothetical prote	c 190	6	6.5	109	2	G71249	hypothetical prote
118	7	7.6	1161	2	S18738	pol protein - simi	c 191	6	6.5	110	2	G69609	cytochrome-c oxida
119	7	7.6	1338	2	T18287	protein-tyrosine k	c 192	6	6.5	110	2	B72713	hypothetical prote
120	7	7.6	1339	2	T40245	probable transcrip	c 193	6	6.5	110	2	E26683	hypothetical prote
121	7	7.6	1463	2	T30290	AAS surface protei	c 194	6	6.5	111	2	AC1648	hypothetical prote
122	7	7.6	1859	2	T15666	hypothetical prote	c 195	6	6.5	113	2	A85906	probable ybhH sigm
123	7	7.6	1726	2	T30810	chromatin structur	c 196	6	6.5	113	2	D91061	probable ybhH sigm
124	7	7.6	2055	2	T30259	multiple PDZ domai	c 197	6	6.5	113	2	Q5ECPA	calgranulin B [val
125	7	7.6	2163	2	S0675	pre-mRNA splicing	c 198	6	6.5	114	1	B31848	hypothetical prote
126	7	7.6	2164	1	GNV989	genome polyprotein	c 199	6	6.5	114	2	S75565	IS66 family elemen
127	7	7.6	2182	2	T28634	variant-specific s	c 200	6	6.5	116	2	G95167	degenerate transpo
128	7	7.6	2285	2	T12796	probable transglyc	c 201	6	6.5	116	2	A9034	hypothetical prote
129	7	7.6	3570	2	T45025	mucin MUC5B, trach	c 202	6	6.5	116	2	S12685	hypothetical prote
130	7	7.6	7829	2	T15789	hypothetical prote	c 203	6	6.5	117	2	F90084	hypothetical prote
131	6	6.5	20	2	S18582	hypothetical prote	c 204	6	6.5	117	2	T49382	conserved hypotet
132	6	6.5	20	2	T50757	puK protein limpo	c 205	6	6.5	120	2	H81728	response regulator
133	6	6.5	29	2	S01448	hypothetical prote	c 206	6	6.5	121	2	B82244	heat-labile entero
134	6	6.5	34	2	F81919	hypothetical prote	c 207	6	6.5	122	2	B33959	ribonuclease P (EC
135	6	6.5	38	2	I46861	macrophage migrati	c 208	6	6.5	123	2	C98103	ribonuclease P pro
136	6	6.5	39	2	I40555	rap60B protein - B	c 209	6	6.5	123	2	T38675	DNA-directed RNA p
137	6	6.5	46	1	S66584	hypothetical prote	c 210	6	6.5	124	2	S40348	Ig kappa chain V-J
138	6	6.5	46	1	S66591	hypothetical prote	c 211	6	6.5	125	2	AC1862	hypothetical prote
139	6	6.5	46	2	PC4400	crotoxin-binding p	c 212	6	6.5	126	2	A70886	hypothetical prote
140	6	6.5	47	2	E89810	hypothetical prote	c 213	6	6.5	126	2	S76349	hypothetical prote
141	6	6.5	52	2	A81042	hypothetical prote	c 214	6	6.5	126	2	C95887	probable translati
142	6	6.5	53	2	G70246	conserved hypotet	c 215	6	6.5	127	2	C95887	beta-lactamase rep
143	6	6.5	55	2	E91155	hypothetical prote	c 216	6	6.5	128	2	B28183	hypothetical prote
144	6	6.5	55	2	B86001	hypothetical prote	c 217	6	6.5	129	2	S76962	translation initia
145	6	6.5	55	2	JV0064	hypothetical 6K pr	c 218	6	6.5	130	2	A69216	hypothetical prote
146	6	6.5	56	2	AF0385	hypothetical prote	c 219	6	6.5	130	2	E83532	hypothetical prote
147	6	6.5	61	2	C69260	hypothetical prote	c 220	6	6.5	130	2	T11570	hypothetical prote
148	6	6.5	71	1	IHPC	high potential iro	c 221	6	6.5	131	2	F70908	hypothetical prote
149	6	6.5	72	2	T07369	ubiquinol-cytochro	c 222	6	6.5	134	2	D70474	hypothetical prote
150	6	6.5	74	2	T18183	hypothetical prote	c 223	6	6.5	134	2	AB2502	hypothetical prote
151	6	6.5	79	1	KL0246	calcium-binding pr	c 224	6	6.5	135	1	A61244	natriuretic peptid
152	6	6.5	79	1	KL001	calcium-binding pr	c 225	6	6.5	135	2	AG1244	hypothetical 135 p
153	6	6.5	79	1	KLPGI	calcium-binding pr	c 226	6	6.5	135	2	F86239	protein F20B24.4 [
154	6	6.5	81	2	T10743	RNA-directed DNA p	c 227	6	6.5	138	2	E73347	hypothetical prote
155	6	6.5	82	2	D82577	hypothetical prote	c 228	6	6.5	138	2	T33495	hypothetical prote
156	6	6.5	82	2	AH2065	hypothetical prote	c 229	6	6.5	138	2	AD0368	probable membrane
157	6	6.5	84	2	D83423	hypothetical prote	c 230	6	6.5	139	2	H89287	protein par-1 (imp
158	6	6.5	84	2	A13563	hypothetical prote	c 231	6	6.5	139	2	H87305	phosphoribosyl-AMP
159	6	6.5	84	2	AD2158	hypothetical prote	c 232	6	6.5	139	2	AC1418	B. subtilis stress
160	6	6.5	87	2	H84234	hypothetical prote	c 233	6	6.5	139	2	AE1793	B. subtilis stress

c 234	6	6.5	140	2	C69963	conserved hypothet	307	6	6.5	183	2	F75086	hypothetical prote
235	6	6.5	145	2	AG3166	hypothetical prote	308	6	6.5	183	2	T25102	hypothetical prote
c 236	6	6.5	146	2	T51473	calmodulin-like pr	c 309	6	6.5	183	2	S70307	hypothetical prote
c 237	6	6.5	146	2	G71181	hypothetical prote	c 310	6	6.5	183	2	C97017	probable membrane
c 238	6	6.5	147	1	G65063	hypothetical prote	c 311	6	6.5	184	2	T06673	response reactor 2
c 239	6	6.5	147	2	I46467	luteinizing hormon	c 312	6	6.5	184	2	T50855	two-component resp
c 240	6	6.5	147	2	AC0864	conserved hypothet	c 313	6	6.5	184	2	T50856	response regulator
c 241	6	6.5	147	2	A85933	hypothetical prote	c 314	6	6.5	186	2	T50857	hypothetical prote
c 242	6	6.5	147	2	G91087	hypothetical prote	c 315	6	6.5	187	2	F82929	hypothetical prote
c 243	6	6.5	148	2	F86701	hypothetical prote	c 316	6	6.5	189	2	F82969	hypothetical prote
c 244	6	6.5	148	2	G64466	hypothetical prote	c 317	6	6.5	190	2	S66981	ribosomal protein
c 245	6	6.5	149	2	B48083	chromosome segrega	c 318	6	6.5	190	2	S2729	ribosomal protein
c 246	6	6.5	149	2	E83088	hypothetical prote	c 319	6	6.5	191	2	H87330	hypothetical prote
c 247	6	6.5	149	2	JC4983	hypothetical 17.1k	c 320	6	6.5	192	2	T12775	hypothetical yokk
c 248	6	6.5	149	2	A95105	conserved hypothet	c 321	6	6.5	192	2	S52249	response regulator
c 249	6	6.5	149	2	A97973	conserved hypothet	c 322	6	6.5	193	2	E95340	hypothetical prote
c 250	6	6.5	150	2	S42203	avidin-related pro	c 323	6	6.5	194	2	D87648	conserved hypothet
c 251	6	6.5	150	2	S42202	avidin-related pro	c 324	6	6.5	194	2	T46920	hypothetical prote
c 252	6	6.5	150	2	S42204	avidin-related pro	c 325	6	6.5	195	2	I40573	hypothetical prote
c 253	6	6.5	150	2	T44952	flagella-related p	c 326	6	6.5	195	2	Q0BED6	hypothetical prote
c 254	6	6.5	150	2	S37018	transposase (clone	c 327	6	6.5	197	1	Q0BED6	hypothetical prote
c 255	6	6.5	151	2	JC2321	hypothetical 17.0k	c 328	6	6.5	197	2	B95309	probable ABC sugar
c 256	6	6.5	151	2	T32957	hypothetical prote	c 329	6	6.5	198	2	AF1870	hypothetical prote
c 257	6	6.5	151	2	A64038	hypothetical prote	c 330	6	6.5	198	2	AC2792	conserved hypothet
c 258	6	6.5	151	2	S75732	hypothetical prote	c 331	6	6.5	199	2	B70516	hypothetical prote
c 259	6	6.5	152	2	S31002	gene 57 protein -	c 332	6	6.5	201	2	S72806	hypothetical prote
c 260	6	6.5	153	2	T29391	hypothetical prote	c 333	6	6.5	202	2	T30927	hypothetical prote
c 261	6	6.5	153	2	S67294	hypothetical prote	c 334	6	6.5	203	2	AB2378	hypothetical prote
c 262	6	6.5	155	2	T25845	hypothetical prote	c 335	6	6.5	203	2	S53587	probable membrane
c 263	6	6.5	155	2	AE0333	probable exported	c 336	6	6.5	203	2	T33864	hypothetical prote
c 264	6	6.5	156	2	H72621	hypothetical prote	c 337	6	6.5	203	2	T25222	hypothetical prote
c 265	6	6.5	157	2	H72065	ribosomal protein	c 338	6	6.5	204	2	B85879	hypothetical prote
c 266	6	6.5	160	2	S76609	hypothetical prote	c 339	6	6.5	204	2	H91034	hypothetical prote
c 267	6	6.5	160	2	AE0135	SsrA-binding prote	c 340	6	6.5	209	2	JU0220	probable positive
c 268	6	6.5	160	2	A97496	probable extracell	c 341	6	6.5	209	2	S65767	hypothetical prote
c 269	6	6.5	160	2	AD2714	conserved hypothet	c 342	6	6.5	209	2	S65768	hypothetical prote
c 270	6	6.5	161	2	B64106	small protein smpB	c 343	6	6.5	210	2	T37785	hypothetical prote
c 271	6	6.5	161	2	C84235	hypothetical prote	c 344	6	6.5	210	2	H72585	hypothetical prote
c 272	6	6.5	161	2	H72571	hypothetical prote	c 345	6	6.5	211	2	T25237	hypothetical prote
c 273	6	6.5	161	2	A97805	hypothetical prote	c 346	6	6.5	211	2	D90065	hypothetical prote
c 274	6	6.5	162	2	T50860	response regulator	c 347	6	6.5	213	2	F86310	protein FL13.8 (im
c 275	6	6.5	163	2	E97908	hypothetical prote	c 348	6	6.5	214	2	T13011	hypothetical prote
c 276	6	6.5	163	2	B95038	PTS system, iIB co	c 349	6	6.5	215	1	Q0BEF3	HXLF1 protein prec
c 277	6	6.5	164	2	S43226	homeotic protein P	c 350	6	6.5	215	2	D91177	probable transport
c 278	6	6.5	165	2	S01510	NADH2 dehydrogenas	c 351	6	6.5	215	2	S47728	probable transport
c 279	6	6.5	165	2	T38202	hypothetical serin	c 352	6	6.5	215	2	E86023	probable transport
c 280	6	6.5	165	2	A95161	conserved hypothet	c 353	6	6.5	215	2	S23432	pyroglutamyl-pepti
c 281	6	6.5	165	2	H98026	conserved hypothet	c 354	6	6.5	215	2	C70471	hypothetical prote
c 282	6	6.5	166	2	C86559	S7 ribosomal prote	c 355	6	6.5	216	2	B97926	conserved hypothet
c 283	6	6.5	166	2	C72734	hypothetical prote	c 356	6	6.5	216	2	F95056	hypothetical prote
c 284	6	6.5	167	2	A87150	tuberculin related	c 357	6	6.5	216	2	F95056	PAP2 family protei
c 285	6	6.5	168	2	E84362	GTP cyclohydrolase	c 358	6	6.5	217	2	AF0906	conserved hypothet
c 286	6	6.5	170	2	S56958	probable membrane	c 359	6	6.5	217	2	E70574	probable transcrip
c 287	6	6.5	172	2	G91049	probable outer mem	c 360	6	6.5	217	2	AB3476	hypothetical prote
c 288	6	6.5	172	2	D85894	probable outer mem	c 361	6	6.5	218	2	S32965	probable GTP-bind
c 289	6	6.5	172	2	H65026	hypothetical prote	c 362	6	6.5	218	2	T02384	hypothetical prote
c 290	6	6.5	174	2	S68246	phosphatidylcholin	c 363	6	6.5	219	2	C97571	hypothetical prote
c 291	6	6.5	175	2	H90768	probable copper/z	c 364	6	6.5	220	2	D70450	phosphoglycerate m
c 292	6	6.5	175	2	AE2486	aminoglycoside ade	c 365	6	6.5	220	2	S20064	ribosomal protein
c 293	6	6.5	175	2	A71358	hypothetical prote	c 366	6	6.5	220	2	C65112	sigma cross-reacti
c 294	6	6.5	175	2	E82118	conserved hypothet	c 367	6	6.5	220	2	H91139	sigma cross-reacti
c 295	6	6.5	175	2	G71480	hypothetical prote	c 368	6	6.5	220	2	C85985	conserved flagell
c 296	6	6.5	175	2	B42463	hypothetical prote	c 369	6	6.5	221	2	E87053	probable flagellar
c 297	6	6.5	175	2	C42291	tail fiber assembl	c 370	6	6.5	221	2	AI0089	myosin light chain
c 298	6	6.5	175	2	I38408	neu differentiation	c 371	6	6.5	222	2	A27270	hypothetical prote
c 299	6	6.5	177	2	B84186	inorganic pyrophos	c 372	6	6.5	224	2	T51875	hypothetical prote
c 300	6	6.5	177	2	G72457	hypothetical prote	c 373	6	6.5	225	1	ADPSGP	2-dehydro-3-deoxy-
c 301	6	6.5	178	2	A49014	20K protein - rabb	c 374	6	6.5	225	2	C88633	protein F56B3.3 [i
c 302	6	6.5	178	2	T42661	hypothetical prote	c 375	6	6.5	226	2	B64500	ribose-5-phosphate
c 303	6	6.5	179	2	F97683	hypothetical prote	c 376	6	6.5	226	2	D70540	probable dethiobio
c 304	6	6.5	179	2	AF2908	S0S ribosomal prot	c 377	6	6.5	226	2	E70769	hypothetical prote
c 305	6	6.5	179	2	T07057	hypothetical prote	c 378	6	6.5	227	2	A47635	MHC class II histo
c 306	6	6.5	182	2	AG1508	protein involved i	c 379	6	6.5	227	2	T03807	hypothetical prote

C 380 6 6.5 227 2 T02413 probable RING zinc
 C 381 6 6.5 227 2 C89839 conserved hypothet
 C 382 6 6.5 228 2 A53271 MHC class II histo
 C 383 6 6.5 228 2 E87612 cytochrome c, memb
 C 384 6 6.5 229 1 H77336 uncharacterized co
 C 385 6 6.5 229 1 F75267 probable cytochrom
 C 386 6 6.5 229 2 S30486 hypohetical 25.6K
 C 387 6 6.5 229 2 AG2390 hypohetical prote
 C 388 6 6.5 230 2 S14686 hypohetical prote
 C 389 6 6.5 230 2 A56210 neu differentiatio
 C 390 6 6.5 231 2 T50827 superoxide dismuta
 C 391 6 6.5 233 2 AB2107 hypohetical prote
 C 392 6 6.5 234 2 C83587 hypohetical prote
 C 393 6 6.5 234 2 E96957 HAD superfamily hy
 C 394 6 6.5 234 2 D98932 ABC transporter, A
 C 395 6 6.5 235 2 T42096 ATP-dependent Clp
 C 396 6 6.5 235 2 S51813 photosystem-I PSI-
 C 397 6 6.5 235 2 T03139 hypohetical prote
 C 398 6 6.5 236 2 T36399 probable alcohol d
 C 399 6 6.5 236 2 T06462 glutathione peroxi
 C 400 6 6.5 237 2 H69820 conserved hypohet
 C 401 6 6.5 237 2 T01359 fatty acid hydroxy
 C 402 6 6.5 238 2 T07921 probable starch sy
 C 403 6 6.5 238 2 E64416 hypohetical prote
 C 404 6 6.5 238 2 G64117 nifs protein homol
 C 405 6 6.5 239 2 B70465 probable export pr
 C 406 6 6.5 239 2 C65222 probable 2-compone
 C 407 6 6.5 239 2 B91267 two-component tran
 C 408 6 6.5 239 2 G86107 probable Y-protein
 C 409 6 6.5 240 2 AF0570 fimbriae Y protein
 C 410 6 6.5 240 2 A45273 fimA expression re
 C 411 6 6.5 240 2 H69846 hypohetical prote
 C 412 6 6.5 241 2 C64006 probable S-adenosy
 C 413 6 6.5 241 2 D43273 heregulin precursor
 C 414 6 6.5 241 2 S32359 glial growth facto
 C 415 6 6.5 242 2 T16804 hypohetical prote
 C 416 6 6.5 242 2 G87545 transcription regu
 C 417 6 6.5 244 2 T37686 hypohetical prote
 C 418 6 6.5 245 2 T47878 hypohetical prote
 C 419 6 6.5 245 2 H88642 protein C54E4.1 [i
 C 420 6 6.5 246 2 A72370 regulatory protein
 C 421 6 6.5 246 2 T20049 hypohetical prote
 C 422 6 6.5 246 2 F95155 ABC transporter, A
 C 423 6 6.5 247 2 S03546 hypohetical prote
 C 424 6 6.5 247 2 T13811 hypohetical prote
 C 425 6 6.5 247 2 T12957 hypohetical prote
 C 426 6 6.5 249 2 T21083 hypohetical prote
 C 427 6 6.5 249 2 T26482 hypohetical prote
 C 428 6 6.5 250 2 E83823 ABC transporter (A
 C 429 6 6.5 251 2 A75482 oxidoreductase, sh
 C 430 6 6.5 251 2 F86942 conserved hypohet
 C 431 6 6.5 251 2 G81923 probable ABC-trans
 C 432 6 6.5 251 2 A81180 ABC transporter, A
 C 433 6 6.5 252 2 AF1278 indol-3-glycerol p
 C 434 6 6.5 252 2 A98022 hypohetical prote
 C 435 6 6.5 253 1 R52PD4 ribosomal protein
 C 436 6 6.5 253 2 H69046 hypohetical prote
 C 437 6 6.5 253 2 G73350 conserved hypohet
 C 438 6 6.5 254 2 S63465 trypsin-like prote
 C 439 6 6.5 254 2 F90107 60S ribosomal prot
 C 440 6 6.5 254 2 S50243 ribosomal protein
 C 441 6 6.5 255 2 I47092 MHC OVAR-DQ-ALPHA-
 C 442 6 6.5 255 2 I47093 MHC OVAR-DQ-ALPHA-
 C 443 6 6.5 255 2 B97861 hypohetical prote
 C 444 6 6.5 256 2 T44452 amidase yedB limpo
 C 445 6 6.5 257 1 R5RTL8 ribosomal protein
 C 446 6 6.5 257 2 JN0923 ribosomal protein
 C 447 6 6.5 257 2 S42725 ribosomal protein
 C 448 6 6.5 258 2 C84559 60S ribosomal prot
 C 449 6 6.5 258 2 T04582 ribosomal protein
 C 450 6 6.5 259 2 S30950 gene 2 protein - M
 C 451 6 6.5 259 2 T29727 hypohetical prote
 C 452 6 6.5 260 1 R5TOL8 ribosomal protein

453 6 6.5 260 2 S22641 ribosomal protein
 454 6 6.5 260 2 T18676 hypohetical prote
 455 6 6.5 260 2 T45750 ribosomal protein
 C 456 6 6.5 260 2 S04647 hypohetical 28.2K
 C 457 6 6.5 262 2 B84668 hypohetical prote
 458 6 6.5 262 2 C84563 hypohetical prote
 459 6 6.5 262 2 T02724 gag protein homolo
 C 460 6 6.5 262 2 C56084 interleukin-1beta
 C 461 6 6.5 263 2 AG2280 glutathione S-tran
 462 6 6.5 264 2 B82619 exodeoxyribonuclea
 C 463 6 6.5 264 2 B69937 hypohetical prote
 464 6 6.5 264 2 T08939 RING zinc finger p
 C 465 6 6.5 268 2 AG2594 enoyl-(acyl-carrie
 C 466 6 6.5 268 2 A81864 probable NMA1686 [i
 467 6 6.5 269 2 T37073 hypohetical prote
 468 6 6.5 269 2 T08811 hypohetical prote
 469 6 6.5 269 2 J04899 proline rich prote
 C 470 6 6.5 270 2 H97376 enoyl-(acyl-carrie
 471 6 6.5 270 2 AF2159 hypohetical prote
 472 6 6.5 270 2 S73705 adhesin P1 precurs
 473 6 6.5 271 2 H84337 spermidine/putresc
 C 474 6 6.5 271 2 B60176 hypohetical prote
 C 475 6 6.5 273 2 E37293 probable transcrip
 C 476 6 6.5 273 2 AC1169 hypohetical prote
 C 477 6 6.5 273 2 T44657 protein GP80 limpo
 C 478 6 6.5 273 2 T19174 hypohetical prote
 C 479 6 6.5 273 2 A80848 iron transport pro
 C 480 6 6.5 273 2 S20069 ribonucleoprotein
 C 481 6 6.5 274 2 F85741 hypohetical prote
 482 6 6.5 274 2 T15134 hypohetical prote
 483 6 6.5 274 2 T19466 hypohetical prote
 C 484 6 6.5 274 2 E71119 metal dependent hy
 485 6 6.5 274 2 A12870 hypohetical prote
 486 6 6.5 274 2 C97647 myb-related trans
 487 6 6.5 274 2 T07393 nitrate transport
 488 6 6.5 275 2 S77388 conserved hypohet
 489 6 6.5 275 2 F82325 conserved hypohet
 C 490 6 6.5 276 2 D70953 noaY protein precu
 C 491 6 6.5 276 2 S13585 conserved hypohet
 492 6 6.5 276 2 F35259 conserved hypohet
 C 493 6 6.5 277 2 A99525 conserved hypohet
 C 494 6 6.5 277 2 I51270 myelin proteolipid
 C 495 6 6.5 277 2 AF3024 hypohetical prote
 C 496 6 6.5 277 2 C98260 hypohetical prote
 C 497 6 6.5 277 2 F97409 hypohetical prote
 C 498 6 6.5 278 2 B40825 hypohetical prote
 499 6 6.5 279 2 AG1307 hypohetical prote
 500 6 6.5 279 2 AG1679 hypohetical prote

ALIGNMENTS

RESULT 1

A55406 calgranulin c - pig
 C:Species: Sus scrofa domestica (domestic pig)
 C>Date: 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 09-Jul-2004
 C:Accession: A55406
 R:Dell'Angelica, E.C.; Schleicher, C.H.; Santome, J.A.
 J. Biol. Chem. 269, 28929-28936, 1994
 A:Title: Primary structure and binding properties of calgranulin C, a novel S100-like cal-
 A:Reference number: A55406; MUID:95050708; PMID:7961855
 A:Accession: A55406
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-91
 A:Cross-references: UNIPROT:P80310
 C:Superfamily: S-100 protein; calmodulin repeat homology
 C:Keywords: calcium binding; EF hand
 F:48-80/Domain: calmodulin repeat homology <EF2>

Alignment Scores: 2.45e-12 Length: 91
 Pred. No.:

Score: 20.00 Matches: 20
Percent Similarity: 100.00% Conservatively: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 21.74% Indels: 0
DB: Gaps: 0

US-09-910-208B-1 (1-276) x A55406 (1-91)

QY 4 ACTAAGCTGGAGATCACCTCGAGGGAATCATCAACATCTTCCACCAGTACTCCGTTCCG 63

Db 1 ThrLysLeuGluAspHisLeuGluGlyIleAsnIlePheHisGlnTyrSerValArg 20

RESULT 2

A42628
calgranulin B - bovine (fragment)
N/Alternate names: calcium-binding protein MRP-14; macrophage migration inhibitory factor in 2

C:Species: Bos primigenius taurus (cattle)
C>Date: 30-Sep-1993 #sequence_revision 23-May-1997 #text_change 23-May-1997
C:Accession: B22309; A42628
R:Tang, T.K.; Hong, T.M.; Lin, C.Y.; Lai, M.L.; Liu, C.H.L.; Lo, H.J.; Wang, M.E.; Chen, submitted to the Protein Sequence Database, July 1992

A:Reference number: A22309

A:Accession: B22309

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-122 <TAN>

R:Dianoux, A.C.; Stasia, M.J.; Garin, J.; Gagnon, J.; Vignais, P.V.

Biochemistry 31, 5898-5905, 1992

A:Title: The 23-kilodalton protein, a substrate of protein kinase C, in bovine neutrophil
A:Reference number: A42628; MUID:92304974; PMID:1610833

A:Accession: A42628

A:Molecule type: protein

A:Residues: 4-32, 'F', 34-56 <DIA>

C:Complex: heterodimer and higher complexes with calgranulin A

C:Superfamily: S-100 protein; calmodulin repeat homology

C:Keywords: blocked amino end; calcium binding; EF hand; heterodimer; inflammation; phospho-
F:50-82/Domain: calmodulin repeat homology <EF2>

Alignment Scores:

Pred. No.:	0.00638	Length:	122
Score:	11.00	Matches:	11
Percent Similarity:	100.00%	Conservatively:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	11.96%	Indels:	0
DB:	1	Gaps:	0

US-09-910-208B-1 (1-276) x A42628 (1-122)

QY 31 ATCATCAACATCTTCCACCAGTACTCCGTTCCG 63

Db 11 IleIleAsnIlePheHisGlnTyrSerValArg 21

RESULT 3

JC4712
S-100 calcium-binding protein A12 - human
N/Alternate names: calcium-binding amniotic fluid protein 1 (CAAF1); calgranulin C; calgranulin protein

C:Species: Homo sapiens (man)

C>Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004

C:Accession: JC4712; JC4717; JC4891; S56113; S56114

R:Yamamura, T.; Hitomi, J.; Nagasaka, K.; Suzuki, M.; Takahashi, E.; Saio, S.; Tsukada, Biochem. Biophys. Res. Commun. 221, 356-360, 1996

A:Title: Human CAAF1 gene - molecular cloning, gene structure, and chromosome mapping.

A:Reference number: JC4712; MUID:96192053; PMID:8619860

A:Accession: JC4712

A:Molecule type: mRNA

A:Residues: 1-92 <YAM>

A:Cross-references: UNIPROT:P80511; DDBJ:D83657; NID:G1502284; PID:BAA12030.1; PID:G150

R:Warti, T.; Ertmann, K.D.; Gallin, M.Y.

Biochem. Biophys. Res. Commun. 221, 454-458, 1996

A:Title: Host-parasite interaction in human onchocerciasis: Identification and sequence

A:Reference number: JC4717; MUID:96192069; PMID:8619876

A:Accession: JC4717

A:Molecule type: protein

A:Residues: 2-92 <MAR>

A:Experimental source: Onchocerca volvulus infecting human tissue

R:Ilig, E.C.; Troxler, H.; Buerigisser, D.M.; Kuster, T.; Markert, M.; Guignard, F.; Hunz

Biochem. Biophys. Res. Commun. 225, 146-150, 1996

A:Title: Amino acid sequence determination of human S100 A12 (P6, Calgranulin C, CGRP,

A:Reference number: JC4891; MUID:96332419; PMID:8769108

A:Accession: JC4891

A:Molecule type: protein

A:Residues: 2-92 <ILIG>

R:Guignard, F.; Maue, J.; Markert, M.

Biochem. J. 309, 395-401, 1995

A:Title: Identification and characterization of a novel human neutrophil protein relate

A:Reference number: S56113; MUID:95351965; PMID:7626002

A:Accession: S56113

A>Status: preliminary

A:Molecule type: protein

A:Residues: 'XX', 4-14, 'X', 16-17, 'XXXX', <GUI1>

A:Experimental source: isoform 6a

A:Accession: S56114

A>Status: preliminary

A:Molecule type: protein

A:Residues: 2-21 <GUI2>

A:Experimental source: isoform 6b

C:Comment: This protein is released by activated neutrophils in the course of inflammat

C:Genetics:

A:Gene: GDB:S100A12; P6; MRP6; CGRP; CAAFI

A:Cross-references: GDB:S218374

A:Map position: 1q21-1q21

C:Complex: monomer

C:Superfamily: S-100 protein; calmodulin repeat homology

F:2-92/Product: S-100 calcium-binding protein A12 #status experimental <MAY>

F:6-39/Domain: calmodulin repeat homology <EF1>

F:49-81/Domain: calmodulin repeat homology <EF2>

F:86-90/Region: zinc binding #status predicted

Alignment Scores:

Pred. No.:	0.81	Length:	92
Score:	9.00	Matches:	9
Percent Similarity:	100.00%	Conservatively:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	9.78%	Indels:	0
DB:	2	Gaps:	0

US-09-910-208B-1 (1-276) x JC4712 (1-92)

QY 37 AACATCTTCCACCAGTACTCCGTTCCG 63

Db 13 AsnIlePheHisGlnTyrSerValArg 21

RESULT 4

Ti2854

hypothetical protein yopT - Bacillus subtilis phage SPBc2

C:Species: Bacillus subtilis phage SPBc2

C>Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004

C:Accession: Ti2854; S69918

R:Razarevic, V.; Duesterhoeft, A.; Soldo, B.; Hilbert, H.; Maue, C.; Karamata, D.

submitted to the EMBL Data Library, August 1997

A:Description: The complete nucleotide sequence of the Bacillus subtilis SPbetac2 proph

A:Reference number: Z17583

A:Accession: Ti2854

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-72 <LAZ>

A:Cross-references: UNIPROT:O64103; EMBL:AF020713; NID:G3025478; PID:G3025568; PIDN:AAC

R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte

C.; Bron, S.; Brouillette, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch

A.; Enrich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.

Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galie

iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Koester, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A.; Authors: Schleith, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron, Akeuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpestra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K. A.; Authors: Yoshikawa, H.F.; Zumschein, E.; Yoshikawa, H.; Danchin, A.

A:Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: B69918
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-72 <KUN>
A:Cross-references: GB:299114; GB:299115; GB:AL009136; NID:G2634478; PIDN:CAB13995.1; PI
A:Experimental source: strain 168
C:Genetics:
A:Gene: yopT

Alignment Scores:
Pred. No.: 9.19 Length: 72
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 8.70% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-1 (1-276) x T12854 (1-72)

QY 219 TTCTTCAAGCTGACGGCTCCGTC 196

Db 45 PheLeuArgSerGlyGlyAlaPheVal 52

RESULT 5

T22414

hypothetical protein F49C12.10 - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T22414

R:Gardner, A.

A:Reference number: Z19562

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Accession: T22414

A:Molecule type: DNA

A:Residues: 1-275 <WIL>

A:Cross-references: UNIPROT:Q20587; EMBL:Z68227; PIDN:CAA92513.1; GSPDB:GN00022; CESP:F4

A:Experimental source: clone F49C12

C:Genetics:

A:Gene: CESP:F49C12.10

A:Map position: 4

A:Introns: 69/1; 112/2; 152/1; 191/3; 233/3

Alignment Scores:
Pred. No.: 8.35 Length: 275
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 8.70% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-1 (1-276) x T22414 (1-275)

QY 51 GTACTCCGTCGGTGGGCATT 74

Db 174 ValLeuArgSerGlyGlyAlaPhe 181

RESULT 6

G71228

hypothetical protein PH0089 - *Pyrococcus horikoshii*

C:Species: *Pyrococcus horikoshii*

C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 09-Jul-2004

C:Accession: G71228
R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi DNA Res. 5, 55-76, 1998
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic A:Reference number: A71000; MUID:98344137; PMID:9679194
A:Accession: G71228
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-334 <KAW>
A:Cross-references: UNIPROT:O57833; GB:AP000001; NID:G3236128; PIDN:BAA29158.1; PID:G325 A:Experimental source: strain OT3
A:Note: this accession replaces an interim accession for a sequence replaced by GenBank C:Genetics:
A:Gene: PH0089

Alignment Scores:
Pred. No.: 8.24 Length: 334
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 8.70% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-1 (1-276) x G71228 (1-334)

QY 150 ATCTTTGGTCTTCGAGGGTTTT 127

Db 272 IlePheGlyValLeuGluGlyPhe 279

RESULT 7

AF2375

hypothetical protein all4558 [imported] - *Nostoc* sp. (strain PCC 7120)

C:Species: *Nostoc* sp. PCC 7120

A:Note: *Nostoc* sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120

C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004

C:Accession: AF2375

R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.

DNA Res. 8, 205-213, 2001

A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Ana*

A:Reference number: AB1807; MUID:21595285; PMID:11759840

A:Accession: AF2375

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-363 <KUR>

A:Cross-references: UNIPROT:Q8YKN7; GB:BA000019; PIDN:BA076257.1; PID:G17133694; GSPDB:G

A:Experimental source: strain PCC 7120

C:Genetics:

A:Gene: all4558

Alignment Scores:
Pred. No.: 8.19 Length: 363
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 8.70% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-1 (1-276) x AF2375 (1-363)

QY 131 GTTTGGGAAGTTCCTTTGTGATC 108

Db 156 ValLeuGlySerPheValIle 163

RESULT 8

A41258

a-agglutinin core protein AGA1 - yeast (*Saccharomyces cerevisiae*)

N:Alternate names: a-agglutinin attachment protein AGA1; protein N3431; protein YNR044w

C:Species: *Saccharomyces cerevisiae*

C:Date: 03-Apr-1992 #sequence_revision 03-Apr-1992 #text_change 09-Jul-2004

C:Accession: A41258; S63375; S17031

R:Roy, A.; Lu, C.F.; Marykwas, D.L.; Lipke, P.N.; Kurjan, J.

Mol. Cell. Biol. 11, 4196-4206, 1991
A;Title: The AGAL product is involved in cell surface attachment of the Saccharomyces cerevisiae
A;Reference number: A41258; MUID: 91304412; PMID: 2072914
A;Accession: A41258
A;Molecule type: DNA
A;Residues: 1-725 <ROY>

A;Cross-references: UNIPROT:P32323; GB:M60590; NID:g170963; PIDN:AAA34382.1; PID:g170964
R;Pohl, T.M.
submitted to the Protein Sequence Database, April 1996
A;Reference number: S63346
A;Accession: S63375
A;Molecule type: DNA
A;Residues: 1-725 <POH>
A;Cross-references: EMBL:Z71659; NID:g1302551; PIDN:CAA96325.1; PID:e239834; PID:g130255
A;Experimental source: strain S288C
C;Genetics:

A;Gene: SGD:AGAL1
A;Cross-references: SGD:S0005327; MIPS:YNR044W
A;Map position: 14R
C;Keywords: glycoprotein; transmembrane protein
F;8-24/Domain: transmembrane #status predicted <TM1>
F;708-724/Domain: transmembrane #status predicted <TM2>

Alignment Scores:
Pred. No.: 7.79 Length: 725
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 8.70% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-1 (1-276) x A41258 (1-725)

QY 71 ATTTGACACCCCTCAACACGCG 94

Db 634 ILESerThrProSerThrSerVal 641

RESULT 9

T19351

hypothetical protein C17E4.2 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C;Accession: T19351

submitted to the EMBL Data Library, October 1996

A;Reference number: Z19113

A;Accession: T19351

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-819 <WIL>

A;Cross-references: UNIPROT:Q93228; EMBL:Z81037; PIDN:Z81037; GSPDB:GN00019; CESP:CL

C;Genetics:

A;Gene: CESP:C17E4.2

A;Map position: 1

A;Introns: 151/3; 346/3; 376/2; 446/3; 669/3; 707/3

Alignment Scores:

Pred. No.: 7.73 Length: 819
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 8.70% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-1 (1-276) x T19351 (1-819)

QY 29 GAATCATCAACATCTCCACCACT 52

Db 799 GluSerSerThrSerThrSer 806

RESULT 10

B41655

sucrose catabolism protein Scry' - Salmonella thompson plasmid Sac (fragment)
C;Species: Salmonella thompson
C;Date: 10-Jul-1992 #sequence_revision 10-Jul-1992 #text_change 09-Jul-2004
C;Accession: B41655
R;Cowan, P.J.; Nagesha, H.; Leonard, L.; Howard, J.L.; Pittard, A.J.
J. Bacteriol. 173, 7464-7470, 1991
A;Title: Characterization of the major promoter for the plasmid-encoded sucrose genes
A;Reference number: A41655; MUID: 92041657; PMID: 1938944

A;Accession: B41655

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-41 <COM>

A;Cross-references: UNIPROT:P24262; GB:M63038; NID:g154360; PIDN:AAA27218.1; PID:g154360

C;Genetics:

A;Genome: plasmid

Alignment Scores:
Pred. No.: 107 Length: 41
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 7.61% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-1 (1-276) x B41655 (1-41)

QY 109 TCAGCTGCTTCAGCTCACGCT 89

Db 16 SerAlaAlaSerAlaHisAla 22

RESULT 11

AH2906

conserved hypothetical protein Atu2689 [imported] - Agrobacterium tumefaciens (strain

C;Species: Agrobacterium tumefaciens

C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004

C;Accession: AH2906

R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo,

; Karp, P.; Romero, P.; Grant, C.; Guenther, D.; Kuttyavin, T.; Levy, R.; Li, M.; McGle

Science 294, 2317-2323, 2001

A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,

ster, E.W.

A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A;Reference number: AB2577; MUID: 21608550; PMID: 11743193

A;Accession: AH2906

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-57 <KUR>

A;Cross-references: UNIPROT:Q8UC09; GB:AE008688; PIDN:AAL43670.1; PID:g17741195; GSPDB:

A;Experimental source: strain C58 (Dupont)

C;Genetics:

A;Gene: Atu2689

A;Map position: circular chromosome

Alignment Scores:

Pred. No.: 104 Length: 57
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 7.61% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-1 (1-276) x AH2906 (1-57)

QY 88 AGCGTGACCTGAAGCAGCTG 108

Db 33 LysArgGluLeuLysGlnLeu 39

RESULT 12

T03670

reverse transcriptase - rice copia-like retrotransposon Rrt7 (fragment)

C;Species: Oryza sativa (rice)

C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 24-Mar-1999

Wed Feb 23 12:50:01 2005

C;Accession: T03670
R;Wang, S.
submitted to the EMBL Data Library, June 1996
A;Description: Copia-like retrotransposons in rice: sequence heterogeneity, species distribution
A;Reference number: Z14979
A;Accession: T03670
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-78 <WNA>
A;Cross-references: EMBL:Z75502; NID:e995599; PID:e250631
A;Experimental source: subsp. Japonica, cv. Nongken 58S, leaf
C;Genetics:
A;Mobile element: copia-like retrotransposon Rrt7

Alignment Scores:
Pred. No.: 102 Length: 78
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 7.61% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-1 (1-276) x T03670 (1-78)

QY 188 GCATCCAGGCTTGGAAATATT 168
|||||
Db 47 AlaSerArgSerTrpAsnIle 53

RESULT 13
T03707
reverse transcriptase homolog - rice retrotransposon Tos11 (fragment)
C;Species: Oryza sativa (rice)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C;Accession: T03707
R;Hirochika, H.; Sugimoto, K.; Otsuki, Y.; Tsugawa, H.; Kanda, M.
Proc. Natl. Acad. Sci. U.S.A. 93, 7783-7788, 1996
A;Title: Retrotransposons of rice involved in mutations induced by tissue culture.
A;Reference number: Z15023; MUID:96353895; PMID:8755553
A;Accession: T03707
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-81 <HIR>
A;Cross-references: UNIPROT:O24195; EMBL:D85869; NID:q1621478; PIDN:BAA12895.1; PID:g162
A;Experimental source: subsp. Japonica, cv. Nipponbare
C;Genetics:
A;Mobile element: retrovirus-related polyprotein
C;Superfamily: retrovirus-related polyprotein

Alignment Scores:
Pred. No.: 102 Length: 81
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 7.61% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-1 (1-276) x T03707 (1-81)

QY 188 GCATCCAGGCTTGGAAATATT 168
|||||
Db 41 AlaSerArgSerTrpAsnIle 47

RESULT 14
T06548
RNA-directed DNA polymerase (EC 2.7.7.49) - wheat Ty1-copia type retrotransposon (fragment)
N;Alternate names: reverse transcriptase
C;Species: Triticum aestivum (common wheat)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T06548
R;Hirochika, H.; Hirochika, R.
Jpn. J. Genet. 68, 35-46, 1993
A;Title: Ty1-copia group retrotransposons as ubiquitous components of plant genomes.
A;Reference number: Z15147; MUID:93305354; PMID:8391285

A;Accession: T06548
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-81 <HIR>
A;Cross-references: UNIPROT:Q9ZRL6; EMBL:D12832; NID:g218342; PIDN:BAA02262.1; PID:g2183
C;Genetics:
A;Gene: pol
A;Mobile element: Ty1-copia type retrotransposon
A;Superfamily: retrovirus-related polyprotein
C;Keywords: nucleotidyltransferase

Alignment Scores:
Pred. No.: 102 Length: 81
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 7.61% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-1 (1-276) x T06548 (1-81)

QY 188 GCATCCAGGCTTGGAAATATT 168
|||||
Db 41 AlaSerArgSerTrpAsnIle 47

RESULT 15
T03937
reverse transcriptase - maize Ty1-copia type retrotransposon (fragment)

C;Species: Zea mays (maize)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T03937
R;Hirochika, H.; Hirochika, R.
Jpn. J. Genet. 68, 35-46, 1993

A;Title: Ty1-copia group retrotransposons as ubiquitous components of plant genomes.
A;Reference number: Z15147; MUID:93305354; PMID:8391285
A;Accession: T03937
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-81 <HIR>
A;Cross-references: UNIPROT:Q9ZRL8; EMBL:D12830; NID:g217965; PIDN:BAA02262.1; PID:g217

C;Genetics:
A;Gene: pol
A;Mobile element: Ty1-copia type retrotransposon
A;Superfamily: retrovirus-related polyprotein
C;Keywords: reverse transcriptase

Alignment Scores:
Pred. No.: 102 Length: 81
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 7.61% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-1 (1-276) x T03937 (1-81)

QY 188 GCATCCAGGCTTGGAAATATT 168
|||||
Db 41 AlaSerArgSerTrpAsnIle 47

Search completed: February 23, 2005, 11:45:04
Job time : 38 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: February 23, 2005, 11:36:26 ; Search time 116 Seconds
(without alignments)
2436.791 Million cell updates/sec

Title: US-09-910-208B-1

Perfect score: 92

Sequence: 1 atgactaagctgaagatca.....acatagatatccacaagag 276

Scoring table:

OLIGO	
Xgapop 60.0 , Xgapext 60.0	
Ygapop 60.0 , Ygapext 60.0	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 1612378 seqs, 512079187 residues

Word size: 1

Total number of hits satisfying chosen parameters: 3224408

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Command line parameters:

```
-MODEL=frame+ n2p.model -DEV=xlp
-Q=/cgn2.1/USPTO.spool_p/HADDAD-09-910208/runat_23022005_101829_14952/app_query.fasta_1
-DB=UniProt_03 -QFMT=fastan -SUFFIX=oligo.rup -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=500 -DOALIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=HADDAD-09-910208 @CGN 1.1 244 @runat_23022005_101829_14952 -NCPU=6
-ICPU=3 -NO_MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DRV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOF=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7
```

Database :

UniProt 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	91	98.9	91	1 S112 BOVIN	P79105 bos taurus
2	64	69.6	70	2 Q9TR16	Q9TR16 bos taurus
3	20	21.7	91	1 S112 FIG	P80310 sus scrofa
4	13	14.1	118	1 S109 RABIT	P50117 oryctolagus
5	11	12.0	122	1 S109 BOVIN	P28783 bos taurus
6	10	10.9	81	1 S112 RABIT	Q77791 oryctolagus
7	9	9.8	91	1 S112_HUMAN	P80511 homo sapien
8	9	9.8	568	2 F78947	P78947 schizosacch
9	9	9.8	605	2 Q9HGP1	Q9HGP1 schizosacch
10	8	8.7	72	2 O64103	O64103 bacterioph
11	8	8.7	72	2 O34498	O34498 bacillus su
12	8	8.7	158	2 Q94577	Q94577 heliocidari
13	8	8.7	225	2 Q48597	Q48597 mycobacteri
14	8	8.7	275	2 Q20587	Q20587 caenorhabdi
15	8	8.7	319	2 Q7MSF1	Q7MSF1 wolinnella s
16	8	8.7	334	2 O57833	O57833 pyrococcus

17	8	8.7	338	2	Q94500	Q94500 dictyosteli
18	8	8.7	353	2	Q6DY57	Q6DY57 pseudopleur
19	8	8.7	363	2	Q8YMK7	Q8YMK7 anabaena sp
20	8	8.7	382	2	Q9V5S3	Q9V5S3 drosophila
21	8	8.7	442	2	Q6FUB7	Q6FUB7 candida gla
22	8	8.7	447	2	Q88W85	Q88W85 lactobacill
23	8	8.7	456	2	Q6CUX7	Q6CUX7 kluyveromyc
24	8	8.7	461	2	Q6C2X8	Q6C2X8 yarrowia li
25	8	8.7	463	2	Q6FW57	Q6FW57 candida gla
26	8	8.7	576	2	Q754B7	Q754B7 ashbya goss
27	8	8.7	578	2	Q6CPE3	Q6CPE3 kluyveromyc
28	8	8.7	600	2	Q941I3	Q941I3 arabisopsis
29	8	8.7	617	2	Q6FNK6	Q6FNK6 candida gla
30	8	8.7	725	1	AGA1 YEAST	P32323 saccharomyc
31	8	8.7	744	2	Q9C2N3	Q9C2N3 neurospora
32	8	8.7	767	2	Q94543	Q94543 drosophila
33	8	8.7	800	2	Q8TFG4	Q8TFG4 schizosacch
34	8	8.7	819	2	Q93228	Q93228 caenorhabdi
35	8	8.7	820	2	Q96035	Q96035 ciona savig
36	8	8.7	846	2	Q6GQ76	Q6GQ76 xenopus lae
37	8	8.7	916	2	Q7VZ10	Q7VZ10 monosiga br
38	8	8.7	1164	2	Q7YU46	Q7YU46 drosophila
39	8	8.7	1241	2	Q75JC0	Q75JC0 dictyosteli
40	8	8.7	1541	2	Q9V8M7	Q9V8M7 drosophila
41	8	8.7	1873	2	Q6S003	Q6S003 dictyosteli
42	8	8.7	2516	2	Q9RN43	Q9RN43 photorhabdu
43	8	8.7	2525	2	Q7N7Y9	Q7N7Y9 photorhabdu
44	8	8.7	3171	2	Q7BSE3	Q7BSE3 plasmodium
45	7	7.6	37	2	Q8CKB1	Q8CKB1 yersinia pe
46	7	7.6	41	1	SCRY_SALTH	P24262 salmonella
47	7	7.6	54	2	Q6ZXC4	Q6ZXC4 rattus norv
48	7	7.6	57	2	Q8UC09	Q8UC09 agrobacteri
49	7	7.6	80	2	Q93XU6	Q93XU6 diospyros k
50	7	7.6	81	2	O24195	O24195 oryza sativ
51	7	7.6	81	2	Q92RK8	Q92RK8 spinacia ol
52	7	7.6	81	2	Q92RL6	Q92RL6 triticum ae
53	7	7.6	81	2	Q92RL8	Q92RL8 zea mays (m
54	7	7.6	88	2	Q8W216	Q8W216 setaria ita
55	7	7.6	88	2	Q82BV5	Q82BV5 streptomyce
56	7	7.6	92	2	Q8W2H1	Q8W2H1 setaria vir
57	7	7.6	92	2	Q8W2H2	Q8W2H2 setaria ver
58	7	7.6	92	2	Q8W2H4	Q8W2H4 setaria ita
59	7	7.6	92	2	Q8W2I3	Q8W2I3 setaria ita
60	7	7.6	92	2	Q8W2I4	Q8W2I4 setaria ita
61	7	7.6	92	2	Q8W2I7	Q8W2I7 setaria fab
62	7	7.6	92	2	Q8W2J4	Q8W2J4 setaria ita
63	7	7.6	92	2	Q7NRK7	Q7NRK7 chromobacte
64	7	7.6	94	2	Q94EP3	Q94EP3 zea mays (m
65	7	7.6	94	2	Q94EP4	Q94EP4 zea mays (m
66	7	7.6	94	2	Q94EP5	Q94EP5 zea mays (m
67	7	7.6	94	2	Q94EP7	Q94EP7 zea mays (m
68	7	7.6	94	2	Q94KN8	Q94KN8 oryza sativ
69	7	7.6	94	2	Q94KP0	Q94KP0 oryza sativ
70	7	7.6	100	2	Q91LA4	Q91LA4 white spot
71	7	7.6	101	2	Q93395	Q93395 salvelinus
72	7	7.6	105	2	Q7PYA7	Q7PYA7 anopheles q
73	7	7.6	105	2	O711Z2	O711Z2 lactobacill
74	7	7.6	109	1	PRVB_BOACO	P02615 boa constri
75	7	7.6	111	2	Q9F181	Q9F181 alcaligenes
76	7	7.6	112	2	Q9FJE9	Q9FJE9 arabisopsis
77	7	7.6	114	2	Q9XU17	Q9XU17 caenorhabdi
78	7	7.6	118	2	Q6PVY2	Q6PVY2 bos taurus
79	7	7.6	120	2	Q92420	Q92420 pseudomonas
80	7	7.6	120	2	Q88IN4	Q88IN4 pseudomonas
81	7	7.6	122	2	Q96T26	Q96T26 neurospora
82	7	7.6	124	2	Q754L7	Q754L7 ashbya goss
83	7	7.6	124	2	Q41609	Q41609 tulipa gesn
84	7	7.6	127	2	O8YRG2	O8YRG2 anabaena sp
85	7	7.6	132	2	Q70KK3	Q70KK3 bacillus am
86	7	7.6	132	2	Q6N535	Q6N535 rhodospseudo
87	7	7.6	133	2	Q7SR05	Q7SR05 human immun
88	7	7.6	133	2	Q7SR06	Q7SR06 human immun
89	7	7.6	133	2	Q7SR07	Q7SR07 human immun

90	7	7.6	133	2	Q7SR08	Q7sr08 human immun	163	7	7.6	219	2	Q9BXF1	Q9bxf1 homo sapien
91	7	7.6	133	2	Q7SR09	Q7sr09 human immun	c 164	7	7.6	219	2	Q6QVY9	Q6cvy9 eyringa vul
92	7	7.6	133	2	Q7SR10	Q7sr10 human immun	165	7	7.6	220	2	Q6EPS0	Q6eps0 oryza sativ
93	7	7.6	133	2	Q7SR11	Q7sr11 human immun	166	7	7.6	223	2	Q6RTAO	Q6rtao bovine papu
94	7	7.6	133	2	Q7SR12	Q7sr12 human immun	167	7	7.6	230	2	Q6MKX6	Q6mkx6 bdellovibri
95	7	7.6	133	2	Q7SR13	Q7sr13 human immun	168	7	7.6	230	2	Q8BUL4	Q8bul4 m mus muscu
96	7	7.6	133	2	Q7SR14	Q7sr14 human immun	169	7	7.6	231	2	Q86K19	Q86k19 dictyosteli
97	7	7.6	133	2	Q7SR15	Q7sr15 human immun	170	7	7.6	232	2	Q8BNV5	Q8bnv5 debaryomyce
98	7	7.6	133	2	Q7SR16	Q7sr16 human immun	171	7	7.6	236	2	Q8SJK3	Q8sjk3 arabidopsis
99	7	7.6	133	2	Q7SR17	Q7sr17 human immun	172	7	7.6	239	2	Q9CUK4	Q9cuk4 mus musculus
100	7	7.6	133	2	Q7SR18	Q7sr18 human immun	173	7	7.6	241	2	Q86LY4	Q86ly4 myxine glut
101	7	7.6	133	2	Q7SR19	Q7sr19 human immun	174	7	7.6	243	2	Q8VYMO	Q8vymo arabidopsis
102	7	7.6	133	2	Q7SR20	Q7sr20 human immun	175	7	7.6	243	2	Q82G51	Q82g51 streptomyce
103	7	7.6	133	2	Q7SR21	Q7sr21 human immun	176	7	7.6	244	2	Q9WVW6	Q9wvw6 pseudomonas
104	7	7.6	133	2	Q7SR22	Q7sr22 human immun	177	7	7.6	245	2	Q9X6H3	Q9x6h3 streptococ
105	7	7.6	133	2	Q7SR23	Q7sr23 human immun	c 178	7	7.6	249	1	CDSA_ECOLI	P04666 e phosphati
106	7	7.6	133	2	Q7SR24	Q7sr24 human immun	179	7	7.6	251	2	Q97CT4	Q97ct4 thermoplasm
107	7	7.6	133	2	Q7SR25	Q7sr25 human immun	c 180	7	7.6	253	1	SOJ_BACHD	Q97k50 bacillus ha
108	7	7.6	133	2	Q7SR26	Q7sr26 human immun	181	7	7.6	253	2	Q7XZHG	Q7xzh6 oryza sativ
109	7	7.6	133	2	Q7SR27	Q7sr27 human immun	c 182	7	7.6	255	1	PLSC_NEIGO	Q59601 neisseria g
110	7	7.6	133	2	Q7SR28	Q7sr28 human immun	c 183	7	7.6	255	1	PLSC_NEINA	Q9ju41 neisseria m
111	7	7.6	133	2	Q7SR29	Q7sr29 human immun	c 184	7	7.6	256	2	PLSC_NEIMB	Q9ju47 neisseria m
112	7	7.6	136	2	Q9VYV7	Q9vyv7 pseudomonas	c 185	7	7.6	257	2	Q9F5M2	Q9f5m2 rhodocyclu
113	7	7.6	138	1	GSPI_XANCP	P31738 xanthomonas	c 186	7	7.6	261	2	Q97VM6	Q59618 neisseria m
114	7	7.6	138	2	O8PGS6	Q8pgs6 xanthomonas	187	7	7.6	261	2	Q97VM6	Q97vw6 sulfobolus
115	7	7.6	138	2	O6APC2	O6apc2 desulfotale	188	7	7.6	264	2	Q95UR4	Q9eur4 arabidopsis
116	7	7.6	139	2	O87VZ4	Q87vz4 pseudomonas	189	7	7.6	268	2	Q95PK4	Q95pk4 tribolium c
117	7	7.6	140	2	O86Q31	Q86q31 hydra atten	190	7	7.6	269	2	Q8ATR6	Q8atr6 oryza sativ
118	7	7.6	140	2	O9XCQ6	Q9xcq6 mus musculus	191	7	7.6	271	1	OLGI_HUMAN	Q8tak6 homo sapien
119	7	7.6	141	2	O58631	O58631 pyrococcus	192	7	7.6	271	2	Q8NTB2	Q8ntb2 corynebacte
120	7	7.6	145	2	O8VU96	O8vu96 lactobacill	193	7	7.6	271	2	Q88T01	Q88t01 lactobacill
121	7	7.6	149	2	O6VAQ6	O6vaq6 onchidella	194	7	7.6	272	2	O64594	O64594 arabidopsis
122	7	7.6	149	2	O7FIU4	Q7fiu4 oryza sativ	195	7	7.6	276	2	Q8PWY0	Q8pwy0 rattus norv
123	7	7.6	151	2	Q8BK94	Q8bk94 mus musculus	c 196	7	7.6	277	2	Q8ROB6	Q8rob6 mus musculu
124	7	7.6	152	2	Q7QCA9	Q7qca9 anopheles g	c 197	7	7.6	277	2	Q8BG34	Q8bg34 m mus muscu
125	7	7.6	156	2	Q7PWZ0	Q7pwz0 anopheles g	c 198	7	7.6	277	2	Q8BP58	Q8bp58 mus musculus
126	7	7.6	158	2	Q6J654	Q6j654 dendrolimus	199	7	7.6	281	2	Q9P632	Q9p632 neurospora
127	7	7.6	163	2	O88167	O88167 agrobacteri	200	7	7.6	281	2	Q8XU00	Q8xuu0 ralstonia s
128	7	7.6	169	2	O8VAM8	Q8vaw8 white spot	c 201	7	7.6	283	2	Q96IJ0	Q96ij0 homo sapien
129	7	7.6	170	2	Q9XSE5	Q9xse5 sus scrofa	202	7	7.6	284	2	Q7QOS7	Q7qos7 giardia lam
130	7	7.6	171	2	Q75CM7	Q75cm7 ashbya goss	c 203	7	7.6	285	2	Q7XKP6	Q7xkp6 oryza sativ
131	7	7.6	185	2	Q9B0V5	Q9b0v5 locustacaru	c 204	7	7.6	285	2	Q74K23	Q74k23 lactobacill
132	7	7.6	185	2	Q9B9T8	Q9b9t8 locustacaru	c 205	7	7.6	285	2	Q6O501	Q6o501 cricetus
133	7	7.6	185	2	Q9B9T9	Q9b9t9 locustacaru	206	7	7.6	291	2	Q8V7H6	Q8v7h6 tt virus. o
134	7	7.6	185	2	Q9B9U0	Q9b9u0 locustacaru	207	7	7.6	293	2	P96725	P96725 bacillus su
135	7	7.6	185	2	Q9B9U1	Q9b9u1 locustacaru	208	7	7.6	301	2	Q9W417	Q9w417 drosophila
136	7	7.6	185	2	Q9B9U2	Q9b9u2 locustacaru	c 209	7	7.6	303	2	Q84RT8	Q84rt8 bacteroides
137	7	7.6	188	2	Q6CT23	Q6ct23 kluyveromyc	c 210	7	7.6	303	2	Q72XR9	Q72xr9 xenopus lae
138	7	7.6	199	2	Q8Y0T8	Q8y0t8 ralstonia s	c 211	7	7.6	305	2	Q65KP7	Q65kp7 bacillus li
139	7	7.6	202	2	O8IXO8	O8ixg8 homo sapien	212	7	7.6	306	2	Q8NXP4	Q8nxp4 staphylococ
140	7	7.6	202	2	O65136	O65136 syringa vul	213	7	7.6	306	2	O7A2V4	Q7a2v4 staphylococ
141	7	7.6	204	2	O05652	O05652 bacillus ce	214	7	7.6	306	2	O7A6W0	Q7a6w0 staphylococ
142	7	7.6	204	2	Q72Y51	Q72y51 bacillus ce	215	7	7.6	306	2	Q8CTI6	Q8cti6 staphylococ
143	7	7.6	204	2	Q815V1	Q815v1 bacillus ce	216	7	7.6	306	2	Q9KWK1	Q9kwk1 staphylococ
144	7	7.6	204	2	Q6HBM6	Q6hbm6 bacillus th	217	7	7.6	306	2	Q6GBD1	Q6gbd1 staphylococ
145	7	7.6	204	2	Q7TS73	Q7ts73 mus musculus	218	7	7.6	306	2	Q6GIU3	Q6giu3 staphylococ
146	7	7.6	208	2	Q18579	Q18579 caenorhabdi	c 219	7	7.6	308	2	Q8WUI3	Q8wui3 homo sapien
147	7	7.6	208	2	Q8MU76	Q8mu76 anopheles g	c 220	7	7.6	308	2	O6I9Z2	Q6i9z2 homo sapien
148	7	7.6	208	2	Q8T5H7	Q8t5h7 anopheles g	c 221	7	7.6	308	2	Q9H5P9	Q9h5p9 homo sapien
149	7	7.6	208	2	Q7PKT5	Q7pkt5 anopheles g	c 222	7	7.6	308	2	Q8VGA4	Q8vga4 mus musculu
150	7	7.6	210	1	INSR_MACMU	Q28516 macaca mula	c 223	7	7.6	309	1	CEOI_LACLA	Q9cg73 lactococcus
151	7	7.6	211	2	Q6PS86	Q6ps86 streptococ	c 224	7	7.6	309	2	Q6IF41	Q6if41 homo sapien
152	7	7.6	210	2	Q9SNI6	Q9sni6 tribolium c	c 225	7	7.6	310	2	Q8NGT8	Q8ngt8 homo sapien
153	7	7.6	211	2	Q95UA8	Q95ua8 tribolium c	226	7	7.6	311	2	Q6BUW0	Q6buw0 debaryomyce
154	7	7.6	212	1	KAD_STRRR6	Q8drd4 streptococ	227	7	7.6	312	2	Q9BK04	Q9bk04 tribolium c
155	7	7.6	212	2	Q9S4J5	Q9s4j5 streptococ	228	7	7.6	312	2	Q9NHB7	Q9nhb7 tribolium c
156	7	7.6	213	2	Q7XPT0	Q7xpt0 oryza sativ	c 229	7	7.6	313	1	CEO2_LACLA	P15244 lactococcus
157	7	7.6	214	2	Q9Q8T1	Q9q8t1 rabbit fibr	230	7	7.6	314	2	O28600	O28600 archaeoglob
158	7	7.6	215	2	Q6CIH4	Q6cih4 kluyveromyc	c 231	7	7.6	315	2	Q6NX20	Q6nx20 xenopus tro
159	7	7.6	215	2	Q6H5V7	Q6h5v7 oryza sativ	c 232	7	7.6	315	2	Q8VGA2	Q8vga2 mus musculu
160	7	7.6	217	1	GT27_FASHE	P31670 fasciola he	233	7	7.6	315	2	Q7TR60	Q7tr60 mus musculu
161	7	7.6	218	2	Q9XYL9	Q9xyl9 fasciola gi	234	7	7.6	318	2	Q9KM43	Q9km43 vibrio chol
162	7	7.6	219	2	Q9P3F8	Q9p3f8 neurospora	235	7	7.6	320	2	Q75WE6	Q75we6 penicillium

236	7	7.6	320	2	Q6SL44	06s144 armillifer	C 309	7	7.6	421	2	Q6W2X0	Q6w2x0 human immun
C 237	7	7.6	323	2	Q36000	Q36000 trichomitus	310	7	7.6	422	2	Q65CX1	Q65cx1 bacillus li
C 238	7	7.6	325	2	Q8W580	Q8w580 arabidopsis	311	7	7.6	424	2	Q61444	Q61444 drosophila
C 239	7	7.6	327	1	NITI1_HUMAN	Q86x76 homo sapien	312	7	7.6	424	2	Q7KPK6	Q7kpk6 drosophila
240	7	7.6	328	2	Q88282	Q88x82 lactobacilli	313	7	7.6	424	2	Q7KPK5	Q7kpk5 drosophila
241	7	7.6	330	2	Q6BAP9	Q6bap9 debaryomyce	314	7	7.6	426	2	Q9NF73	Q9nf73 drosophila
C 242	7	7.6	332	2	Q92XE3	Q92xe3 rhizobium m	C 315	7	7.6	426	2	Q8SD13	Q8sd13 arabidopsis
243	7	7.6	332	2	Q02796	Q02796 saccharomyc	316	7	7.6	430	2	Q8LSR8	Q8lsr8 oryza sativ
244	7	7.6	332	2	Q6Q5I8	Q6q5i8 saccharomyc	317	7	7.6	434	2	Q9C979	Q9c979 arabidopsis
245	7	7.6	334	2	Q9ABN8	Q9abn8 caulobacter	318	7	7.6	436	2	Q18714	Q18714 leishmania
C 246	7	7.6	338	2	Q6P4C0	Q6p4c0 homo sapien	C 319	7	7.6	438	2	Q9HUD9	Q9hud9 pseudomonas
247	7	7.6	338	2	Q44936	Q44936 strongyloce	320	7	7.6	439	2	Q86MJ3	Q86mj3 caenorhabdi
248	7	7.6	338	2	Q95Y19	Q95y19 caenorhabdi	321	7	7.6	440	2	Q9P566	Q9p566 neurospora
249	7	7.6	342	2	Q06148	Q06148 saccharomyc	322	7	7.6	441	2	Q6M4A0	Q6m4a0 corynebacte
C 250	7	7.6	344	2	Q9LG29	Q9lg29 arabidopsis	323	7	7.6	441	2	Q8NP94	Q8np94 corynebacte
251	7	7.6	344	2	Q9RWF7	Q9rfw7 deinococcus	C 324	7	7.6	448	2	Q7R090	Q7r090 giardia lam
252	7	7.6	345	2	Q8WZ17	Q8wz17 penicillium	325	7	7.6	456	2	Q9LQA0	Q9lqa0 arabidopsis
253	7	7.6	347	1	DTX3_HUMAN	Q8n919 homo sapien	C 326	7	7.6	456	2	Q9XCK8	Q9xck8 streptococ
254	7	7.6	347	1	DTX3_MOUSE	Q80v91 mus musculu	C 327	7	7.6	462	2	Q7XVS1	Q7xvs1 oryza sativ
255	7	7.6	347	1	Q8JFW8	Q8jfw8 brachydanio	328	7	7.6	463	2	Q7S427	Q7s427 neurospora
256	7	7.6	349	2	Q9AR58	Q9ar58 solanum tub	329	7	7.6	463	2	Q6UU50	Q6uu50 oryza sativ
257	7	7.6	349	2	Q92P53	Q9zp53 solanum tub	330	7	7.6	463	2	Q803Y5	Q803y5 brachydanio
258	7	7.6	349	2	Q8FSE8	Q8fse8 corynebacte	331	7	7.6	464	2	Q8MZR6	Q8mzr6 ctenocephal
259	7	7.6	351	2	Q88536	Q88536 mus musculu	332	7	7.6	464	2	Q86MJ4	Q86mj4 caenorhabdi
C 260	7	7.6	353	2	Q7SF02	Q7sf02 neurospora	333	7	7.6	465	2	Q9HFT4	Q9hit4 pleurotus s
C 261	7	7.6	353	2	Q98BM1	Q98bm1 rhizobium l	334	7	7.6	466	2	Q8BH11	Q8bh11 debaryomyce
262	7	7.6	353	2	Q74012	Q74012 mycobacteri	335	7	7.6	469	2	Q8U254	Q8u254 pyrococcus
C 263	7	7.6	363	2	Q7T2F4	Q7t2f4 brachydanio	336	7	7.6	469	2	Q8MQS2	Q8mq82 drosophila
C 264	7	7.6	366	2	Q8VQW5	Q8vqw5 azotobacter	337	7	7.6	469	2	Q91QP5	Q91qp5 melon yello
C 265	7	7.6	368	2	Q6VL75	Q6al75 desulfotale	338	7	7.6	469	2	Q9WB52	Q9wbs2 physalis se
C 266	7	7.6	368	2	Q8VCV4	Q8vcv4 mus musculu	C 339	7	7.6	474	2	Q28424	Q28424 archaeoglob
267	7	7.6	369	2	Q7S4Z9	Q7s4z9 neurospora	340	7	7.6	475	1	SIM1_YEAST	P40472 saccharomyc
268	7	7.6	369	2	Q8XXD5	Q8xxd5 ralstonia s	C 341	7	7.6	475	2	Q7CUZ5	Q7cu25 agrobacteri
C 269	7	7.6	370	2	Q6ZOL8	Q6zol8 oryza sativ	C 342	7	7.6	476	2	Q651C2	Q651c2 oryza sativ
270	7	7.6	372	1	YLUP_PICAN	F34735 picchia angu	C 343	7	7.6	477	2	Q6MP47	Q6mp47 bdellovibri
271	7	7.6	376	1	MID2_YEAST	P36027 saccharomyc	C 344	7	7.6	478	2	Q6CFN8	Q6cfn8 yarrowia li
272	7	7.6	377	2	Q8P7Z1	Q8p7z1 xanthomonas	345	7	7.6	481	2	Q989D0	Q989d0 rhizobium l
273	7	7.6	378	2	Q6W1Z4	Q6w1z4 drosophila	C 346	7	7.6	482	2	Q29120	Q29120 archaeoglob
274	7	7.6	379	2	Q6MYT6	Q6myt6 aspergillus	C 347	7	7.6	488	2	Q18545	Q18545 caenorhabdi
C 275	7	7.6	379	2	Q8VMJ5	Q8vmj5 anabaena sp	C 348	7	7.6	490	2	Q7NQA3	Q7nqa3 chromobacte
C 276	7	7.6	380	2	Q15885	Q15885 homo sapien	C 349	7	7.6	495	2	Q6IMF0	Q6imf0 mus musculu
C 277	7	7.6	381	2	Q67LH1	Q67lh1 symbiobacte	C 350	7	7.6	496	2	Q6C7M6	Q6c7m6 yarrowia li
C 278	7	7.6	384	2	Q916I9	Q916i9 pseudomonas	351	7	7.6	496	2	Q88VA6	Q88va6 lactobacill
279	7	7.6	387	2	Q8SYN0	Q8syn0 drosophila	352	7	7.6	496	2	Q8BX37	Q8bx37 m mus muscu
280	7	7.6	387	2	Q9ZJN7	Q9zjn7 helicobacte	353	7	7.6	499	2	Q95ZK5	Q95zk5 caenorhabdi
C 281	7	7.6	388	2	Q73GJ2	Q73gj2 wolbachia p	C 354	7	7.6	501	2	Q7XMT3	Q7xmt3 oryza sativ
C 282	7	7.6	389	2	Q84SE0	Q84se0 oryza sativ	355	7	7.6	503	1	PUR1_PASMU	Q916b8 pasceurella
283	7	7.6	390	2	Q6C4X7	Q6c4x7 yarrowia li	356	7	7.6	504	2	Q9HR41	Q9hr41 halobacteri
284	7	7.6	393	2	Q9RX12	Q9rx12 deinococcus	C 357	7	7.6	505	1	SCRY_SALTY	P22340 salmonella
C 285	7	7.6	394	2	Q6C8P0	Q6c8p0 aquifex aeo	C 358	7	7.6	505	2	Q6RZ11	Q6rz11 escherichia
C 286	7	7.6	397	2	Q6C8P0	Q6c8p0 yarrowia li	C 359	7	7.6	505	2	Q8PQ85	Q8pq85 xanthomonas
C 287	7	7.6	399	2	Q9HJE6	Q9hje6 thermoplasma	360	7	7.6	506	2	Q9CA74	Q9ca74 arabidopsis
288	7	7.6	399	2	Q9LPK4	Q9lpk4 arabidopsis	361	7	7.6	510	2	Q6SCJ8	Q6scj8 aspergillus
289	7	7.6	401	2	Q6AU99	Q6au99 oryza sativ	C 362	7	7.6	512	2	Q95SN6	Q95sn6 drosophila
C 290	7	7.6	402	1	OXAL_YEAST	Q39952 saccharomyc	C 363	7	7.6	513	2	Q7WU11	Q7wuh1 escherichia
291	7	7.6	405	1	HMX_STRPU	Q26656 strongyloce	C 364	7	7.6	513	2	Q8VVV9	Q8vvv9 arabidopsis
292	7	7.6	407	2	Q7M566	Q7ma66 wolinnella s	365	7	7.6	514	2	Q73QS1	Q73qs1 treponema d
293	7	7.6	407	2	Q9RI96	Q9ri96 streptomyce	C 366	7	7.6	518	2	Q97DP7	Q97dp7 clostridium
C 294	7	7.6	409	2	Q7BT32	Q7bt32 streptomyce	367	7	7.6	519	2	Q755V0	Q755v0 ashbya goss
295	7	7.6	410	2	P72472	P72472 streptomyce	368	7	7.6	524	2	Q8W4X8	Q8w4x8 nicotiana a
C 296	7	7.6	410	2	Q92EP3	Q92ep3 listeria in	369	7	7.6	524	2	Q86MJ5	Q86mj5 caenorhabdi
297	7	7.6	410	2	Q89NX8	Q89nx5 bradyrhizob	C 370	7	7.6	525	1	NU59_YEAST	Q723a6 homo sapien
C 298	7	7.6	411	2	Q63MR8	Q63mr8 burkholderi	371	7	7.6	528	1	Q6B1V8	Q6b1v8 saccharomyc
C 299	7	7.6	414	2	Q6W2W2	Q6w2w2 human immun	372	7	7.6	528	2	Q6B1V8	Q6b1v8 saccharomyc
300	7	7.6	417	2	Q7PS00	Q7ps00 anopheles g	373	7	7.6	528	2	Q6B1V8	Q6b1v8 saccharomyc
301	7	7.6	421	2	Q07009	Q07009 bacillus su	374	7	7.6	529	1	LAC1_PLEOS	Q12729 pleurotus o
C 302	7	7.6	421	2	Q6W2V9	Q6w2v9 human immun	375	7	7.6	529	2	Q8WZJ4	Q8wzj4 penicillium
C 303	7	7.6	421	2	Q6W2W4	Q6w2w4 human immun	376	7	7.6	529	2	Q68HC2	Q68hc2 penicillium
C 304	7	7.6	421	2	Q6W2W5	Q6w2w5 human immun	377	7	7.6	529	2	Q6RYA4	Q6rya4 pleurotus o
C 305	7	7.6	421	2	Q6W2W6	Q6w2w6 human immun	378	7	7.6	530	2	Q8RW07	Q8rw07 solanum tub
C 306	7	7.6	421	2	Q6W2W7	Q6w2w7 human immun	379	7	7.6	531	2	Q6A1A1	Q6aal1 pleurotus s
C 307	7	7.6	421	2	Q6W2W8	Q6w2w8 human immun	C 380	7	7.6	532	2	Q8WZL0	Q8wz10 neurospora
C 308	7	7.6	421	2	Q6W2W9	Q6w2w9 human immun	381	7	7.6	532	2	Q7Z8S3	Q7z8s3 pleurotus s


```
RL J. Cell Sci. 109:805-815(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX Hofmann M.A., Drury S., Fu C., Qu W., Taguchi A., Lu Y., Avila C.,
RA Kambham N., Bierhaus A., Nawroth P., Neurath M.F., Slattery T.,
RA Beach D., McClary J., Nagashima M., Morser J., Stern D., Schmidt A.M.;
RT "RAGE mediates a novel proinflammatory axis: a central cell surface
RT receptor for S100/calgranulin polypeptides.";
RL Cell 97:889-901(1999)
CC -!- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
CC -!- SIMILARITY: Belongs to the S-100 family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D49548; BAA08496.1; -.
DR EMBL; AF011757; AAB65423.1; -.
DR HSSP; P80511; IGQM.
DR InterPro; IPR001751; CaBP_S100.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR010983; EF_Hand_like.
DR Pfam; PF00036; ehand; 1.
DR Pfam; PF01023; S_100; 1.
DR ProDom; PD003407; CaBP_S100; 1.
DR PROSITE; PS00018; EF_HAND; 1.
DR PROSITE; PS00303; S100_CABP; 1.
DR KX Calcium-binding; Metal-binding; Zinc.
FT INIT MET 1 0 0 By similarity.
FT CA_BIND 18 31 EF-hand 1; low affinity (By similarity).
FT CA_BIND 61 72 EF-hand 2; high affinity (By similarity).
SQ SEQUENCE 91 AA; 10554 MW; 66FBC3C1B0354482 CRC64;

Alignment Scores:
Pred. No.: Length: 91
Score: 91.00 Matches: 91
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.91% Indels: 0
DB: 1 Gaps: 0

US-09-910-208B-1 (1-276) x S112_BOVIN (1-91)

QY 4 ACTAAGCTGGAAGATCACCTGGAGGAATCATCAACATCTTCACCACTCTCCAGTACTCCGTTCCG 63
Db 1 ThrLysLeuGluAspHisLeuGluGlyIleAsnIlePheHisGlnTyrSerValArg 20
QY 64 GTGGGGCATTTGACACCTTCAACAGCGTGAGCTGAAGCAGTGTATCATCAAGGAACATT 123
Db 21 ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40
QY 124 CCCAAACCTCCAGAACACCAAGATCAACCTTACCAATATTCACAAATATTTCCAGACCTG 183
Db 41 ProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAspLeu 60
QY 184 GATGCCGATATAA 195
Db 61 AspAlaAspLys 64

RESULT 3
ID S112_PIG STANDARD; PRT; 91 AA.
AC P80310;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Calgranulin C (CAGC).
GN Name=S100A12;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE.
RC TISSUE=Granulocyte;
RX MEDLINE=95050708; PubMed=7961855;
RA Dell'Angelica E.C., Schleicher C.H., Santome J.A.;
RT "Primary structure and binding properties of calgranulin C, a novel
RT S100-like calcium-binding protein from pig granulocytes.";
RL J. Biol. Chem. 269:28929-28936(1994).
CC -!- TISSUE SPECIFICITY: Found essentially in granulocytes with small
```

CC amounts found in lymphocytes.
 CC -!- MISCELLANEOUS: In the absence of zinc binds one calcium ion per
 CC molecule, in the presence of zinc binds two calcium ions per
 CC molecule.
 CC -!- SIMILARITY: Belongs to the S-100 family.
 CC -!- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
 DR PIR, A55406; A55406.
 DR HSP, P00511; IEB.
 DR InterPro; IPR001751; CaBP_S100.
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR010983; EF_Hand_like.
 DR Pfam; PF00036; ehand; 1.
 DR Pfam; PF01023; S_100; 1.
 DR ProDom; PD003407; CaBP_S100; 1.
 DR PROSITE; PS00018; EF_HAND; FALSE_NEG.
 DR PROSITE; PS00303; S100_CaBP; 1.
 KW Calcium-binding; Direct protein sequencing; Metal-binding; Zinc.
 FT CA_BIND 18 31 EF-hand 1; low affinity (By similarity).
 FT CA_BIND 61 72 EF-hand 2; high affinity (By similarity).
 SQ SEQUENCE 91 AA; 10614 MW; B4204461432D7FCE CRC64;
 Alignment Scores:
 Pred. No.: 3,04e-11 Length: 91
 Score: 20.00 Matches: 20
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 21.74% Indels: 0
 DB: 1 Gaps: 0
 US-09-910-208B-1 (1-276) x S112_PIG (1-91)
 QY 4 ACTAAGCTGGAGATCAGCTGGAGGAGATCATCATCATCTTCCACAGTACTCCGTCGG 63
 DB 1 ThrLysLeuGluAspHisLeuGluGlyIleIleAsnIlePheHisGlnTyrSerValArg 20
 RESULT 4
 S109_RABIT STANDARD; PRT; 118 AA.
 ID S109_RABIT
 AC F50117;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Calgranulin B (Migration inhibitory factor-related protein 14) (MRP-14) (Fragment).
 GN Name=S100A9; Synonyms=MRP-14;
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OC NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=New Zealand white; TISSUE=Neutrophils;
 RX MEDLINE=9635278; PubMed=8702689; DOI=10.1074/jbc.271.33.19802;
 RA Yang Z., de Veer M.J., Gardiner E.E., Devenish R.J., Handley C.J.,
 RA Underwood J.R., Robinson H.C.;
 RT "Rabbit polymorphonuclear neutrophils form 35S-labeled S-sulfo-
 calgranulin C when incubated with inorganic [35S]sulfate.";
 RL J. Biol. Chem. 271:19802-19809(1996).
 RN [2]
 RP SEQUENCE OF 45-82 FROM N.A.
 RC STRAIN=New Zealand white;
 RX MEDLINE=94198229; PubMed=8148323;
 RA Mori S., Goto K., Goto F., Matakami K., Ohkawara S., Yoshinaga M.;
 RT "Dynamic changes in mRNA expression of neutrophils during the course
 of acute inflammation in rabbits.";
 RL Int. Immunol. 6:149-156(1994).
 CC -!- SIMILARITY: Belongs to the S-100 family.
 CC -!- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
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 CC -----
 DR EMBL; AF091849; AAC61771.1; -.
 DR EMBL; D17404; BAA04227.1; -.
 DR PIR; I46861; I46861.
 DR HSP; P06702; IIRJ.
 DR InterPro; IPR001751; CaBP_S100.
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR010983; EF_Hand_like.
 DR Pfam; PF00036; ehand; 1.
 DR Pfam; PF01023; S_100; 1.
 DR ProDom; PD003407; CaBP_S100; 1.
 DR PROSITE; PS00018; EF_HAND; 1.
 DR PROSITE; PS00303; S100_CaBP; 1.
 KW Calcium-binding; Repeat.
 FT NON_TER 1 1
 FT CA_BIND 9 22 EF-hand 1; low affinity (Potential).
 FT CA_BIND 53 64 EF-hand 2; high affinity (Potential).
 FT DOMAIN 103 118 2 X 8 AA tandem repeats of G-H-G-H-G-H-S-H.
 FT REPEAT 103 110 1.
 FT REPEAT 111 118 2.
 SQ SEQUENCE 118 AA; 13292 MW; 7496118E21AD5C41 CRC64;
 Alignment Scores:
 Pred. No.: 0.000445 Length: 118
 Score: 13.00 Matches: 13
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 14.13% Indels: 0
 DB: 1 Gaps: 0
 US-09-910-208B-1 (1-276) x S109_RABIT (1-118)
 QY 31 ATCATCAACATCTCCACAGTACTCCGTCGGTGGGG 69
 DB 1 IleIleAsnIlePheHisGlnTyrSerValArgValGly 13
 RESULT 5
 S109_BOVIN STANDARD; PRT; 122 AA.
 ID S109_BOVIN
 AC P28783;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Calgranulin B (Neutrophil cytosolic 23 kDa protein) (P23) (BEE22) (Fragment).
 DE (Fragment).
 GN Name=S100A9;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=oesophageal epithelium;
 RX MEDLINE=93280230; PubMed=8505358;
 RA Tang T.K., Hong T.-M., Lin C.-Y., Lai M.-L., Liu C.H.L., Lo H.-J.,
 RA Wang M.-E., Chen L.B., Chen W.-T., Ip W., Lin D.C., Lin J.J.-C.,
 RA Lin S., Sun T.-T., Wang E., Wang J.L., Wu R., Wu C.-W., Chien S.;
 RT "Nuclear proteins of the bovine esophageal epithelium. I. Monoclonal
 antibody W2 specifically reacts with condensed nuclei of
 differentiated superficial cells.";
 RL J. Cell Sci. 104:237-247(1993).
 RN [2]
 RP SEQUENCE OF 4-56.
 RC TISSUE=Neutrophils;
 RX MEDLINE=92304974; PubMed=1610833;
 RA Dianoux A.-C., Stasia M.-J., Garin J., Gagnon J., Vignais P.V.;
 RT "The 23-kilodalton protein, a substrate of protein kinase C, in bovine
 neutrophil cytosol is a member of the S100 family.";

RL Biochemistry 31:5898-5905(1992).
 CC -I- SUBUNIT: Disulfide linked heterodimer of a 7/11 kDa and a 22/23
 CC kDa subunits.
 CC -I- SUBCELLULAR LOCATION: Cytoplasmic; loosely associated to the
 CC cytoskeleton.
 CC -I- TISSUE SPECIFICITY: Found essentially in phagocytic cells.
 CC -I- PTM: Phosphorylated by protein kinase C.
 CC -I- SIMILARITY: Belongs to the S-100 family.
 CC -I- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
 DR HSSP; P06702; IIRJ.
 DR InterPro: IPR001751; CaBP_S100.
 DR InterPro: IPR002048; EF-hand.
 DR InterPro: IPR010983; EF_Hand_like.
 DR Pfam; PF00036; ehand; 1.
 DR ProDom; PD003407; CaBP_S100; 1.
 DR PROSITE; PS00018; EF_HAND; PARTIAL.
 DR PROSITE; PS00303; S100_CABP; 1.
 KW Calcium-binding; Direct protein sequencing.
 FT NON_TER 1 1
 FT CA_BIND 19 32 EF-hand 1; low affinity (Potential).
 FT CA_BIND 63 74 EF-hand 2; high affinity (Potential).
 SQ SEQUENCE 122 AA; 13673 MW; F3CA8C4806BECCD CRC64;

Alignment Scores:
 Pred. No.: 0.0498 Length: 122
 Score: 11.00 Matches: 11
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 11.96% Indels: 0
 DB: 1 Gaps: 0

US-09-910-208B-1 (1-276) x S109_BOVIN (1-122)

QY 31 ATCAACATCTTCACACGACTCCGTCGG 63
 Db 11 IIEIAAAsnIlePheHisGlnTyrSerValArg 21

RESULT 6

S112_RABIT
 ID S112_RABIT STANDARD; PRT; 81 AA.
 AC O77791;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Calgranulin C (CAGC) (Fragment).
 GN Name=S100A12;
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Lagomorpha; Leporidae; Oryctolagus.
 OC NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC STRAIN=New Zealand white; TISSUE=Neutrophils;
 RX MEDLINE=96355278; PubMed=8702688; DOI=10.1074/jbc.271.33.19802;
 RA Yang Z., Deveer M.J., Gardiner E.E., Devenish R.J., Handley C.J.,
 RA Underwood J.R., Robinson H.C.;
 RT "Rabbit polymorphonuclear neutrophils form 35S-labeled S-sulfo-
 calgranulin C when incubated with inorganic [35S]sulfate.";
 RL J. Biol. Chem. 271:19802-19809(1996).
 CC -I- SIMILARITY: Belongs to the S-100 family.
 CC -I- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
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 CC -----
 CC EMBL; AF091848; AAC61770.1; -;
 DR HSSP; P80511; 1E8A.

DR InterPro: IPR001751; CaBP_S100.
 DR InterPro: IPR002048; EF-hand.
 DR InterPro: IPR010983; EF_Hand_like.
 DR Pfam; PF00036; ehand; 1.
 DR ProDom; PD003407; CaBP_S100; 1.
 DR PROSITE; PS00018; EF_HAND; 1.
 DR PROSITE; PS00303; S100_CABP; 1.
 KW Calcium-binding; Direct protein sequencing.
 FT NON_TER 1 1
 FT CA_BIND 8 21 EF-hand 1; low affinity (By similarity).
 FT CA_BIND 51 62 EF-hand 2; high affinity (By similarity).
 SQ SEQUENCE 81 AA; 9401 MW; 95E67A209180CB66 CRC64;

Alignment Scores:
 Pred. No.: 0.554 Length: 81
 Score: 10.00 Matches: 10
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 10.87% Indels: 0
 DB: 1 Gaps: 0

US-09-910-208B-1 (1-276) x S112_RABIT (1-81)

QY 34 ATCAACATCTTCACACGACTCCGTCGG 63
 Db 1 IIEAAsnIlePheHisGlnTyrSerValArg 10

RESULT 7

S112_HUMAN
 ID S112_HUMAN STANDARD; PRT; 91 AA.
 AC P80511; P83219;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Calgranulin c (CAGC) (CGRP) (Neutrophil S100 protein) (Calcium-binding
 DE protein in amniotic fluid 1) (CAAF1) (p6) [Contains: Calcitermin].
 GN Name=S100A12;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97138564; PubMed=8985590; DOI=10.1016/S0143-4160(96)90087-1;
 RA Wicki R., Marenholz I., Mischke D., Schaefer B.W., Heizmann C.W.;
 RT "Characterization of the human S100A12 (calgranulin C, p6, CAAF1,
 CGRP) gene, a new member of the S100 gene cluster on chromosome
 RT 1q21.";
 RT Cell Calcium 20:459-464(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96192053; PubMed=8619860; DOI=10.1006/bbrc.1996.0600;
 RA Yamamura T., Hitomi J., Nagasaki K., Suzuki M., Takahashi E.,
 RA Saito S., Tsukada T., Yamaguchi K.;
 RT "Human CAAF1 gene -- molecular cloning, gene structure, and chromosome
 RT mapping.";
 RL Biochem. Biophys. Res. Commun. 221:356-360(1996).
 RN [3]
 RP SEQUENCE.
 RX MEDLINE=96192069; PubMed=8619876; DOI=10.1006/bbrc.1996.0616;
 RA Marti T., Ertmann K.D., Gallin M.Y.;
 RT "Host-parasite interaction in human onchocerciasis: identification and
 RT sequence analysis of a novel human calgranulin.";
 RL Biochem. Biophys. Res. Commun. 221:454-458(1996).
 RN [4]
 RP SEQUENCE.
 RC TISSUE=Neutrophils;
 RX MEDLINE=96332419; PubMed=8769108; DOI=10.1006/bbrc.1996.1144;
 RA Ilg E.C., Irozier H., Buergisser D.M., Kueter T., Markert M.,
 RA Guignard F., Hunziker P., Birchler N., Heizmann C.W.;
 RT "Amino acid sequence determination of human S100A12 (p6, calgranulin
 RT C, CGRP, CAAF1) by tandem mass spectrometry.";

RL Biochem. Biophys. Res. Commun. 225:146-150(1996).
RN [5]
RP SEQUENCE OF 1-20.
RX MEDLINE=95351965; PubMed=7626002;
RA Guignard F., Maue J., Markert M.;
RT "Identification and characterization of a novel human neutrophil
protein related to the S100 family.";
RL Biochem. J. 309:395-401(1995).
RN [6]
RP SEQUENCE OF 77-91, ANTIMICROBIAL ACTIVITY, AND MASS SPECTROMETRY.
RC TISSUE=Nasal mucus;
RX MEDLINE=21413725; PubMed=11522286; DOI=10.1016/S0014-5793(01)02731-4;
RA Cole A.M., Kim Y.-H., Tahk S., Hong T., Weis P., Waring A.J., Ganz T.;
RT "Calcitermin, a novel antimicrobial peptide isolated from human airway
secretions.";
RL FEBS Lett. 504:5-10(2001).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (1.95 ANGSTROMS).
RX MEDLINE=21065388; PubMed=11134923; DOI=10.1107/S090744490001458X;
RA Moroz O.V., Antson A.A., Murshudov G.N., Maitland N.J., Dodson G.G.,
RA Wilson K.S., Skibshoj I., Lukanidin E.M., Bronstein I.B.;
RT "The three-dimensional structure of human S100A12.";
RL Acta Crystallogr. D 57:20-29(2001).
CC -!- FUNCTION: Calcitermin possesses antifungal activity against
C. albicans and is also active against E.coli and P.aeruginosa but
not L.mohocytogenes and S.aureus.
CC -!- SUBUNIT: Homodimer.
CC -!- TISSUE SPECIFICITY: Monocytes and lymphocytes.
CC -!- MASS SPECTROMETRY: MW=10444; METHOD=Electrospray; RANGE=1-91;
NOTE=Ref.6.
CC -!- MASS SPECTROMETRY: MW=1688.9; METHOD=MALDI; RANGE=77-91;
NOTE=Ref.6.
CC -!- SIMILARITY: Belongs to the S-100 family.
CC -!- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
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DR EMBL; X97859; CAA66453.1; -
DR EMBL; X98288; CAA66934.1; -
DR EMBL; X98289; CAA66934.1; JOINED.
DR EMBL; X98290; CAA66934.1; JOINED.
DR EMBL; X98289; CAB94792.1; -
DR EMBL; X98290; CAB94792.1; JOINED.
DR EMBL; D49549; BAA08497.1; -
DR EMBL; D83654; BAA12036.1; -
DR EMBL; D83657; BAA12030.1; -
DR PIR; JC4712; JC4712.
DR PDB; 1E8A; X-ray; A/B=1-91.
DR PDB; 1QGB; X-ray; A/B/C/D/E/F/G/H/I/J/K/L=1-91.
DR PDB; 1QDB; X-ray; A/B/C/D/E/F=1-91.
DR Genew; HGNC:10489; S100A12.
DR MIM; 603112; -
DR GO; GO:0005829; Cytosol; TAS.
DR GO; GO:0005626; C:insoluble fraction; TAS.
DR GO; GO:0005509; F:calcium ion binding; TAS.
DR GO; GO:0006954; P:inflammatory response; TAS.
DR InterPro; IPR001751; CaBP_S100.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR010983; EF_Hand_like.
DR Pfam; PF00036; ehand; 1.
DR Pfam; PF01023; S_100; 1.
DR ProDom; PD003407; CaBP_S100; 1.
DR PROSITE; PS00018; EF_HAND; FALSE_NEG.
DR PROSITE; PS00303; S100_CaBP; 1.
KW 3D-structure; Antibiotic; Calcium-binding; Direct protein sequencing;
KW Fungicide; Metal-binding; Zinc.
FT INIT_MET 0 0

FT PEPTIDE 77 91 Calcitermin.
FT CA_BIND 18 31 EF-hand 1; low affinity (By similarity).
FT CA_BIND 61 72 EF-hand 2; high affinity (By similarity).
FT HELIX 2 18
FT TURN 19 19
FT TURN 24 25
FT STRAND 26 27
FT HELIX 29 39
FT TURN 41 43
FT TURN 45 48
FT HELIX 50 60
FT TURN 62 63
FT STRAND 68 69
FT HELIX 70 85
SQ SEQUENCE 91 AA; 10444 MW; 325685EA8695F6B7 CRC64;
Alignment Scores:
Pred. No.: 5.79 Length: 91
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 9.78% Indels: 0
DB: 1 Gaps: 0
US-09-910-208B-1 (1-276) x S112_HUMAN (1-91)
QY 37 AACATCTCCACGACTCCGTCGG 63
DB 12 AenIIePheHisGlnTyrSerValArg 20
RESULT 8
P78947 PRELIMINARY; PRT; 568 AA.
ID P78947
AC P78947; 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Similar to p1r: S52731.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972h-;
RA Kohnosu A., Niwa O., Yano M., Saitoh S., Katayama T., Nagao K.,
RA Yanagida M.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; D83993; BAA12197.1; -
SQ SEQUENCE 568 AA; 64255 MW; CBF7BD60B8F0DFA6 CRC64;
Alignment Scores:
Pred. No.: 4.7 Length: 568
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 9.78% Indels: 0
DB: 2 Gaps: 0
US-09-910-208B-1 (1-276) x P78947 (1-568)
QY 200 CGGTCTTTATCGCATCCAGGTCCTGG 174
DB 154 ProSerLeuSerAlaSerArgSerIrp 162
RESULT 9
Q9HGP1 PRELIMINARY; PRT; 605 AA.
ID Q9HGP1
AC Q9HGP1; 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE SPBC29B5.04c protein.
GN Names:SPBC29B5.04c;
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972h-;
RX MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne S., Lyne R., Stewart A.,
RA Scourto J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odeil C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weijtens I., Vanstreels E., Rieger M., Schafer M., Muller-Auer S.,
RA Gabel C., Fuchs M., Dusterhoft A., Fritz C., Holzer E., Moestl D.,
RA Hilbert H., Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R.,
RA Pohl T.M., Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RL "The genome sequence of Schizosaccharomycetes pombe";
RT Nature 415:871-880(2002).
DR EMBL; AL391603; CAC05513.1; -;
DR GeneDB SPombe; SPBC29B5.04c; -;
SQ SEQUENCE 605 AA; 68508 MW; 24558A5C0357448F CRC64;

Alignment Scores:
Pred. No.: 4.67 Length: 605
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 9.78% Indels: 0
DB: 2 Gaps: 0

US-09-910-208b-1 (1-276) x Q9HGP1 (1-605)
QY 200 CCCTCTTTATCGCATCCAGTCTTGG 174
Db 154 ProSerLeuSerAlaSerArgSerTrp 162
|||||

RESULT 10
O64103 PRELIMINARY; PRT; 72 AA.
AC O64103;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein yopt.
GN Names:yopt;
OS Bacteriophage SPBc2.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
OX NCBI_TaxID=66797;
RN [1]
RP SEQUENCE FROM N.A.
RA Lazarevic V., Dusterhoft A., Soldo B., Hilbert H., Muel C.,
RA Karamata D.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF020713; AAC13063.1; -;

DR PIR; T12854; T12854.
KW Hypothetical protein.
SQ SEQUENCE 72 AA; 8078 MW; EF0EFA5D3DE275A4 CRC64;
Alignment Scores:
Pred. No.: 63.1 Length: 72
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 8.70% Indels: 0
DB: 2 Gaps: 0

US-09-910-208b-1 (1-276) x O64103 (1-72)
QY 219 TTCTCAAAAGCTGACGGCTCCGTC 196
|||||
Db 45 PreLeuLyAlaAspGlySerVal 52
|||||

RESULT 11
O34498 PRELIMINARY; PRT; 72 AA.
AC O34498;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Yopt protein.
GN Names:yopt; OrderedLocusNames=BSU20770;
DE Bacillus subtilis.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377; DOI=10.1038/36786;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Entian K.-D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Gallizi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guiseppe G., Guy B.J., Haga K., Haech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullio M.F., Itaya M.,
RA Jones L.-M., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M.,
RA Klein C., Kobayashi Y., Koetter P., Koningsstein G., Krogh S.,
RA Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J.,
RA Lazarevic V., Lee S.M., Levine A., Liu H., Masuda S., Mael C.,
RA Medigue C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S.,
RA Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B.,
RA Park S.H., Parro V., Pohl T.M., Portetelle D., Porwollik S.,
RA Prescott A.M., Pressecan E., Fujic P., Purnelle B., Rapoport G.,
RA Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B.,
RA Rose M., Sadaie Y., Sato T., Scanlan E., Schleich S., Schroeter R.,
RA Scoffone F., Sekiguchi J., Sekowska A., Seror S.J., Seror P.,
RA Shin B.S., Soldo B., Sorokin A., Tacconi B., Takagi T., Takahashi H.,
RA Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpestra P.,
RA Tognoni A., Tosato V., Uchiyama S., Vandenbol M., Vannier F.,
RA Vassarotti A., Viari A., Wambutt R., Wedler H., Wedler H.,
RA Weitzengger T., Winters P., Wipat A., Yamamoto H., Yamane K.,
RA Yasumoto K., Yata K., Yoshida K., Yoshikawa H., Zumstein E.,
RA Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis";
RL Nature 390:249-256(1997).
RL EMBL; Z99114; CAB13969.1; -;
KW Complete proteome.
SQ SEQUENCE 72 AA; 8078 MW; EF0EFA5D3DE275A4 CRC64;

Alignment Scores:
Pred. No.: 63.1 Length: 72
Score: 8.00 Matches: 8

Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 8.70% Indels: 0
 DB: 2 Gaps: 0

US-09-910-208B-1 (1-276) x Q34498 (1-72)

QY 219 TTCTCAAGCTGAGCGCTCCGTC 196
 DB 45 PheLeuLySAlaSpGlySerVal 52

RESULT 12

Q94577
 ID Q94577 PRELIMINARY; PRT; 158 AA.
 AC Q94577;
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE HEHBOX7 (Fragment).
 GN Name=Hehbox7;
 OS Helicoidaris erythrogramma (Sea urchin).
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 OC Echinoidea; Euechinozoa; Echinacea; Echinozoa; Echinometridae;
 OC Helicoidaris.
 OX NCBI_TaxID=7634;
 RN [1]_
 RP SEQUENCE FROM N.A.
 RA Popodi E., Andrews M.E., Kissinger J.C., Raff R.A.;
 RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
 CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
 DR EMBL; U31564; AAB09407.1; -.
 DR HSSP; P09631; 1PUF.
 DR TRANSFAC; T03769; -.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR001356; Homeobox.
 DR InterPro; IPR009057; Homeodomain like.
 DR InterPro; IPR000047; HTH_lambrepresr.
 DR Pfam; PF00046; Homeobox; 1.
 DR PRINTS; PR00024; HOMEBOX.
 DR PRINTS; PR00031; HTHREPRESS.
 DR SMART; SM00389; HOX; 1.
 DR PROSITE; PS00027; HOMEBOX_1; 1.
 DR PROSITE; PS50071; HOMEBOX_2; 1.
 KW DNA-binding; Homeobox; Nuclear protein.
 FT NON_TER
 SQ SEQUENCE 158 AA; 18102 MW; B92185PEAA4CB148 CRC64;

Alignment Scores:
 Pred. No.: 57.7 Length: 158
 Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 8.70% Indels: 0
 DB: 2 Gaps: 0

US-09-910-208B-1 (1-276) x Q94577 (1-158)

QY 32 TCATCAACATCTTCCACCGAGTACT 55
 DB 102 SerSerThrSerSerThrSerThr 109

RESULT 13

Q9597
 ID Q9597 PRELIMINARY; PRT; 225 AA.
 AC Q9597;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE MK35 lipoprotein precursor.
 OS Mycobacterium kansasii.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1768;
 RN [1]_
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bostrom;
 RX MEDLINE=96036229; PubMed=7582031;
 RA Armoa G.R., Rouse D.A., Nair J., Mackall J.C., Morris S.L.;
 RT "A highly immunogenic putative Mycobacterium kansasii lipoprotein."
 RL Microbiology 141:2705-2712(1995).
 DR EMBL; U20446; AAA90989.1; -.
 KW Lipoprotein; Signal.
 FT SIGNAL
 FT CHAIN 6 13 Potential.
 FT CHAIN 14 225 MK35 lipoprotein.
 SQ SEQUENCE 225 AA; 23083 MW; F5B90E23CCCAAB4D CRC64;

Alignment Scores:

Pred. No.: 55.4 Length: 225
 Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 8.70% Indels: 0
 DB: 2 Gaps: 0

US-09-910-208B-1 (1-276) x Q49597 (1-225)

QY 32 TCATCAACATCTTCCACCGAGTACT 55
 DB 34 SerSerThrSerSerThrSerThr 41

RESULT 14

Q20587
 ID Q20587 PRELIMINARY; PRT; 275 AA.
 AC Q20587;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein F49C12.10.
 GN ORFNames=F49C12.10;
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
 OC Rhabditidae; Rhabditinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]_
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA none;
 RT "Genome sequence of the nematode C.elegans: A platform for
 RT investigating biology."
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Gardner A.E.;
 RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Z68227; CAA92513.1; -.
 DR PIR; T22414; T22414.
 DR WormBase; WBGene00009879; F49C12.10.
 DR WormPep; F49C12.10; CE03370.
 KW Hypothetical protein.
 SQ SEQUENCE 275 AA; 32355 MW; 5CDD0DCE7381F9E CRC64;

Alignment Scores:

Pred. No.: 54.2 Length: 275
 Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 8.70% Indels: 0
 DB: 2 Gaps: 0

US-09-910-208B-1 (1-276) x Q20587 (1-275)

QY 51 GTACTCCGTTCCGGTGGGCAATT 74

```
|||||
Db      174 ValLeuArgSerGlyAlaPhe 181

RESULT 15
Q7MSF1
ID Q7MSF1 PRELIMINARY; PRT; 319 AA.
AC Q7MSF1;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
DE OrderedLocusNames=WS0523;
GN Wolinella succinogenes.
OS Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC Helicobacteraceae; Wolinella.
OX NCBI_TaxID=844;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=DSMZ 1740;
RX MEDLINE=2282897; PubMed=14500908; DOI=10.1073/pnas.1932838100;
RA Baar C., Eppinger M., Raddatz G., Simon J., Lanz C., Klimmek O.,
RA Nandakumar R., Gross R., Rosinus A., Keller H., Jagtap P., Linke B.,
RA Meyer F., Lederer H., Schuster S.C.;
RT "Complete genome sequence and analysis of Wolinella succinogenes.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:11690-11695(2003).
DR EMBL; BX571658; CAE09660.1; -.
DR InterPro; IPR001440; TPR.
DR InterPro; IPR008941; TPR-like.
DR PROSITE; PS50293; TPR_REGION; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 319 AA; 35080 MW; 6BDBF2D7D8D7DEB4 CRC64;

Alignment Scores:
Pred. No.: 53.2 Length: 319
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 8.70% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-1 (1-276) x Q7MSF1 (1-319)

QY 74 TCGACACCTCAACAGCGTGAGC 97
Db 15 SerThrProSerThrSerValSer 22

Search completed: February 23, 2005, 11:49:08
Job time : 134 secs
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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: February 23, 2005, 11:23:55 ; Search time 113.5 Seconds
(without alignments)
1880.984 Million cell updates/sec

Title: US-09-910-208B-1
Perfect score: 92
Sequence: 1 atgactaagctggaagatca.....acatagatatccacaagag 276

Scoring table: OLIGO

Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2105692 seqs, 386760381 residues

Word size: 1

Total number of hits satisfying chosen parameters: 3967864

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Command line parameters:

-MODEL=frame+n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO_epool_p/HADDAD-09-910208/runat_23022005_101828_14945/app_query.fasta_1
-DB=A_Geneseq_16Dec04 -QMTI=fastan -SUFFIX=oligo.rag -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=500 -DOCLALIGN=200 -HAPS SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL
-USER=HADDAD-09-910208 -HEAPSZE=500 -MINLEN=0 -MAXLEN=2000000000
-ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORE=0 -WAIT -DSFBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : A_Geneseq_16Dec04:*

- 1: Geneseq1980s:*
- 2: Geneseq1990s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001s:*
- 5: Geneseq2002s:*
- 6: Geneseq2003as:*
- 7: Geneseq2003bs:*
- 8: Geneseq2004as:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	92	100.0	92	AAW03563	Calcium b
2	90	97.8	90	AA90765	AA90765 Bovine CA
3	90	97.8	90	AA90764	AA90764 Bovine co
4	20	21.7	91	AAW01826	AAW01826 Component
5	20	21.7	91	AAW93819	AAW93819 Angiotrop
6	18	19.6	18	AA90766	AA90766 Endo Lys
7	15	16.3	30	AAE85169	AAE85169 Bovine se
8	15	16.3	50	AA90763	AA90763 Human EN
9	9	9.8	46	ABB43183	ABB43183 Peptide #
10	9	9.8	46	AAW37021	AAW37021 Peptide #

11	9	9.8	46	4	ABB26281	Abb26281 Protein #
12	9	9.8	46	4	AAW76914	Aam76914 Human bon
13	9	9.8	46	4	AAW64093	Aam64093 Human bra
14	9	9.8	46	4	ABG58579	Abg58579 Human liv
15	9	9.8	46	5	ABG46027	Abg46027 Human pep
16	9	9.8	91	4	AAW31909	Aab31909 Amino aci
17	9	9.8	92	2	AAW03564	Aaw03564 Calcium b
18	9	9.8	92	2	AAW24137	Aaw24137 Human che
19	9	9.8	92	3	AAW45542	Aab45542 Human S10
20	9	9.8	92	4	AAW31911	Aab31911 Amino aci
21	9	9.8	92	4	AAW31907	Aab31907 Amino aci
22	9	9.8	92	4	AAW31908	Aab31908 Amino aci
23	9	9.8	92	7	ADA93649	Ada93649 Human cal
24	9	9.8	92	8	ADN04192	Adn04192 Antipsori
25	9	9.8	92	8	ADO19540	Ado19540 Human PRO
26	9	9.8	92	8	ADR14333	Adr14333 Human NF-
27	9	9.8	92	8	ADP23921	Adp23921 PRO polyP
28	9	9.8	92	8	ADS74331	Ads74331 PRO polyP
29	8	8.7	61	8	ABO56539	Abos6539 Human gen
30	8	8.7	142	5	ABP00813	Abp00813 Human ORF
31	8	8.7	153	3	AAW32827	Abw32827 Eucalyptu
32	8	8.7	382	4	ABW63454	Abw63454 Drosophil
33	8	8.7	584	3	AAW46902	Aag46902 Arabidops
34	8	8.7	628	8	ADL04785	Adl04785 M. catar
35	8	8.7	666	4	ABG19647	Abg19647 Novel hum
36	8	8.7	723	8	ADS23460	Ads23460 Bacterial
37	8	8.7	725	8	ADN19351	Adn19351 Bacterial
38	8	8.7	845	2	AAW17890	Aaw17890 Photorhab
39	8	8.7	845	2	AAW56579	Aaw56579 Fragment
40	8	8.7	1849	2	AAW17900	Aaw17900 Photorhab
41	8	8.7	1849	2	AAW56573	Aaw56573 Toxin Tcd
42	8	8.7	2516	2	AAW17899	Aaw17899 Photorhab
43	8	8.7	2516	2	AAW56572	Aaw56572 Toxin Tcd
44	8	8.7	2516	4	AAW72609	Aab72609 Photorhab
45	8	8.7	2516	5	ABG32651	Abg32651 P. lumine
46	8	8.7	2516	8	ADP18614	Adp18614 Photorhab
47	8	8.7	2516	8	ADR21575	Adr21575 Photorhab
48	8	8.7	2517	4	AAW72611	Aaw72611 Modified
49	8	8.7	2522	2	AAW33729	Aay33729 Photorhab
50	8	8.7	2526	6	ABM70229	Abm70229 Photorhab
51	8	8.7	2537	4	ABW72614	Aab72614 TcdA toxi
52	8	8.7	1938	6	ABW98398	Abw98398 Streptomy
53	7	7.6	29	4	AAW17878	Aam17878 Peptide #
54	7	7.6	29	4	ABW36899	Abw36899 Peptide #
55	7	7.6	29	4	AAW30385	Aam30385 Peptide #
56	7	7.6	29	4	ABW31682	Abw31682 Peptide #
57	7	7.6	29	4	ABW22223	Abw22223 Protein #
58	7	7.6	29	4	AAW70049	Aam70049 Human bon
59	7	7.6	29	4	AAW57642	Aam57642 Human bra
60	7	7.6	29	4	ABG51744	Abg51744 Human liv
61	7	7.6	29	4	AAW05526	Aam05526 Peptide #
62	7	7.6	29	5	ABG39680	Abg39680 Human pep
63	7	7.6	51	4	AAU57122	Aau57122 Propionib
64	7	7.6	51	6	ABW53641	Abw53641 Propionib
65	7	7.6	53	4	ABW42820	Abw42820 Peptide #
66	7	7.6	53	4	AAW36633	Aam36633 Peptide #
67	7	7.6	53	4	AAW76526	Aam76526 Human bon
68	7	7.6	53	4	AAU65772	Aau65772 Propionib
69	7	7.6	53	4	AAU49027	Aau49027 Propionib
70	7	7.6	53	4	AAW63712	Aam63712 Human bra
71	7	7.6	53	4	ABW58226	Abw58226 Human liv
72	7	7.6	53	6	ABM62291	Abm62291 Propionib
73	7	7.6	53	6	ABW45546	Abw45546 Propionib
74	7	7.6	73	4	AAU44124	Aau44124 Propionib
75	7	7.6	73	6	ABW40643	Abw40643 Propionib
76	7	7.6	74	4	AAW81097	Aam81097 Human hae
77	7	7.6	74	4	AAW81541	Aam81541 Human hae
78	7	7.6	77	7	ABO80252	Abos80252 Pseudomon
79	7	7.6	78	3	AAW19967	Aag19967 Arabidops
80	7	7.6	79	5	ABP32302	Abp32302 Human ORF
81	7	7.6	85	4	ABW52953	Abw52953 Human tra
82	7	7.6	86	3	AAW39135	Aaw39135 Human sec
83	7	7.6	98	3	AAW19966	Aag19966 Arabidops

C 84	7	7.6	103	5	ABP69193	Abp69193 Human pol	C 157	7	7.6	309	4	AAU24751	Aau24751 Human olf
C 85	7	7.6	104	6	ADA57076	Ada57076 Human sec	C 158	7	7.6	309	5	ABG76845	Abg76845 Human G-p
C 86	7	7.6	104	6	ADA40928	Ada40928 Human sec	C 159	7	7.6	309	5	ABB54573	Abb54573 Lactococc
C 87	7	7.6	104	7	ADD37928	Add37928 Human sec	C 160	7	7.6	309	5	AAU85371	Aau85371 G-coupled
C 88	7	7.6	105	2	AAW88615	Aaw88615 Secreted	C 161	7	7.6	310	3	AAG23168	Aag23168 Arabidops
C 89	7	7.6	105	4	ABW50382	Abw50382 Human sec	C 162	7	7.6	310	3	AAG45838	Aag45838 Arabidops
C 90	7	7.6	105	6	ABO44639	Ab044639 Novel hum	C 163	7	7.6	310	6	ABP97070	Abp97070 Human G p
C 91	7	7.6	105	6	ABO26119	Ab026119 Human pro	C 164	7	7.6	310	6	ADC85653	Adc85653 Human GPC
C 92	7	7.6	109	8	AQ65397	Aq65397 Novel hum	C 165	7	7.6	310	7	ADG84279	Adg84279 Human TMD
C 93	7	7.6	117	7	ADF59399	Adf59399 Human pol	C 166	7	7.6	310	7	ADG84279	Adg84279 Human TMD
C 94	7	7.6	123	5	ADK35204	Adk35204 Novel hum	C 167	7	7.6	312	5	ABP40738	Abp40738 Staphyloc
C 95	7	7.6	135	4	ABB71040	Abb71040 Drosophil	C 168	7	7.6	312	8	ADS08044	Ads08044 Staphyloc
C 96	7	7.6	137	4	AAO06256	Aao06256 Human pol	C 169	7	7.6	315	5	ABG77246	Abg77246 Selected
C 97	7	7.6	138	4	AAO12339	Aao12339 Novel hum	C 170	7	7.6	318	6	ABU49698	Abu49698 Protein e
C 98	7	7.6	164	5	AAE20651	Aae20651 Human gen	C 171	7	7.6	320	4	AAU67615	Aau67615 Propionib
C 99	7	7.6	170	4	AAE20651	Aae20651 Human gen	C 172	7	7.6	320	6	ABM64976	Abm64976 Propionib
C 100	7	7.6	176	8	ABO58920	Ab058920 Human gen	C 173	7	7.6	320	6	ABM64134	Abm64134 Propionib
C 101	7	7.6	179	2	AAW80659	Aaw80659 Human tra	C 174	7	7.6	320	8	ADR68708	Adr68708 Penicilli
C 102	7	7.6	183	7	ADC95884	Adc95884 E. faeciu	C 175	7	7.6	325	3	AAG45837	Aag45837 Arabidops
C 103	7	7.6	186	4	ABB69467	Abb69467 Drosophil	C 176	7	7.6	325	3	AAG45837	Aag45837 Arabidops
C 104	7	7.6	194	4	AAU19319	Aau19319 Human G-p	C 177	7	7.6	327	5	ADI16806	Adi16806 Human NOV
C 105	7	7.6	200	4	ABU78511	Abu78511 Pseudomon	C 178	7	7.6	327	5	ADI16806	Adi16806 Human NOV
C 106	7	7.6	204	4	ABU52951	Abu52951 Human tra	C 179	7	7.6	327	6	ABM65919	Abm65919 Propionib
C 107	7	7.6	210	3	ADH85669	Adh85669 Enterococ	C 180	7	7.6	331	4	AAU51834	Aau51834 Propionib
C 108	7	7.6	210	3	ABW44543	Abw44543 Virulence	C 181	7	7.6	331	6	ABM48353	Abm48353 Propionib
C 109	7	7.6	212	5	ABP54495	Abp54495 Pasteurel	C 182	7	7.6	334	8	ADS27736	Ads27736 Bacterial
C 110	7	7.6	212	4	AAU37626	Aau37626 Streptoco	C 183	7	7.6	334	8	ADS27736	Ads27736 Bacterial
C 111	7	7.6	212	6	ABU45820	Abu45820 Protein e	C 184	7	7.6	338	4	ABG01710	Abg01710 Novel hum
C 112	7	7.6	224	3	AAW57054	Aaw57054 Human pro	C 185	7	7.6	340	5	ABP58974	Abp58974 Human I k
C 113	7	7.6	226	6	ABU69133	Abu69133 Human NOV	C 186	7	7.6	347	4	ABW50177	Abw50177 Human tra
C 114	7	7.6	226	8	ADO08269	Ado08269 Human NOV	C 187	7	7.6	347	4	ABW50177	Abw50177 Human tra
C 115	7	7.6	227	7	ABO81633	Ab081633 Pseudomon	C 188	7	7.6	347	8	ADC31185	Adc31185 Human nov
C 116	7	7.6	231	7	ABO68943	Ab068943 Pseudomon	C 189	7	7.6	347	8	ADR08626	Adr08626 Human pro
C 117	7	7.6	236	7	ABO80020	Ab080020 Pseudomon	C 190	7	7.6	349	8	ADJ49117	Adj49117 Oil-assoc
C 118	7	7.6	243	7	ADD11648	Add11648 Arabidops	C 191	7	7.6	350	8	ADJ50144	Adj50144 Oil-assoc
C 119	7	7.6	243	7	ADD30318	Add30318 Plant yie	C 192	7	7.6	351	8	ADM03905	Adm03905 Human pro
C 120	7	7.6	243	8	ADI44237	Adi44237 Plant tra	C 193	7	7.6	351	8	ADH58986	Adh58986 Mouse GPC
C 121	7	7.6	245	8	ADR16225	Adr16225 Streptoco	C 194	7	7.6	351	8	ADH58986	Adh58986 Mouse GPC
C 122	7	7.6	245	8	ABU30320	Abu30320 Bacterial	C 195	7	7.6	351	8	ADO29714	Ado29714 Mouse GPC
C 123	7	7.6	249	6	ABU28502	Abu28502 Protein e	C 196	7	7.6	351	8	ADO29714	Ado29714 Mouse GPC
C 124	7	7.6	250	4	ABG12917	Abg12917 Novel hum	C 197	7	7.6	399	7	ABO77270	Ab077270 Pseudomon
C 125	7	7.6	254	6	ABU06072	Abu06072 N. mening	C 198	7	7.6	402	7	ABO78963	Ab078963 Pseudomon
C 126	7	7.6	255	4	ABE69299	Abb69299 Drosophil	C 199	7	7.6	407	5	ABO09999	Ab009999 Human pro
C 127	7	7.6	255	6	AAE37037	Aae37037 Human nuc	C 200	7	7.6	407	5	ABG64626	Abg64626 Human alb
C 128	7	7.6	257	6	ABP78820	Abp78820 N. gonorr	C 201	7	7.6	407	8	ADL77893	Adl77893 Albumin f
C 129	7	7.6	263	4	AAU62592	Aau62592 Propionib	C 202	7	7.6	418	7	ABO83887	Ab083887 Pseudomon
C 130	7	7.6	263	6	ABM59111	Abm59111 Propionib	C 203	7	7.6	424	4	ABW64620	Abw64620 Drosophil
C 131	7	7.6	264	3	AAG40069	Aag40069 Arabidops	C 204	7	7.6	426	4	ABW64620	Abw64620 Drosophil
C 132	7	7.6	264	3	AAG04977	Aag04977 Arabidops	C 205	7	7.6	434	6	ADA57216	Ada57216 Human sec
C 133	7	7.6	264	5	ABG32883	Abg32883 Human zlm	C 206	7	7.6	434	6	ADA41095	Ada41095 Human sec
C 134	7	7.6	270	6	ABU17017	Abu17017 Protein e	C 207	7	7.6	434	7	ADB91664	Abd91664 Human sec
C 135	7	7.6	270	6	ABU70000	Abu70000 Alloolococ	C 208	7	7.6	438	4	AAU33707	Aau33707 Pseudomon
C 136	7	7.6	270	7	ADH85668	Adh85668 Enterococ	C 209	7	7.6	438	6	ABU15597	Abu15597 Protein e
C 137	7	7.6	271	4	AAAG90190	Aag90190 C. glutami	C 210	7	7.6	441	4	AAG91857	Aag91857 C. glutami
C 138	7	7.6	271	6	ABR43441	Ab43441 Human mal	C 211	7	7.6	442	4	AAG65742	Aag65742 Flea epox
C 139	7	7.6	271	7	ADI21201	Adi21201 Novel hum	C 212	7	7.6	442	4	AAU51012	Aau51012 Flea epox
C 140	7	7.6	272	3	AAG29929	Aag29929 Arabidops	C 213	7	7.6	446	5	ABJ11117	Abj11117 Yeast sel
C 141	7	7.6	282	3	AAG04976	Aag04976 Arabidops	C 214	7	7.6	456	5	ABN91513	Abn91513 Herbicida
C 142	7	7.6	282	3	AAG04068	Aag04068 Arabidops	C 215	7	7.6	456	8	ADR16242	Adr16242 Streptoco
C 143	7	7.6	289	5	ABG76864	Abg76864 Human G-p	C 216	7	7.6	460	1	AAU81061	Aau81061 Sequence
C 144	7	7.6	292	6	ADA34549	Ada34549 Acinetoba	C 217	7	7.6	464	2	AAU24003	Aau24003 A flea ep
C 145	7	7.6	296	6	ABU65257	Abu65257 Novel hum	C 218	7	7.6	464	2	AAU24004	Aau24004 A flea ep
C 146	7	7.6	301	4	ABW59924	Abw59924 Drosophil	C 219	7	7.6	464	3	AAU68739	Aau68739 Amino aci
C 147	7	7.6	302	4	ABG10947	Abg10947 Novel hum	C 220	7	7.6	464	4	AAU36983	Aau36983 Protein s
C 148	7	7.6	303	4	AAU33897	Aau33897 Staphyloc	C 221	7	7.6	464	4	AAU36983	Aau36983 Protein s
C 149	7	7.6	306	4	AAU36707	Aau36707 Staphyloc	C 222	7	7.6	464	4	AAG65736	Aag65736 Flea epox
C 150	7	7.6	306	6	ADH89524	Adh89524 Staphyloc	C 223	7	7.6	464	4	AAG65736	Aag65736 Flea epox
C 151	7	7.6	306	6	ABU16314	Abu16314 Protein e	C 224	7	7.6	464	4	AAU51005	Aau51005 Flea epox
C 152	7	7.6	306	6	ABU42743	Abu42743 Protein e	C 225	7	7.6	464	4	AAU51005	Aau51005 Flea epox
C 153	7	7.6	306	6	ABU44001	Abu44001 Protein e	C 226	7	7.6	470	6	ABR40853	Ab40853 Catalpa s
C 154	7	7.6	306	6	ABM72329	Abm72329 Staphyloc	C 227	7	7.6	475	3	AAU34722	Aau34722 Human sec
C 155	7	7.6	308	6	ADA83766	Ada83766 Human SLC	C 228	7	7.6	483	7	ABO70478	Ab070478 Pseudomon
C 156	7	7.6	308	8	ADP25135	Adp25135 PRO polyp	C 229	7	7.6	485	5	ABP69693	Abp69693 Human pol

c 230	7	7.6	500	6	AAB30796	Aae30796 Human tra	303	7	7.6	674	8	ADL15347	Adl15347 B thuring
c 231	7	7.6	503	3	ABO83917	AbO83917 Pseudomon	304	7	7.6	675	8	ADL15377	Adl15377 B thuring
c 232	7	7.6	504	3	AAB44568	Aab44568 Virulence	305	7	7.6	675	8	ADL15351	Adl15351 B thuring
c 233	7	7.6	504	5	ABP54520	Abp54520 Pasteurel	306	7	7.6	675	8	ADL15349	Adl15349 B thuring
c 234	7	7.6	504	8	ADS17616	Adsl7616 Aspergill	307	7	7.6	675	8	ADL15345	Adl15345 B thuring
c 235	7	7.6	505	8	ADG73740	Adg73740 Ampicilli	308	7	7.6	675	8	ADL15381	Adl15381 B thuring
c 236	7	7.6	506	5	ABB91594	Abb91594 Herbicida	309	7	7.6	675	8	ADL15383	Adl15383 B thuring
c 237	7	7.6	519	4	ABG07249	Abg07249 Novel hum	c 310	7	7.6	675	8	ADN20157	Adn20157 Bacterial
c 238	7	7.6	529	4	AAB81926	Aab81926 Acromoni	311	7	7.6	676	8	ADL15343	Adl15343 B thuring
c 239	7	7.6	533	3	AAV933953	Aay933953 Amino aci	312	7	7.6	676	8	ADL15375	Adl15375 B thuring
c 240	7	7.6	533	3	AAV933952	Aay933952 Amino aci	313	7	7.6	677	8	ADL15355	Adl15355 B thuring
c 241	7	7.6	548	8	ADG61981	Adg61981 Transcrip	314	7	7.6	677	8	ADL15387	Adl15387 B thuring
c 242	7	7.6	548	8	ADS23189	AdS23189 Bacterial	315	7	7.6	687	8	ABR53552	AbR53552 Protein s
c 243	7	7.6	556	8	ADN22789	Adn22789 Bacterial	316	7	7.6	687	8	ADK64396	AdK64396 Disease t
c 244	7	7.6	558	8	ABO78932	AbO78932 Pseudomon	317	7	7.6	692	8	ADR68709	Adr68709 Penicilli
c 245	7	7.6	559	8	ADJ67952	Adj67952 G. stearo	c 318	7	7.6	698	8	ADS21451	AdS21451 Bacterial
c 246	7	7.6	559	8	ADJ68164	Adj68164 G. stearo	319	7	7.6	702	4	ABE01160	Abe01160 Drosophil
c 247	7	7.6	559	8	ADK01242	AdK01242 DNA polym	320	7	7.6	702	4	ABE71509	AbE71509 Drosophil
c 248	7	7.6	559	8	ADJ79461	Adj79461 G. stearo	c 321	7	7.6	714	6	AAO31003	Aao31003 Human tra
c 249	7	7.6	559	8	ADJ84901	Adj84901 B. stearo	c 322	7	7.6	714	8	ADR09688	Adr09688 Human pro
c 250	7	7.6	559	8	ADM77689	Adm77689 DNA polym	323	7	7.6	717	4	ABB60361	Abb60361 Drosophil
c 251	7	7.6	559	8	ADM66356	Adm66356 G. stearo	c 324	7	7.6	730	6	ABU12299	Abu12299 Human aut
c 252	7	7.6	559	8	ADO04409	Ado04409 B. steart	325	7	7.6	786	7	ABE57208	AbE57208 Rat Prote
c 253	7	7.6	559	8	ADP82486	Adp82486 B. stearo	326	7	7.6	786	7	ABE57204	AbE57204 Rat Prote
c 254	7	7.6	563	8	ADR50793	Adr50793 Human c-b	c 327	7	7.6	812	6	ABM68038	Abm68038 Photorhab
c 255	7	7.6	571	4	ABB62038	Abb62038 Drosophil	328	7	7.6	837	4	ABB68265	Abb68265 Drosophil
c 256	7	7.6	583	4	ABG09959	Abg09959 Novel hum	c 329	7	7.6	848	6	ADA38354	Ada38354 Vibrio ha
c 257	7	7.6	602	8	ADS43991	AdS43991 Bacterial	330	7	7.6	859	4	ABB71182	Abb71182 Drosophil
c 258	7	7.6	609	7	ADJ70515	Adj70515 Human hea	331	7	7.6	860	8	ADL04498	AdL04498 M. catarr
c 259	7	7.6	613	8	ADJ35082	Adj35082 Xylanase	c 332	7	7.6	861	6	ABU12316	Abu12316 Human PAT
c 260	7	7.6	625	8	ADRI0287	Adri0287 Human pro	333	7	7.6	864	2	AAV03636	Aav03636 Hypoxia-r
c 261	7	7.6	635	7	ADSE61270	Adse61270 Rat prote	334	7	7.6	864	6	ABU63755	Abu63755 Rat prote
c 262	7	7.6	644	2	AAW13821	Aaw13821 Yeast tra	335	7	7.6	864	7	ADC69799	Adc69799 Rat neuro
c 263	7	7.6	646	5	AAO20518	Aao20518 Protein o	336	7	7.6	864	7	ABW01151	Abw01151 Hypoxia-r
c 264	7	7.6	651	6	ABG74687	Abg74687 Human CGD	337	7	7.6	877	6	ABR53890	AbR53890 Protein s
c 265	7	7.6	655	4	ABE70771	AbE70771 Murine ne	338	7	7.6	877	7	ADK64848	Adk64848 Disease c
c 266	7	7.6	657	7	ABO79255	AbO79255 Pseudomon	c 339	7	7.6	894	6	ADB12663	AdB12663 Alloococ
c 267	7	7.6	663	8	ADQ08650	Adq08650 Ciona int	c 340	7	7.6	895	6	ABU12304	Abu12304 Human PAT
c 268	7	7.6	667	5	AAU99258	Aau99258 Bacillus	c 341	7	7.6	901	6	ADB12661	AdB12661 Alloococ
c 269	7	7.6	667	5	AAU99257	Aau99257 Bacillus	c 342	7	7.6	922	3	AAAB36515	Aab36515 Candida a
c 270	7	7.6	669	5	AAU99259	Aau99259 Maize opt	343	7	7.6	922	5	ABP73838	Abp73838 Candida a
c 271	7	7.6	669	5	AAU99262	Aau99262 Bacillus	c 344	7	7.6	933	6	ABU12307	Abu12307 Human PAT
c 272	7	7.6	669	8	ADL15309	Adl15309 B thuring	c 345	7	7.6	938	6	ADB12659	AdB12659 Human pro
c 273	7	7.6	669	8	ADL15315	Adl15315 B thuring	346	7	7.6	949	8	ADM87258	Adm87258 Human pro
c 274	7	7.6	670	5	AAU99273	Aau99273 Bacillus	c 347	7	7.6	958	3	AAV51120	Aav51120 Human SAR
c 275	7	7.6	670	5	AAU99266	Aau99266 Bacillus	c 348	7	7.6	958	8	ADL83102	AdL83102 Human PRO
c 276	7	7.6	673	5	AAU99265	Aau99265 Bacillus	c 349	7	7.6	965	7	ADC31607	AdC31607 Human nov
c 277	7	7.6	673	5	AAU99271	Aau99271 Bacillus	350	7	7.6	982	4	ABE59353	AbE59353 Drosophil
c 278	7	7.6	673	5	AAU99263	Aau99263 Bacillus	351	7	7.6	982	4	ABB67401	Abb67401 Drosophil
c 279	7	7.6	673	5	AAU99260	Aau99260 Bacillus	c 352	7	7.6	993	6	ABU12300	Abu12300 Human PAT
c 280	7	7.6	673	8	ADL15325	Adl15325 B thuring	353	7	7.6	1013	4	ABE60789	AbE60789 Drosophil
c 281	7	7.6	673	8	ADL15325	Adl15325 B thuring	354	7	7.6	1023	6	ABU48443	Abu48443 Protein e
c 282	7	7.6	673	8	ADL15317	Adl15317 B thuring	c 355	7	7.6	1024	5	ABE04861	AbE04861 LDL recep
c 283	7	7.6	673	8	ADL15365	Adl15365 B thuring	c 356	7	7.6	1026	6	ABU12314	Abu12314 Human PAT
c 284	7	7.6	673	8	ADL15337	Adl15337 B thuring	357	7	7.6	1031	4	AAU35339	Aau35339 Enterococ
c 285	7	7.6	673	8	ADL15389	Adl15389 B thuring	c 358	7	7.6	1044	6	ABU12310	Abu12310 Human PAT
c 286	7	7.6	673	8	ADL15311	Adl15311 B thuring	359	7	7.6	1061	6	ABU29451	Abu29451 Protein e
c 287	7	7.6	673	8	ADL15333	Adl15333 B thuring	360	7	7.6	1077	4	ABE58720	AbE58720 Drosophil
c 288	7	7.6	673	8	ADL15371	Adl15371 B thuring	361	7	7.6	1083	8	ADM87238	Adm87238 Human pro
c 289	7	7.6	673	8	ADL15361	Adl15361 B thuring	362	7	7.6	1157	2	AAE28900	Aae28900 Toxin SOC
c 290	7	7.6	673	8	ADL15369	Adl15369 B thuring	363	7	7.6	1157	2	AAE25997	Aae25997 Delta-end
c 291	7	7.6	673	8	ADL15391	Adl15391 B thuring	364	7	7.6	1157	2	AAE27343	Aae27343 B thuring
c 292	7	7.6	673	8	ADL15395	Adl15395 B thuring	365	7	7.6	1157	2	AAE44208	Aae44208 Bacillus
c 293	7	7.6	673	8	ADL15367	Adl15367 B thuring	366	7	7.6	1157	2	AAE33768	Aae33768 Bt isolat
c 294	7	7.6	673	8	ADL15357	Adl15357 B thuring	367	7	7.6	1157	2	AAW06418	Aaw06418 Antiscara
c 295	7	7.6	673	8	ADL15373	Adl15373 B thuring	368	7	7.6	1157	8	ADR89430	Adr89430 cry8Aa. 1
c 296	7	7.6	673	8	ADL15397	Adl15397 B thuring	369	7	7.6	1169	2	AAW06417	Aaw06417 Antiscara
c 297	7	7.6	673	8	ADL15329	Adl15329 B thuring	370	7	7.6	1193	7	ADJ70742	Adj70742 Human hea
c 298	7	7.6	673	8	ADL15359	Adl15359 B thuring	371	7	7.6	1206	5	AAU99255	Aau99255 Bacillus
c 299	7	7.6	673	8	ADL15363	Adl15363 B thuring	372	7	7.6	1206	8	ADL15305	Adl15305 B thuring
c 300	7	7.6	674	8	ADL15385	Adl15385 B thuring	373	7	7.6	1210	5	AAU99256	Aau99256 Bacillus
c 301	7	7.6	674	8	ADL15379	Adl15379 B thuring	374	7	7.6	1210	8	ADL15307	Adl15307 B thuring
c 302	7	7.6	674	8	ADL15353	Adl15353 B thuring	375	7	7.6	1222	8	ADR39771	Adr39771 Human kin

376	7	7.6	1248	2	AAW19783	Aaw19783 Human mul	449	6	6.5	14	3	ADC16845	Adc16845 Human sin
377	7	7.6	1384	8	ADN61482	Adn61482 Human kpp	450	6	6.5	14	7	ADW70233	Adw70233 Human gpa
378	7	7.6	1392	8	ADJ96675	Adj96675 Human pro	451	6	6.5	15	2	AAW47391	Aaw47391 Spruce bu
379	7	7.6	1468	4	ABB65329	Abb65329 Drosophil	c 452	6	6.5	15	2	AAy33077	Aay33077 Carbohydr
380	7	7.6	1551	4	ABE64459	Abbe64459 Drosophil	c 453	6	6.5	15	2	AAy01479	Aay01479 N-termina
381	7	7.6	1603	5	ABB81171	Abb81171 Human put	c 454	6	6.5	15	2	AAy14549	Aay14549 Rat LSR-g
382	7	7.6	1603	8	ADJ57844	Adj57844 MRB prote	455	6	6.5	15	3	AAy49463	Aay49463 Spruce bu
383	7	7.6	1655	4	ABG17466	Abg17466 Novel hum	456	6	6.5	15	5	AAO15974	Aao15974 Human mac
384	7	7.6	1726	2	AAW19784	Aaw19784 Human mul	457	6	6.5	15	5	ABB80709	Abb80709 Thermal h
385	7	7.6	1726	7	ADW79869	Adw79869 Rat putat	c 458	6	6.5	15	6	ABU87162	Abu87162 Carbohydr
c 386	7	7.6	1759	5	ABP69142	Abp69142 Human pol	459	6	6.5	15	7	ADF09362	Adf09362 Human cal
c 387	7	7.6	1784	8	ADR86368	Adr86368 Aspergill	460	6	6.5	15	8	ADN65117	Adn65117 HLA bindi
388	7	7.6	2000	7	ADK62360	Adk62360 Disease t	461	6	6.5	15	8	ADN19434	Adn19434 TRPI deri
389	7	7.6	2015	4	ABB65890	Abb65890 Drosophil	462	6	6.5	16	2	AAW52159	Aaw52159 Mouse lig
390	7	7.6	2164	1	AAW19784	Aaw19784 Human mul	463	6	6.5	17	2	AAW52159	Aaw52159 Mouse lig
391	7	7.6	2164	1	AAW19784	Aaw19784 Human mul	464	6	6.5	17	2	AAW52159	Aaw52159 Mouse lig
c 392	7	7.6	2182	3	AAW22476	Aaw22476 Plasmodiu	c 465	6	6.5	17	7	ADD36497	Add36497 NRI3 C-t
c 393	7	7.6	2182	3	AAW22476	Aaw22476 Plasmodiu	465	6	6.5	20	2	AAW04992	Aaw04992 Papilloma
394	7	7.6	2285	2	AAW98149	Aaw98149 Bacillus	c 466	6	6.5	20	2	AAW76825	Aaw76825 Xenopus s
395	7	7.6	2285	3	AAW98149	Aaw98149 Bacillus	c 467	6	6.5	20	2	AAW76824	Aaw76824 Human CTN
396	7	7.6	2870	3	AAW95559	Aay95559 Caenorhab	c 468	6	6.5	20	4	AAW72830	Aay72830 Human bet
397	7	7.6	2870	8	ADN07634	Adn07634 Caenorhab	c 469	6	6.5	20	4	AAW72828	Aay72828 Human bet
398	7	7.6	3178	3	AAW95556	Aay95556 Caenorhab	c 470	6	6.5	20	4	AAW72826	Aay72826 Xenopus b
399	7	7.6	3178	3	AAW95556	Aay95556 Caenorhab	c 471	6	6.5	20	4	AAW72826	Aay72826 Xenopus b
c 400	7	7.6	4315	5	ABP43908	Abp43908 MUC5B par	472	6	6.5	20	4	AAW72826	Aay72826 Xenopus b
c 401	7	7.6	4773	7	ADJ95094	Adj95094 Novel NOV	473	6	6.5	20	5	AAO18146	Aao18146 HPV type
402	6	6.5	5703	8	ADL23265	Adl23265 Human MUC	474	6	6.5	20	5	ABP47327	Abp47327 HPV18 E7
c 403	6	6.5	5703	8	ADL23265	Adl23265 Human MUC	475	6	6.5	20	5	ABP47327	Abp47327 HPV18 E7
c 404	6	6.5	5703	8	ADL23265	Adl23265 Human MUC	476	6	6.5	20	5	ABP47327	Abp47327 HPV18 E7
c 405	6	6.5	5703	8	ADL23265	Adl23265 Human MUC	477	6	6.5	20	5	ABP47327	Abp47327 HPV18 E7
c 406	6	6.5	5703	8	ADL23265	Adl23265 Human MUC	478	6	6.5	20	5	ABP47327	Abp47327 HPV18 E7
c 407	6	6.5	5703	8	ADL23265	Adl23265 Human MUC	479	6	6.5	20	5	ABP47327	Abp47327 HPV18 E7
c 408	6	6.5	5703	8	ADL23265	Adl23265 Human MUC	480	6	6.5	20	5	ABP47327	Abp47327 HPV18 E7
c 409	6	6.5	5703	8	ADL23265	Adl23265 Human MUC	481	6	6.5	20	5	ABP47327	Abp47327 HPV18 E7
c 410	6	6.5	5703	8	ADL23265	Adl23265 Human MUC	482	6	6.5	20	5	ABP47327	Abp47327 HPV18 E7
c 411	6	6.5	5703	8	ADL23265	Adl23265 Human MUC	483	6	6.5	20	5	ABP47327	Abp47327 HPV18 E7
c 412	6	6.5	5703	8	ADL23265	Adl23265 Human MUC	484	6	6.5	20	5	ABP47327	Abp47327 HPV18 E7
c 413	6	6.5	5703	8	ADL23265	Adl23265 Human MUC	485	6	6.5	20	5	ABP47327	Abp47327 HPV18 E7
c 414	6	6.5	5703	8	ADL23265	Adl23265 Human MUC	486	6	6.5	20	5	ABP47327	Abp47327 HPV18 E7
c 415	6	6.5	5703	8	ADL23265	Adl23265 Human MUC	487	6	6.5	20	5	ABP47327	Abp47327 HPV18 E7
c 416	6	6.5	5703	8	ADL23265	Adl23265 Human MUC	488	6	6.5	20	5	ABP47327	Abp47327 HPV18 E7
c 417	6	6.5	5703	8	ADL23265	Adl23265 Human MUC	489	6	6.5	20	5	ABP47327	Abp47327 HPV18 E7
c 418	6	6.5	5703	8	ADL23265	Adl23265 Human MUC	490	6	6.5	20	5	ABP47327	Abp47327 HPV18 E7
c 419	6	6.5	5703	8	ADL23265	Adl23265 Human MUC	491	6	6.5	20	5	ABP47327	Abp47327 HPV18 E7
c 420	6	6.5	5703	8	ADL23265	Adl23265 Human MUC	492	6	6.5	20	5	ABP47327	Abp47327 HPV18 E7
c 421	6	6.5	5703	8	ADL23265	Adl23265 Human MUC	493	6	6.5	20	5	ABP47327	Abp47327 HPV18 E7
c 422	6	6.5	5703	8	ADL23265	Adl23265 Human MUC	494	6	6.5	20	5	ABP47327	Abp47327 HPV18 E7
c 423	6	6.5	5703	8	ADL23265	Adl23265 Human MUC	495	6	6.5	20	5	ABP47327	Abp47327 HPV18 E7
c 424	6	6.5	5703	8	ADL23265	Adl23265 Human MUC	496	6	6.5	20	5	ABP47327	Abp47327 HPV18 E7
c 425	6	6.5	5703	8	ADL23265	Adl23265 Human MUC	497	6	6.5	20	5	ABP47327	Abp47327 HPV18 E7
c 426	6	6.5	5703	8	ADL23265	Adl23265 Human MUC	498	6	6.5	20	5	ABP47327	Abp47327 HPV18 E7
c 427	6	6.5	5703	8	ADL23265	Adl23265 Human MUC	499	6	6.5	20	5	ABP47327	Abp47327 HPV18 E7
c 428	6	6.5	5703	8	ADL23265	Adl23265 Human MUC	500	6	6.5	20	5	ABP47327	Abp47327 HPV18 E7
c 429	6	6.5	5703	8	ADL23265	Adl23265 Human MUC	501	6	6.5	20	5	ABP47327	Abp47327 HPV18 E7
c 430	6	6.5	5703	8	ADL23265	Adl23265 Human MUC	502	6	6.5	20	5	ABP47327	Abp47327 HPV18 E7
c 431	6	6.5	5703	8	ADL23265	Adl23265 Human MUC	503	6	6.5	20	5	ABP47327	Abp47327 HPV18 E7
c 432	6	6.5	5703	8	ADL23265	Adl23265 Human MUC	504	6	6.5	20	5	ABP47327	Abp47327 HPV18 E7
c 433	6	6.5	5703	8	ADL23265	Adl23265 Human MUC	505	6	6.5	20	5	ABP47327	Abp47327 HPV18 E7
c 434	6	6.5	5703	8	ADL23265	Adl23265 Human MUC	506	6	6.5	20	5	ABP47327	Abp47327 HPV18 E7
c 435	6	6.5	5703	8	ADL23265	Adl23265 Human MUC	507	6	6.5	20	5	ABP47327	Abp47327 HPV18 E7
c 436	6	6.5	5703	8	ADL23265	Adl23265 Human MUC	508	6	6.5	20	5	ABP47327	Abp47327 HPV18 E7
c 437	6	6.5	5703	8	ADL23265	Adl23265 Human MUC	509	6	6.5	20	5	ABP47327	Abp47327 HPV18 E7
c 438	6	6.5	5703	8	ADL23265	Adl23265 Human MUC	510	6	6.5	20	5	ABP47327	Abp47327 HPV18 E7
c 439	6	6.5	5703	8	ADL23265	Adl23265 Human MUC	511	6	6.5	20	5	ABP47327	Abp47327 HPV18 E7
c 440	6	6.5	5703	8	ADL23265	Adl23265 Human MUC	512	6	6.5	20	5	ABP47327	Abp47327 HPV18 E7
c 441	6	6.5	5703	8	ADL23265	Adl23265 Human MUC	513	6	6.5	20	5	ABP47327	Abp47327 HPV18 E7
c 442	6	6.5	5703	8	ADL23265	Adl23265 Human MUC	514	6	6.5	20	5	ABP47327	Abp47327 HPV18 E7
c 443	6	6.5	5703	8	ADL23265	Adl23265 Human MUC	515	6	6.5	20	5	ABP47327	Abp47327 HPV18 E7
c 444	6	6.5	5703	8	ADL23265	Adl23265 Human MUC	516	6	6.5	20	5	ABP47327	Abp47327 HPV18 E7
c 445	6	6.5	5703	8	ADL23265	Adl23265 Human MUC	517	6	6.5	20	5	ABP47327	Abp47327 HPV18 E7
c 446	6	6.5	5703	8	ADL23265	Adl23265 Human MUC	518	6	6.5	20	5	ABP47327	Abp47327 HPV18 E7
c 447	6	6.5	5703	8	ADL23265	Adl23265 Human MUC	519	6	6.5	20	5	ABP47327	Abp47327 HPV18 E7
c 448	6	6.5	5703	8	ADL23265	Adl23265 Human MUC	520	6	6.5	20	5	ABP47327	Abp47327 HPV18 E7

ALIGNMENTS

RESULT 1

AAW03563
ID AAW03563 standard; protein; 92 AA.

XX AC AAW03563;

XX DT 01-MAY-1997 (first entry)

XX DE Calcium binding protein CAAFL1.

XX KW Calcium binding protein; bovine; amniotic fluid; S100 protein family;

XX KW intracellular signal transduction; squamous epithelial cell; neutrophil;

XX KW macrophage; cancer; cancerous lesion; inflammation; neoplasia; cervix;

XX KW squamous cell carcinoma; skin; oesophagus; CAAFL1; lung; blood disease.

XX OS Bos taurus.

XX

PN EP731166-A2;
 XX 11-SEP-1996;
 XX 04-DEC-1995; 95EP-00119045.
 XX 06-MAR-1995; 95JP-00045564.
 PR 06-MAR-1995; 95JP-00070468.
 XX (TOFU) TONEN CORP.
 PA (HITO/) HITOMI J.
 XX Hitomi J, Yamaguchi K, Yamamura T, Kimura T;
 PI WPI; 1996-403989/41.
 DR N-PSDB; AAT39345.
 XX New human of bovine calcium binding protein and related nucleic acid - is
 PT a marker for inflammation, neoplasia, skin and blood diseases.
 XX Claim 1; Page 21; 36pp; English.
 PS This sequence represents the CAAF1 calcium-binding protein isolated from
 CC bovine amniotic fluid. CAAF1 belongs to the S100 protein family, which
 CC includes calyculin, MRP8, and MRP14. Intracellular calcium ion
 CC concentration is one of the key factors for intracellular signal
 CC transduction. The calcium signals are transduced by various calcium-
 CC binding proteins, such as the protein encoded by this sequence. CAAF1 is
 CC normally expressed in squamous epithelial cells, neutrophils and
 CC macrophages, but atypical epithelial cells are negative for CAAF1 and
 CC overexpression is observed in several types of cancer cells and
 CC neutrophils/macrophages infiltrating cancerous lesions. Detection of
 CC CAAF1 (using antibodies in usual immunoassays) can be used to diagnose
 CC (or monitor) inflammation, neoplasia (particularly squamous cell
 CC carcinoma of the skin, oesophagus, lung and cervix), and skin and blood
 CC diseases
 XX SQ Sequence 92 AA;
 Alignment Scores:
 Pred. No.: 1.23e-83 Length: 92
 Score: 92.00 Matches: 92
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 2 Gaps: 0
 US-09-910-208B-1 (1-276) x AAW03563 (1-92)
 QY 1 ATGACTAAGCTGGAAGATCACCTGGAGGGAATCATCAACATCTTCCACAGTACTCCGTT 60
 DB 1 MetThrLysLeuGluAspHisLeuGluGlyIleIleAsnIlePheHisGlnTyrSerVal 20
 QY 61 CGGTGGGGCAATTCGACACCTCCACAGCTGAGCTGAAGCAGCTGATCAAAAGGAA 120
 DB 21 ArgValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGlu 40
 QY 121 CTTCCCAAAACCTCCAGACACCAAGATCAACCTACCATTCACAAATATTTCCAAAG 180
 DB 41 LeuProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAsp 60
 QY 181 CTGGATGCGGATAAAGACGGAGCCCTGAGCTTTGAGGAAATTCGTAGTCTCTGGTGCCAGG 240
 DB 61 LeuAspAlaAspLysAspGlyAlaValSerPheGluGluPheValValLeuValSerArg 80
 QY 241 GTGCTGAACACGCCACATAGATATCCAAAGAG 276
 DB 81 ValLeuLysThrAlaHisIleAspIleHisLysGlu 92
 RESULT 2
 AAY90765
 ID AAY90765 standard; protein; 90 AA.
 XX

AC AAY90765;
 XX 18-AUG-2000 (first entry)
 XX Bovine CAAF1 acid sequence SEQ ID NO:4.
 XX Bovine; EN-RAGE; extracellular novel RAGE binding protein;
 KW receptor for advanced glycation endproduct; inflammation; inhibition;
 KW antiinflammatory; immunoglobulin; cell surface molecule; septic shock;
 KW systemic lupus erythematosus; inflammatory lupus nephritis; endotoxaemia;
 KW autoimmune disorder; inflammatory disorder.
 XX OS Bos taurus.
 XX WO200020621-A1.
 XX 13-APR-2000.
 XX 06-OCT-1999; 99WO-US023303.
 XX 06-OCT-1998; 98US-00167705.
 PR 05-MAR-1999; 99US-00263312.
 XX (UYCO) UNIV COLUMBIA NEW YORK.
 PA Schmidt AM, Stern D;
 XX WPI; 2000-303794/26.
 XX New human EN-RAGE (extracellular novel receptor for advanced glycation
 PT end products) peptide, useful for identifying anti-inflammatory compounds
 PT that inhibit its interaction with RAGE.
 XX Claim 2; Page 41; 132pp; English.
 XX The present invention describes an isolated human EN-RAGE (extracellular
 CC novel receptor for advanced glycation end products) peptide (P1). The EN-
 CC RAGE peptide binds to RAGE which is a member of the immunoglobulin
 CC superfamily of cell-surface molecules. A compound capable of inhibiting
 CC the interaction of EN-RAGE with RAGE is useful for the suppression of
 CC inflammation resulting from systemic lupus erythematosus, inflammatory
 CC lupus nephritis, septic shock, endotoxaemia, or an autoimmune or
 CC inflammatory disorder in which the recruitment of EN-RAGE containing
 CC inflammatory cells occurs. The compound is also useful for the treatment
 CC of systemic lupus erythematosus, inflammatory lupus nephritis in a
 CC subject. The human EN-RAGE peptide is useful for identifying compounds
 CC that inhibit its interaction with RAGE. The present sequence represents
 CC the bovine CAAF1 which shows homology to the human EN-RAGE N-terminal
 CC amino acid sequence
 XX SQ Sequence 90 AA;
 Alignment Scores:
 Pred. No.: 1.28e-81 Length: 90
 Score: 90.00 Matches: 90
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 97.83% Indels: 0
 DB: 3 Gaps: 0
 US-09-910-208B-1 (1-276) x AAY90765 (1-90)
 QY 4 ACTAAGCTGGAAGATCACCTGGAGGGAATCATCAACATCTTCCACAGTACTCCGTTCCG 63
 DB 1 ThrLysLeuGluAspHisLeuGluGlyIleIleAsnIlePheHisGlnTyrSerValArg 20
 QY 64 GTGGGGCAATTCGACACCTCCACAGCGTGAAGCAGCTGATCAAAAGGAACTT 123
 DB 21 ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40
 QY 124 CCCAAAACCTCCAGAACACCAAGATCAACTACCATTCAGAAATATTTCCAAAGCTTG 183
 DB 41 ProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAspLeu 60

QY 184 GATGCCGATAAAGACGGAGCGTCAGCTTTGAGGAATTCGTAGTCTCGTCCAGGGTG 243
 DB 61 AsplaasplysAspGlyAlaValSerPheGluGluPheValValLeuValSerArgVal 80
 QY 244 CTGAAACAGCCCATAGATATCCACAAA 273
 DB 81 LeulysThrAlaHisIleAspIleHislys 90
 RESULT 3
 AAY90764
 ID AAY90764 standard; protein; 90 AA.
 AC AAY90764;
 XX
 DT 18-AUG-2000 (first entry)
 DE Bovine corneal antigen (B-COAG) acid sequence SEQ ID NO:3.
 KW Bovine; EN-RAGE; extracellular novel RAGE binding protein;
 KW receptor for advanced glycation endproduct; inflammation; inhibition;
 KW antiinflammatory; immunoglobulin; cell surface molecule; septic shock;
 KW systemic lupus erythematosus; inflammatory lupus nephritis; endotoxaemia;
 KW autoimmune disorder; inflammatory disorder.
 XX
 OS Bos taurus.
 XX
 FN WO200020621-A1.
 XX
 PD 13-APR-2000.
 XX
 PF 06-OCT-1999; 99WO-US023303.
 XX
 PR 06-OCT-1998; 98US-00167705.
 PR 05-MAR-1999; 99US-00263312.
 XX
 PA (UYCO) UNIV COLUMBIA NEW YORK.
 XX
 PI Schmidt AM, Stern D;
 XX
 XX WPI; 2000-303794/26.
 DR
 PT New human EN-RAGE (extracellular novel receptor for advanced glycation
 PT end products) peptide, useful for identifying anti-inflammatory compounds
 PT that inhibit its interaction with RAGE.
 XX
 PS Claim 2; Page 41; 132pp; English.
 XX
 CC The present invention describes an isolated human EN-RAGE (extracellular
 CC novel receptor for advanced glycation end products) peptide (Pi). The EN-
 CC RAGE peptide binds to RAGE which is a member of the immunoglobulin
 CC superfamily of cell-surface molecules. A compound capable of inhibiting
 CC the interaction of EN-RAGE with RAGE is useful for the suppression of
 CC inflammation resulting from systemic lupus erythematosus, inflammatory
 CC lupus nephritis, septic shock, endotoxaemia, or an autoimmune or
 CC inflammatory disorder in which the recruitment of EN-RAGE containing
 CC inflammatory cells occurs. The compound is also useful for the treatment
 CC of systemic lupus erythematosus, inflammatory lupus nephritis in a
 CC subject. The human EN-RAGE peptide is useful for identifying compounds
 CC that inhibit its interaction with RAGE. The present sequence represents
 CC the bovine corneal antigen which shows homology to the human EN-RAGE N-
 CC terminal amino acid sequence
 SQ Sequence 90 AA;
 Alignment Scores:
 Pred. No.: 1.28e-81 Length: 90
 Score: 90.00 Matches: 90
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 97.83% Indels: 0
 DB: 3 Gaps: 0

US-09-910-208B-1 (1-276) x AAY90764 (1-90)
 QY 4 ACTAAGCTGGAAGATCACCTGGAGGGAATCATCAATCTTCCACAGTACTCGTTCGG 63
 DB 1 ThrLysLeuGluAspHisLeuGluGlyIleIleAsnIlePheHisGlnTyrSerValArg 20
 QY 64 GTGGGGCATTTTCGACACCCCTCAACAAGCGTGAGCTGAAGCAGCTGATCACAAGGAACCTT 123
 DB 21 ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40
 QY 124 CCCAAACCCCTCCAGACACCAAGATCAACCTACCATTTGACAAATATTTCCAGACCTG 183
 DB 41 ProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAspLeu 60
 QY 184 GATCCGATAAAGACGGAGCGTCAGCTTTGAGGAATTCGTAGTCTCGTCCAGGGTG 243
 DB 61 AsplaasplysAspGlyAlaValSerPheGluGluPheValValLeuValSerArgVal 80
 QY 244 CTGAAACAGCCCATAGATATCCACAAA 273
 DB 81 LeulysThrAlaHisIleAspIleHislys 90
 RESULT 4
 AAW01826
 ID AAW01826 standard; protein; 91 AA.
 AC AAW01826;
 XX
 DT 16-OCT-1997 (first entry)
 DE Component of bioactive metal RNA polypeptide.
 KW Bioactive; metal; RNA polypeptide; RNP; modulation; analysis;
 KW angiogenesis; vascular state; mammalian tissue; transfer; cell;
 KW genetic information; selective; alteration; nucleic acid content;
 KW leukocyte; pig; monocyto-CuRNP.
 XX
 OS Sus scrofa.
 XX
 FN DE19628895-A1.
 XX
 PD 23-JAN-1997.
 XX
 PF 17-JUL-1996; 96DE-01028895.
 PR 17-JUL-1995; 95DE-01025992.
 PR 18-AUG-1995; 95DE-01030500.
 XX
 PA (FRAU) FRAUNHOFER GES FOERDERUNG ANGEWANDTEN.
 XX
 PI Wissler JH, Logemann E, Kiesewetter S, Heilmeyer LMG;
 XX
 WPI; 1997-088586/09.
 DR N-PSDB; AAT62569.
 XX
 PT Bioactive metal RNA polypeptide - useful for modulating angiogenesis,
 PT etc.
 XX
 PS Claim 1; Page 15; 16pp; German.
 CC
 CC A novel bioactive metal RNA polypeptide (RNP) has a RNA component
 CC including the sequence AAT62568 and a polypeptide component having the
 CC sequence AAW01826, which is encoded by AAT62569. The RNP, or anti-RNP
 CC immunoglobulin, can be used to modulate and/or analyse angiogenesis and
 CC the vascular state of mammalian tissue, transfer genetic information in
 CC cells and selectively alter the nucleic acid content of cells. Leukocytes
 CC from pig's blood were cultured in medium, and the supernatant treated
 CC with NH4 sulphate at 35, 45 and 90% saturation to precipitate protein
 CC fractions. The residual supernatant was diluted to 45% NH4 sulphate
 CC saturation and concentrated by ultrafiltration using a 0.5 kD membrane.
 CC The retentate was purified to give 8 mg of product described as monocyto-
 CC CuRNP
 XX

SQ Sequence 91'AA;

Alignment Scores:

Pred. No.: 4.44e-11 Length: 91
 Score: 20.00 Matches: 20
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 21.74% Indels: 0
 DB: 2 Gaps: 0

US-09-910-208B-1 (1-276) x AAW01826 (1-91)

QY 4 ACTAAGCTGGAAGATCACCTGGAGGAATCATCAACATCTTCCACCACTACTCCGTTCCGG 63
 |||||
 Db 1 ThrLysLeuGluAspHisLeuGluGlyIleIleAsnIlePheHisGlnTy-SerValArg 20

RESULT 5

AAW93819

ID AAW93819 standard; peptide; 91 AA.

XX AC AAW93819;

XX DT 21-JUN-1999 (first entry)

XX DE Angiotropin related protein derived peptide.

XX KW Angiotropin related protein; ARP; ternary complex; S100 protein;

KW copper-containing ribonucleoprotein; copper; cell selective;

KW morphogenic action; blood capillary endothelial cell; confluent;

KW non-mitogenic induction; cell phenotype; three-dimensional organoid;

KW spatiotemporal supracellular organisation; chemotropic; blood vessel;

KW tissue neovascularisation; angiogenesis modulation.

XX OS Synthetic.

XX PN DE19811047-C1.

XX PD 15-APR-1999.

XX PF 13-MAR-1998; 98DE-01011047.

XX PR 13-MAR-1998; 98DE-01011047.

XX PA (FRAU) FRAUNHOFER GES FOERDERUNG ANGEWANDTEN.

XX PI Kieseewetter S, Kuhn E, Koch-Pelster B, Brunner H;

XX WPI; 1999-216114/19.

XX PT Copper-containing ribonucleoproteins - useful for modulating angiogenesis.

XX PS Disclosure; Page 2; 16pp; German.

XX CC This invention describes novel copper-containing ribonucleoproteins which are ternary complexes of an S100 protein, copper ions, and RNA comprising the following consensus sequence or its complement GGAAUNNNNNNAUGN1-6CUNNUNNNNNNAAGN0-IUANAACAUN0-SCUUNAGN0-13AGAA-AUN0-16UUACAG where N = G, A, U or C. The ribonucleoproteins are stated to have the following properties (1) cell-selective morphogenic action in vitro on isolated primary and/or cloned blood capillary endothelial cells in culture for the non-mitogenic induction of the change in cell phenotype from the confluent state, for non-mitogenic alteration of the spatiotemporal supracellular organisation of cells into three-dimensional organoid, capillary-like structures in culture, (2) a specific chemotropic action on blood vessels in vivo, (3) induction of directional growth of blood vessels in vivo and (4) induction of neovascularisation of tissues through directed ingrowth of blood vessels. Their use for modulating angiogenesis is claimed

SQ Sequence 91 AA;

Alignment Scores:

Pred. No.: 4.44e-11 Length: 91
 Score: 20.00 Matches: 20
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 21.74% Indels: 0
 DB: 2 Gaps: 0

US-09-910-208B-1 (1-276) x AAW93819 (1-91)

QY 4 ACTAAGCTGGAAGATCACCTGGAGGAATCATCAACATCTTCCACCACTACTCCGTTCCGG 63
 |||||
 Db 1 ThrLysLeuGluAspHisLeuGluGlyIleIleAsnIlePheHisGlnTy-SerValArg 20

RESULT 6

AAW90766

ID AAW90766 standard; protein; 18 AA.

XX AC AAW90766;

XX DT 18-AUG-2000 (first entry)

XX DE Endo Lys C amino acid sequence SEQ ID NO:5.

XX KW Bovine; EN-RAGE; extracellular novel RAGE binding protein;

KW receptor for advanced glycation endproduct; inflammation; inhibition;

KW antiinflammatory; immunoglobulin; cell surface molecule; septic shock;

KW systemic lupus erythematosus; inflammatory lupus nephritis; endotoxaemia;

KW autoimmune disorder; inflammatory disorder.

XX OS Unidentified.

XX PN WO200020621-A1.

XX PD 13-APR-2000.

XX PF 06-OCT-1999; 99WO-US023303.

XX PR 06-OCT-1998; 98US-00167705.

XX PR 05-MAR-1999; 99US-00263312.

XX PA (UYCO) UNIV COLUMBIA NEW YORK.

XX PI Schmidt AM, Stern D;

XX WPI; 2000-303794/26.

XX PT New human EN-RAGE (extracellular novel receptor for advanced glycation end products) peptide, useful for identifying anti-inflammatory compounds that inhibit its interaction with RAGE.

XX PS Claim 2; Page 41; 132pp; English.

XX CC The present invention describes an isolated human EN-RAGE (extracellular novel receptor for advanced glycation end products) peptide (p1). The EN-RAGE peptide binds to RAGE which is a member of the immunoglobulin superfamily of cell-surface molecules. A compound capable of inhibiting the interaction of EN-RAGE with RAGE is useful for the suppression of inflammation resulting from systemic lupus erythematosus, inflammatory lupus nephritis, septic shock, endotoxaemia, or an autoimmune or inflammatory disorder in which the recruitment of EN-RAGE containing inflammatory cells occurs. The compound is also useful for the treatment of systemic lupus erythematosus, inflammatory lupus nephritis in a subject. The human EN-RAGE peptide is useful for identifying compounds that inhibit its interaction with RAGE. The present sequence represents Endo Lys C which shows homology to the human EN-RAGE N-terminal amino acid sequence

SQ Sequence 18 AA;

Alignment Scores:

Pred. No.: 5.06e-09 Length: 18
 Score: 18.00 Matches: 18
 Percent Similarity: 100.00% Conservative: 0

KW Human; foetal liver; gene expression; single exon nucleic acid probe.
XX
OS Homo sapiens.
XX
PN WO200157277-A2.
XX
XX
PD 09-AUG-2001.
XX
XX
PF 30-JAN-2001; 2001WO-US000669.
XX
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX
DR WPI; 2001-483447/52.
XX
XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human fetal liver.
XX
XX
PS Claim 27; SEQ ID NO 35818; 639pp + Sequence Listing; English.
XX
XX
CC The invention relates to a single exon nucleic acid probe for measuring
CC human gene expression in a sample derived from human foetal liver. The
CC single exon nucleic acid probes may be used for predicting, measuring and
CC displaying gene expression in samples derived from human fetal liver. The
CC present sequence is a peptide encoded by a single exon nucleic acid probe
CC of the invention. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX
SQ Sequence 46 AA;
XX
XX
Alignment Scores:
Pred. No.: 5.62 Length: 46
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 9.78% Indels: 0
DB: 4 Gaps: 0
XX
US-09-910-208B-1 (1-276) x ABB43183 (1-46)
XX
OY 37 AACATCTTCCACGACTACTCGTTCGG 63
XX
DB 13 AsnIlePheHisGlnTySerValArg 21
XX
RESULT 10
AAM37021
ID AAM37021 standard; protein; 46 AA.
XX
XX
AC AAM37021;
XX
XX
DT 17-OCT-2001 (first entry)
XX
DE Peptide #11058 encoded by probe for measuring placental gene expression.
XX
KW Probe; microarray; human; placenta; antenatal diagnosis;
KW genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200157272-A2.
XX
XX
PD 09-AUG-2001.
XX
XX

PF 30-JAN-2001; 2001WO-US000663.
XX
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX
DR WPI; 2001-488897/53.
XX
XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human placenta.
XX
XX
PS Claim 27; SEQ ID NO 37290; 654pp; English.
XX
XX
CC The present invention relates to single exon nucleic acid probes (SENPs;
CC see AAI31315-AAI57546). The present sequence is a peptide encoded by one
CC such probe. The probes are useful for producing a microarray for
CC predicting, measuring and displaying gene expression in samples derived
CC from human placenta. The probes are useful for antenatal diagnosis of
CC human genetic disorders
XX
XX
SQ Sequence 46 AA;
XX
XX
Alignment Scores:
Pred. No.: 5.62 Length: 46
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 9.78% Indels: 0
DB: 4 Gaps: 0
XX
US-09-910-208B-1 (1-276) x AAM37021 (1-46)
XX
OY 37 AACATCTTCCACGACTACTCGTTCGG 63
XX
DB 13 AsnIlePheHisGlnTySerValArg 21
XX
RESULT 11
ABB26281
ID ABB26281 standard; protein; 46 AA.
XX
XX
AC ABB26281;
XX
XX
DT 23-JAN-2002 (first entry)
XX
XX
DE Protein #8280 encoded by probe for measuring heart cell gene expression.
XX
XX
KW Human; gene expression; heart; microarray; vascular system;
KW cardiovascular disease; hypertension; cardiac arrhythmia;
KW congenital heart disease.
XX
OS Homo sapiens.
XX
XX
PN WO200157274-A2.
XX
XX
PD 09-AUG-2001.
XX
XX
PF 30-JAN-2001; 2001WO-US000666.
XX
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX

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XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX DR WPI; 2001-488999/53.
XX PT Single exon nucleic acid probes for analyzing gene expression in human
XX PT hearts.
XX PS Claim 15; SEQ ID NO 28051; 530pp; English.
XX CC The present invention relates to single exon nucleic acid probes for
CC measuring human gene expression in a sample derived from human heart (see
CC AB21535-ABA41305). The present sequence is a protein encoded by one such
CC probe. The probes may be used for predicting, measuring and displaying
CC gene expression in samples derived from the human heart via microarrays.
CC By measuring gene expression, the probes are useful for predicting,
CC diagnosing, grading, staging, monitoring and prognosing diseases of the
CC human heart and vascular system e.g. cardiovascular disease.
CC hypertension, cardiac arrhythmias and congenital heart disease. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 46 AA;
XX
Alignment Scores:
Pred. No.: 5.62 Length: 46
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 9.78% Indels: 0
DB: 4 Gaps: 0
XX
US-09-910-208B-1 (1-276) x ABB26281 (1-46)
Oy 37 AACATCTTCCACAGTACTCGTTCGG 63
Db 13 AsnIlePheHisGInty:SerValarg 21
RESULT 12
AAM76914
ID AAM76914 standard; protein; 46 AA.
XX AC AAM76914;
XX
XX 06-NOV-2001 (first entry)
XX DT Human bone marrow expressed probe encoded protein SEQ ID NO: 37220.
XX DE Human; bone marrow expressed exon; gene expression analysis; probe;
XX KW microarray; cancer; leukaemia; lymphoma; myeloma.
XX OS Homo sapiens.
XX XX WO200157276-A2.
XX PN 09-AUG-2001.
XX PD
XX PF 30-JAN-2001; 2001WO-US0000668.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX PT
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XX DR WPI; 2001-488900/53.
XX PI Human genome-derived single exon nucleic acid probes useful for analyzing
XX PT gene expression in human bone marrow.
XX XX
XX PS Example 4; SEQ ID NO 37220; 658pp + Sequence Listing; English.
XX CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC bone marrow. They can be used to measure gene expression in bone marrow
CC samples, which may enable the improved diagnosis and treatment of cancers
CC such as lymphoma, leukaemia and myeloma. The present sequence is a
CC protein encoded by one of the probes of the invention
XX SQ Sequence 46 AA;
XX
Alignment Scores:
Pred. No.: 5.62 Length: 46
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 9.78% Indels: 0
DB: 4 Gaps: 0
XX
US-09-910-208B-1 (1-276) x AAM76914 (1-46)
Oy 37 AACATCTTCCACAGTACTCGTTCGG 63
Db 13 AsnIlePheHisGInty:SerValarg 21
RESULT 13
AAM64093
ID AAM64093 standard; protein; 46 AA.
XX AC AAM64093;
XX
XX 05-NOV-2001 (first entry)
XX DT Human brain expressed single exon probe encoded protein SEQ ID NO: 36198.
XX DE Human; brain expressed exon; gene expression analysis; probe; microarray;
XX KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
XX OS Homo sapiens.
XX XX WO200157275-A2.
XX PN 09-AUG-2001.
XX PD
XX PF 30-JAN-2001; 2001WO-US0000667.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX XX
XX WPI; 2001-483446/52.
XX DR Single exon nucleic acid probes for analyzing gene expression in human
XX PT brains.
XX PS Example 4; SEQ ID NO 36198; 650pp + Sequence Listing; English.
XX CC The present invention provides a number of single exon nucleic acid
XX probes which are derived from genomic sequences expressed in the human
```


CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is a protein encoded by one of
CC the probes of the invention

XX SQ Sequence 46 AA;

Alignment Scores: 5.62 Length: 46
Pred. No.: 9.00 Matches: 9
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
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DB: 4

US-09-910-208B-1 (1-276) x AAM64093 (1-46)

QY 37 AACATCTTCCACAGTACTCGTTCGG 63
Db 13 AenllePheHisGlnTy-SerValArg 21

RESULT 14

ABG58579
ID ABG58579 standard; peptide; 46 AA.

XX AC ABG58579;

XX DT 25-FEB-2003 (first entry)

XX DE Human liver peptide, SEQ ID NO 37227.

XX KW Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
KW hypercholesterolaemia; coronary heart disease.

XX OS Homo sapiens.

XX PN WO200157273-A2.

XX PD 09-AUG-2001.

XX PF 30-JAN-2001; 2001WO-US000664.

XX PR 04-FEB-2000; 2000US-0180312P.

XX PR 26-MAY-2000; 2000US-0207456P.

XX PR 30-JUN-2000; 2000US-00608408.

XX PR 03-AUG-2000; 2000US-00632366.

XX PR 21-SEP-2000; 2000US-0234687P.

XX PR 27-SEP-2000; 2000US-0236359P.

XX PR 04-OCT-2000; 2000GB-00024263.

XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX DR WPI; 2001-488898/53.

XX PT Human genome-derived single exon nucleic acid probes useful for analyzing

XX PT gene expression in human adult liver.

XX PS Claim 27; SEQ ID NO 37227; 658pp; English.

XX CC The invention relates to a single exon nucleic acid probe (SENP) (I) for
CC measuring human gene expression in a sample derived from human adult
CC liver, comprising one of 13109 defined nucleotide sequences given in the
CC specification (or complements/ fragments). The probe hybridises at high
CC stringency to a nucleic acid molecule expressed in the human adult liver.
CC (I) may be used for predicting, measuring and displaying gene expression
CC in samples derived from human adult liver. The genes identified may be
CC involved in genetic liver diseases such as cirrhosis,
CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
CC associated with coronary heart disease. ABG47348-ABG59930 represent human
CC liver single exon encoded peptides of the invention. Note: The sequence

CC information for this patent does not appear in the printed specification
CC but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 46 AA;

Alignment Scores: 5.62 Length: 46
Pred. No.: 9.00 Matches: 9
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 9.78% Gaps: 0
DB: 4

US-09-910-208B-1 (1-276) x ABG58579 (1-46)

QY 37 AACATCTTCCACAGTACTCGTTCGG 63
Db 13 AenllePheHisGlnTy-SerValArg 21

RESULT 15

ABG46027

XX ID ABG46027 standard; peptide; 46 AA.

XX AC ABG46027;

XX DT 19-AUG-2002 (first entry)

XX DE Human peptide encoded by genome-derived single exon probe SEQ ID 35692.

XX KW Human; single exon probe; asthma; lung cancer; COPD; ILD;
KW chronic obstructive pulmonary disease; interstitial lung disease;
KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karsenger syndrome;
KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
KW primary ciliary dyskinesia; pulmonary hypertension;
KW hyaline membrane disease.

XX OS Homo sapiens.

XX PN WO200186003-A2.

XX PD 15-NOV-2001.

XX PF 30-JAN-2001; 2001WO-US000665.

XX PR 04-FEB-2000; 2000US-0180312P.

XX PR 26-MAY-2000; 2000US-0207456P.

XX PR 30-JUN-2000; 2000US-00608408.

XX PR 03-AUG-2000; 2000US-00632366.

XX PR 21-SEP-2000; 2000US-0234687P.

XX PR 27-SEP-2000; 2000US-0236359P.

XX PR 04-OCT-2000; 2000GB-00024263.

XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX DR WPI; 2002-114183/15.

XX PT Spatially-addressable set of single exon nucleic acid probes, used to

XX PT measure gene expression in human lung samples.

XX PS Claim 27; SEQ ID NO 35692; 634pp; English.

XX CC The invention relates to a spatially-addressable set of single exon
XX CC nucleic acid probes for measuring gene expression in a sample derived
XX CC from human lung comprising single exon nucleic acid probes having one of
XX CC 12614 nucleic acid sequences mentioned in the specification, or their
XX CC complements or the 12387 open reading frames derived from the 12614
XX CC probes. Also included are a microarray comprising the novel set of probes

CC ; the novel set of probes which hybridise at high stringency to a nucleic
 CC acid expressed in the human lung; measuring gene expression in a sample
 CC derived from human lung, comprising (a) contacting the array with a
 CC collection of detectably labeled nucleic acids derived from human lung
 CC mRNA, and (b) measuring the label detectably bound to each probe of the
 CC array; identifying exons in a eukaryotic genome, comprising (a)
 CC algorithmically predicting at least one exon from genomic sequences of
 CC the eukaryote; and (b) detecting specific hybridisation of detectably
 CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
 CC having a fragment identical to the predicted exon, the probe is included
 CC in the above mentioned microarray; assigning exons to a single gene,
 CC comprising (a) identifying exons from genomic sequence by the method
 CC above and (b) measuring the expression of each of the exons in several
 CC tissues and/or cell types using hybridisation to a single exon
 CC microarrays having a probe with the exon, where a common pattern of
 CC expression of the exons in the tissues and/or cell types indicates that
 CC the exons should be assigned to a single gene; a peptide comprising one
 CC of 12011 sequences, mentioned in the specification, or encoded by the
 CC probes/open reading frames (ORF). The probes are used for gene expression
 CC analysis, and for identifying exons in a gene, particularly using human
 CC lung derived mRNA and for the study of lung diseases such as asthma, lung
 CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
 CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
 CC tuberous sclérosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
 CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary
 CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,
 CC Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary
 CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The
 CC present sequence is a peptide/protein encoded by a single exon probe of
 CC the invention. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 46 AA;

Alignment Scores:
 Pred. NO.: 5.62 Length: 46
 Score: 9.00 Matches: 9
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 9.78% Indels: 0
 DB: 5 Gaps: 0

US-09-910-208B-1 (1-276) x ABG46027 (1-46)

QY 37 AACATCTTCCACGACTCTCGTCGG 63
 Db 13 AenilePheHisGlnIyrSerValArg 21

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14:	/cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*	15	16.3	15	50	US-09-872-185B-9	Sequence 9, Appli
15:	/cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*	15	16.3	15	50	US-09-872-185B-9	Sequence 9, Appli
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		42	7	7	6	US-09-796-692-1461	Sequence 1461, Ap
		43	7	7	6	US-09-796-692-1905	Sequence 1905, Ap
		44	7	7	6	US-10-040-862-1461	Sequence 1461, Ap
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SUMMARIES

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C 77	7	7.6	212	15	US-10-282-122A-73744	Sequence 73744, A	150	7	7.6	504	16	US-10-854-299-111	Sequence 111, App
C 78	7	7.6	213	15	US-10-425-114-61536	Sequence 61536, A	151	7	7.6	505	15	US-10-442-017-17	Sequence 17, Appl
C 79	7	7.6	215	16	US-10-767-701-32449	Sequence 32449, A	152	7	7.6	508	16	US-10-437-963-146016	Sequence 146016
C 80	7	7.6	220	15	US-10-425-114-60496	Sequence 60496, A	153	7	7.6	534	15	US-10-381-870-3	Sequence 3, Appl
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C 82	7	7.6	226	15	US-10-138-588-16	Sequence 16, Appl	155	7	7.6	548	15	US-10-369-493-12222	Sequence 12222, A
C 83	7	7.6	226	15	US-10-307-817-620	Sequence 620, App	156	7	7.6	556	15	US-10-369-493-5442	Sequence 5442, Ap
C 84	7	7.6	226	14	US-10-156-761-11581	Sequence 11581, A	157	7	7.6	559	15	US-10-671-403-182	Sequence 182, App
C 85	7	7.6	243	15	US-10-402-366-3	Sequence 3, Appl	158	7	7.6	559	15	US-10-671-419-182	Sequence 182, App
C 86	7	7.6	243	15	US-10-225-066A-350	Sequence 350, App	159	7	7.6	559	15	US-10-670-844-182	Sequence 182, App
C 87	7	7.6	243	15	US-10-374-780A-2700	Sequence 2700, App	160	7	7.6	559	15	US-10-671-134-182	Sequence 182, App
C 88	7	7.6	243	15	US-10-369-493-19353	Sequence 19353, A	161	7	7.6	559	15	US-10-673-098-182	Sequence 182, App
C 89	7	7.6	245	16	US-10-771-931-38	Sequence 38, Appl	162	7	7.6	559	15	US-10-672-638-182	Sequence 182, App
C 90	7	7.6	245	16	US-10-771-931-38	Sequence 38, Appl	163	7	7.6	559	15	US-10-673-127-182	Sequence 182, App
C 91	7	7.6	249	13	US-10-136-517-17	Sequence 17, Appl	164	7	7.6	559	16	US-10-670-817-182	Sequence 182, App
C 92	7	7.6	249	13	US-10-282-122A-56426	Sequence 56426, A	165	7	7.6	559	16	US-10-673-119-182	Sequence 182, App
C 93	7	7.6	253	16	US-10-437-963-175539	Sequence 175539,	166	7	7.6	559	16	US-10-671-207-182	Sequence 182, App
C 94	7	7.6	263	15	US-10-424-599-194025	Sequence 194025,	167	7	7.6	567	15	US-10-424-599-227211	Sequence 227211,
C 95	7	7.6	264	9	US-09-990-017-2	Sequence 2, Appl	168	7	7.6	592	16	US-10-437-963-135993	Sequence 135993,
C 96	7	7.6	270	15	US-10-282-122A-44941	Sequence 44941, A	169	7	7.6	592	16	US-10-437-963-194949	Sequence 194949,
C 97	7	7.6	271	9	US-09-738-626-3944	Sequence 3944, Ap	170	7	7.6	600	15	US-10-425-114-38048	Sequence 38048, A
C 98	7	7.6	273	15	US-10-425-114-41693	Sequence 41693, A	171	7	7.6	602	15	US-10-369-493-22421	Sequence 22421, A
C 99	7	7.6	273	15	US-10-767-701-44740	Sequence 44740, A	172	7	7.6	603	15	US-10-408-765A-2321	Sequence 60357, A
C 100	7	7.6	296	15	US-10-136-728-78	Sequence 78, Appl	173	7	7.6	609	16	US-10-408-765A-2321	Sequence 2321, Ap
C 101	7	7.6	303	9	US-09-815-242-5393	Sequence 5393, Ap	174	7	7.6	609	16	US-10-437-963-116491	Sequence 116491,
C 102	7	7.6	306	9	US-09-815-242-5393	Sequence 5393, Ap	175	7	7.6	610	16	US-10-437-963-135993	Sequence 135993,
C 103	7	7.6	306	15	US-10-282-122A-44238	Sequence 44238, A	176	7	7.6	626	16	US-10-437-963-107774	Sequence 107774,
C 104	7	7.6	306	15	US-10-282-122A-70667	Sequence 70667, A	177	7	7.6	631	16	US-10-437-963-194947	Sequence 194947,
C 105	7	7.6	306	15	US-10-282-122A-71525	Sequence 71525, A	178	7	7.6	646	9	US-09-964-899-53	Sequence 53, Appl
C 106	7	7.6	308	14	US-10-157-031-48	Sequence 48, Appl	179	7	7.6	661	16	US-10-437-963-107686	Sequence 107686,
C 107	7	7.6	309	9	US-09-886-055-471	Sequence 471, App	180	7	7.6	661	16	US-10-437-963-194959	Sequence 194959,
C 108	7	7.6	309	14	US-09-804-291-471	Sequence 471, App	181	7	7.6	667	13	US-10-032-717-6	Sequence 6, Appl
C 109	7	7.6	309	14	US-10-017-161-126	Sequence 126, App	182	7	7.6	667	13	US-10-032-717-6	Sequence 6, Appl
C 110	7	7.6	310	15	US-10-292-798-106	Sequence 106, App	183	7	7.6	667	14	US-10-414-637-6	Sequence 6, Appl
C 111	7	7.6	318	15	US-10-282-122A-77622	Sequence 77622, A	184	7	7.6	667	14	US-10-414-637-8	Sequence 8, Appl
C 112	7	7.6	321	15	US-10-424-599-171387	Sequence 171387,	185	7	7.6	669	13	US-10-032-717-10	Sequence 10, Appl
C 113	7	7.6	327	15	US-10-072-012-34	Sequence 34, Appl	186	7	7.6	669	14	US-10-032-717-16	Sequence 16, Appl
C 114	7	7.6	327	15	US-10-072-012-34	Sequence 34, Appl	187	7	7.6	669	14	US-10-414-637-10	Sequence 10, Appl
C 115	7	7.6	327	17	US-10-923-960-21	Sequence 21, Appl	188	7	7.6	669	14	US-10-414-637-16	Sequence 16, Appl
C 116	7	7.6	332	15	US-10-424-599-257165	Sequence 257165,	189	7	7.6	669	15	US-10-606-320-6	Sequence 6, Appl
C 117	7	7.6	334	15	US-10-369-493-16769	Sequence 16769, A	190	7	7.6	669	15	US-10-606-320-12	Sequence 12, Appl
C 118	7	7.6	347	15	US-10-104-047-2844	Sequence 2844, Ap	191	7	7.6	670	13	US-10-032-717-24	Sequence 24, Appl
C 119	7	7.6	347	15	US-10-221-625-28	Sequence 28, Appl	192	7	7.6	670	13	US-10-032-717-44	Sequence 44, Appl
C 120	7	7.6	349	15	US-10-389-566-1121	Sequence 1121, Ap	193	7	7.6	670	14	US-10-414-637-24	Sequence 24, Appl
C 121	7	7.6	349	15	US-10-389-566-2148	Sequence 2148, Ap	194	7	7.6	670	14	US-10-414-637-44	Sequence 44, Appl
C 122	7	7.6	350	15	US-10-108-260A-2590	Sequence 2590, Ap	195	7	7.6	670	16	US-10-437-963-188733	Sequence 188733,
C 123	7	7.6	362	17	US-10-923-960-25	Sequence 25, Appl	196	7	7.6	673	13	US-10-032-717-12	Sequence 12, Appl
C 124	7	7.6	368	16	US-10-437-963-135945	Sequence 135945,	197	7	7.6	673	13	US-10-032-717-18	Sequence 18, Appl
C 125	7	7.6	376	9	US-09-801-368-206	Sequence 206, App	198	7	7.6	673	13	US-10-032-717-22	Sequence 22, Appl
C 126	7	7.6	387	15	US-10-335-977-5987	Sequence 5987, Ap	199	7	7.6	673	13	US-10-032-717-40	Sequence 40, Appl
C 127	7	7.6	389	15	US-10-335-977-5988	Sequence 5988, Ap	200	7	7.6	673	13	US-10-032-717-40	Sequence 40, Appl
C 128	7	7.6	395	16	US-10-437-963-135896	Sequence 135896,	201	7	7.6	673	14	US-10-414-637-12	Sequence 12, Appl
C 129	7	7.6	401	16	US-10-437-963-152476	Sequence 152476,	202	7	7.6	673	14	US-10-414-637-18	Sequence 18, Appl
C 130	7	7.6	404	16	US-10-437-963-135891	Sequence 135891,	203	7	7.6	673	14	US-10-414-637-22	Sequence 22, Appl
C 131	7	7.6	407	11	US-09-833-245-1375	Sequence 1375, Ap	204	7	7.6	673	15	US-10-606-320-8	Sequence 8, Appl
C 132	7	7.6	417	15	US-10-424-599-207190	Sequence 207190,	205	7	7.6	673	15	US-10-606-320-14	Sequence 14, Appl
C 133	7	7.6	428	15	US-10-425-114-55940	Sequence 55940, A	206	7	7.6	673	15	US-10-606-320-22	Sequence 22, Appl
C 134	7	7.6	434	9	US-09-726-643-70	Sequence 70, Appl	207	7	7.6	673	15	US-10-606-320-26	Sequence 26, Appl
C 135	7	7.6	434	13	US-10-042-141-70	Sequence 70, Appl	208	7	7.6	673	15	US-10-606-320-30	Sequence 30, Appl
C 136	7	7.6	434	17	US-10-919-272-70	Sequence 70, Appl	209	7	7.6	673	15	US-10-606-320-34	Sequence 34, Appl
C 137	7	7.6	438	9	US-09-815-242-5203	Sequence 5203, Ap	210	7	7.6	673	15	US-10-606-320-54	Sequence 54, Appl
C 138	7	7.6	438	15	US-10-282-122A-43521	Sequence 43521, A	211	7	7.6	673	15	US-10-606-320-56	Sequence 56, Appl
C 139	7	7.6	441	9	US-09-738-626-5611	Sequence 5611, Ap	212	7	7.6	673	15	US-10-606-320-58	Sequence 58, Appl
C 140	7	7.6	453	16	US-10-437-963-135847	Sequence 135847,	213	7	7.6	673	15	US-10-606-320-60	Sequence 60, Appl
C 141	7	7.6	456	16	US-10-771-931-55	Sequence 55, Appl	214	7	7.6	673	15	US-10-606-320-62	Sequence 62, Appl
C 142	7	7.6	462	16	US-10-437-963-135980	Sequence 135980,	215	7	7.6	673	15	US-10-606-320-64	Sequence 64, Appl
C 143	7	7.6	470	15	US-10-183-667-485	Sequence 485, App	216	7	7.6	673	15	US-10-606-320-66	Sequence 66, Appl

217	7	7.6	673	15	US-10-606-320-68	Sequence 68, Appl	290	7	7.6	1176	16	US-10-437-963-124382	Sequence 124382,
218	7	7.6	673	15	US-10-606-320-70	Sequence 70, Appl	c 291	7	7.6	1188	16	US-10-437-963-135987	Sequence 135987,
219	7	7.6	673	15	US-10-606-320-86	Sequence 86, Appl	292	7	7.6	1193	16	US-10-408-765A-2548	Sequence 2548, Ap
220	7	7.6	673	15	US-10-606-320-88	Sequence 88, Appl	293	7	7.6	1198	16	US-10-437-963-188614	Sequence 188614,
221	7	7.6	673	15	US-10-606-320-90	Sequence 90, Appl	294	7	7.6	1206	13	US-10-032-717-2	Sequence 2, Appli
222	7	7.6	673	15	US-10-606-320-92	Sequence 92, Appl	295	7	7.6	1206	14	US-10-414-637-2	Sequence 2, Appli
223	7	7.6	673	15	US-10-606-320-94	Sequence 94, Appl	296	7	7.6	1206	15	US-10-606-320-2	Sequence 2, Appli
224	7	7.6	673	16	US-10-437-963-178585	Sequence 178585,	297	7	7.6	1210	13	US-10-032-717-4	Sequence 4, Appli
225	7	7.6	674	15	US-10-606-320-44	Sequence 44, Appl	298	7	7.6	1210	14	US-10-414-637-4	Sequence 4, Appli
226	7	7.6	674	15	US-10-606-320-50	Sequence 50, Appl	299	7	7.6	1210	15	US-10-606-320-4	Sequence 4, Appli
227	7	7.6	674	15	US-10-606-320-76	Sequence 76, Appl	c 300	7	7.6	1222	16	US-10-437-963-135849	Sequence 135849,
228	7	7.6	674	15	US-10-606-320-82	Sequence 82, Appl	301	7	7.6	1225	16	US-10-437-963-151401	Sequence 151401,
c 229	7	7.6	675	15	US-10-369-493-2810	Sequence 2810, Ap	302	7	7.6	1244	16	US-10-437-963-130188	Sequence 130188,
230	7	7.6	675	15	US-10-606-320-42	Sequence 42, Appl	303	7	7.6	1261	16	US-10-437-963-107844	Sequence 107844,
231	7	7.6	675	15	US-10-606-320-46	Sequence 46, Appl	304	7	7.6	1296	16	US-10-437-963-136020	Sequence 136020,
232	7	7.6	675	15	US-10-606-320-48	Sequence 48, Appl	c 305	7	7.6	1326	16	US-10-437-963-135935	Sequence 135935,
233	7	7.6	675	15	US-10-606-320-74	Sequence 74, Appl	306	7	7.6	1344	16	US-10-437-963-188626	Sequence 188626,
234	7	7.6	675	15	US-10-606-320-78	Sequence 78, Appl	307	7	7.6	1357	16	US-10-437-963-164009	Sequence 164009,
235	7	7.6	675	15	US-10-606-320-80	Sequence 80, Appl	308	7	7.6	1385	16	US-10-437-963-188572	Sequence 188572,
236	7	7.6	676	15	US-10-606-320-40	Sequence 40, Appl	c 309	7	7.6	1387	16	US-10-437-963-135981	Sequence 135981,
237	7	7.6	676	15	US-10-606-320-72	Sequence 72, Appl	310	7	7.6	1392	16	US-10-618-941-132	Sequence 132, App
238	7	7.6	676	16	US-10-437-963-195110	Sequence 195110,	311	7	7.6	1475	16	US-10-437-963-188611	Sequence 188611,
239	7	7.6	677	15	US-10-606-320-52	Sequence 52, Appl	c 312	7	7.6	1492	16	US-10-437-963-176824	Sequence 176824,
240	7	7.6	677	15	US-10-606-320-84	Sequence 84, Appl	313	7	7.6	1496	16	US-10-437-963-188661	Sequence 188661,
c 241	7	7.6	677	16	US-10-437-963-170932	Sequence 170932,	314	7	7.6	1496	16	US-10-437-963-107849	Sequence 107849,
c 242	7	7.6	685	16	US-10-437-963-151556	Sequence 151556,	315	7	7.6	1497	16	US-10-437-963-124538	Sequence 124538,
243	7	7.6	694	16	US-10-437-963-107642	Sequence 107642,	c 316	7	7.6	1500	16	US-10-437-963-135895	Sequence 135895,
c 244	7	7.6	698	15	US-10-369-493-10484	Sequence 10484, A	317	7	7.6	1511	16	US-10-437-963-161204	Sequence 161204,
c 245	7	7.6	704	16	US-10-437-963-170944	Sequence 170944,	318	7	7.6	1521	16	US-10-437-963-188685	Sequence 188685,
c 246	7	7.6	714	16	US-10-405-310-2	Sequence 2, Appli	319	7	7.6	1538	16	US-10-437-963-164006	Sequence 164006,
247	7	7.6	748	15	US-10-425-114-51679	Sequence 51679, A	c 320	7	7.6	1581	16	US-10-437-963-196981	Sequence 196981,
248	7	7.6	752	16	US-10-437-963-187141	Sequence 187141,	321	7	7.6	1614	16	US-10-437-963-107676	Sequence 107676,
249	7	7.6	752	16	US-10-437-963-107866	Sequence 107866,	322	7	7.6	1627	16	US-10-437-963-195091	Sequence 195091,
c 250	7	7.6	779	16	US-10-437-963-170059	Sequence 170059,	323	7	7.6	1635	16	US-10-437-963-130181	Sequence 130181,
c 251	7	7.6	782	16	US-10-437-963-135938	Sequence 135938,	324	7	7.6	1650	16	US-10-437-963-107776	Sequence 107776,
c 252	7	7.6	798	16	US-10-437-963-187102	Sequence 187102,	325	7	7.6	1651	16	US-10-437-963-194012	Sequence 194012,
c 253	7	7.6	799	16	US-10-437-963-135946	Sequence 135946,	326	7	7.6	1655	16	US-10-437-963-188582	Sequence 188582,
254	7	7.6	799	16	US-10-437-963-185819	Sequence 185819,	327	7	7.6	1663	16	US-10-437-963-146158	Sequence 146158,
255	7	7.6	799	16	US-10-437-963-186962	Sequence 186962,	328	7	7.6	1664	16	US-10-437-963-107768	Sequence 107768,
256	7	7.6	827	16	US-10-437-963-146165	Sequence 146165,	329	7	7.6	1673	16	US-10-437-963-107894	Sequence 107894,
c 257	7	7.6	827	16	US-10-437-963-170936	Sequence 170936,	330	7	7.6	1697	16	US-10-437-963-107733	Sequence 107733,
c 258	7	7.6	847	14	US-10-156-761-15032	Sequence 15032, A	331	7	7.6	1699	16	US-10-437-963-107632	Sequence 107632,
c 259	7	7.6	848	14	US-10-284-084-58	Sequence 58, Appl	332	7	7.6	1701	16	US-10-437-963-188570	Sequence 188570,
c 260	7	7.6	850	15	US-10-425-114-37178	Sequence 37178, A	333	7	7.6	1703	16	US-10-437-963-164013	Sequence 164013,
c 261	7	7.6	852	16	US-10-437-963-135867	Sequence 135867,	334	7	7.6	1705	16	US-10-437-963-188651	Sequence 188651,
c 262	7	7.6	860	16	US-10-437-963-194960	Sequence 194960,	335	7	7.6	1708	16	US-10-437-963-130259	Sequence 130259,
263	7	7.6	864	14	US-10-091-333-11	Sequence 11, Appl	336	7	7.6	1710	16	US-10-437-963-107858	Sequence 107858,
c 264	7	7.6	864	14	US-10-325-878-11	Sequence 11, Appl	337	7	7.6	1713	16	US-10-437-963-194018	Sequence 194018,
c 265	7	7.6	880	16	US-10-437-963-170939	Sequence 170939,	338	7	7.6	1726	14	US-10-205-219-109	Sequence 109, App
c 266	7	7.6	922	14	US-10-032-585-7675	Sequence 7675, Ap	339	7	7.6	1735	16	US-10-437-963-194948	Sequence 194948,
267	7	7.6	926	16	US-10-437-963-107738	Sequence 107738,	340	7	7.6	1737	16	US-10-437-963-164004	Sequence 164004,
c 268	7	7.6	949	15	US-10-112-944-351	Sequence 351, App	341	7	7.6	1750	16	US-10-437-963-194022	Sequence 194022,
c 269	7	7.6	973	16	US-10-437-963-135992	Sequence 135992,	342	7	7.6	1753	16	US-10-437-963-107684	Sequence 107684,
c 270	7	7.6	987	16	US-10-437-963-107641	Sequence 107641,	343	7	7.6	1755	16	US-10-437-963-188692	Sequence 188692,
c 271	7	7.6	996	16	US-10-437-963-135853	Sequence 135853,	344	7	7.6	1757	16	US-10-437-963-107679	Sequence 107679,
c 272	7	7.6	996	16	US-10-437-963-188658	Sequence 188658,	345	7	7.6	1757	16	US-10-437-963-107722	Sequence 107722,
273	7	7.6	997	16	US-10-437-963-201562	Sequence 201562,	346	7	7.6	1757	16	US-10-437-963-188719	Sequence 188719,
274	7	7.6	998	16	US-10-437-963-188648	Sequence 188648,	347	7	7.6	1760	16	US-10-437-963-188619	Sequence 188619,
275	7	7.6	1023	15	US-10-282-122A-76367	Sequence 76367, A	348	7	7.6	1767	16	US-10-437-963-188731	Sequence 188731,
c 276	7	7.6	1024	14	US-10-211-962-84	Sequence 84, Appl	349	7	7.6	1774	16	US-10-437-963-107694	Sequence 107694,
c 277	7	7.6	1031	9	US-09-815-242-10932	Sequence 10932, A	350	7	7.6	1774	16	US-10-437-963-107851	Sequence 107851,
c 278	7	7.6	1031	9	US-09-815-242-10932	Sequence 10932, A	351	7	7.6	1777	16	US-10-437-963-194957	Sequence 194957,
c 279	7	7.6	1050	16	US-10-437-963-135861	Sequence 135861,	352	7	7.6	1778	16	US-10-437-963-188697	Sequence 188697,
c 280	7	7.6	1054	16	US-10-437-963-155594	Sequence 155594,	353	7	7.6	1783	16	US-10-437-963-107816	Sequence 107816,
c 281	7	7.6	1061	15	US-10-282-122A-57375	Sequence 57375, A	354	7	7.6	1786	16	US-10-437-963-107824	Sequence 107824,
282	7	7.6	1077	15	US-10-099-322-110	Sequence 110, App	355	7	7.6	1786	16	US-10-437-963-130264	Sequence 130264,
283	7	7.6	1077	15	US-10-044-564-110	Sequence 110, App	356	7	7.6	1788	16	US-10-437-963-107728	Sequence 107728,
284	7	7.6	1083	15	US-10-112-944-331	Sequence 331, App	357	7	7.6	1788	16	US-10-437-963-188693	Sequence 188693,
c 285	7	7.6	1128	16	US-10-437-963-146164	Sequence 146164,	358	7	7.6	1790	16	US-10-437-963-188682	Sequence 188682,
c 286	7	7.6	1138	16	US-10-437-963-136023	Sequence 136023,	359	7	7.6	1791	16	US-10-437-963-107687	Sequence 107687,
c 287	7	7.6	1154	16	US-10-437-963-128109	Sequence 128109,	360	7	7.6	1793	16	US-10-437-963-188585	Sequence 188585,
c 288	7	7.6	1157	16	US-10-782-141-16	Sequence 16, Appl	361	7	7.6	1794	16	US-10-437-963-107735	Sequence 107735,
c 289	7	7.6	1159	16	US-10-437-963-135940	Sequence 135940,	362	7	7.6	1794	16	US-10-437-963-130262	Sequence 130262,

363	7	7.6	1796	16	US-10-437-963-188666	Sequence 188666,	C 436	6	6.5	10	14	US-10-283-722-486	Sequence 486, App
364	7	7.6	1797	16	US-10-437-963-107888	Sequence 107888,	C 437	6	6.5	10	14	US-10-283-722-506	Sequence 506, App
365	7	7.6	1800	16	US-10-437-963-107766	Sequence 107766,	C 438	6	6.5	10	14	US-10-283-722-610	Sequence 610, App
366	7	7.6	1803	16	US-10-437-963-188627	Sequence 188627,	C 439	6	6.5	10	14	US-10-283-722-613	Sequence 613, App
367	7	7.6	1804	16	US-10-437-963-107887	Sequence 107887,	C 440	6	6.5	10	15	US-10-283-903-173	Sequence 173, App
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ALIGNMENTS

RESULT 1
US-09-826-589-3
; Sequence 3, Application US/09826589
; Patent No. US20020106726A1

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; GENERAL INFORMATION:
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Stern, David
; TITLE OF INVENTION: EXTRACELLULAR NOVEL RAGE BINDING PROTEIN (EN-RAGE) AND USES THERE
; FILE REFERENCE: 0575/55873-B-PCT-US
; CURRENT APPLICATION NUMBER: US/09/826,589
; CURRENT FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 3
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Bovine
US-09-826-589-3

Alignment Scores:
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Query Match: 97.83% Indels: 0
DB: 9 Gaps: 0

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RESULT 2
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; Sequence 4, Application US/09826589
; Patent No. US20020106726A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Stern, David
; TITLE OF INVENTION: EXTRACELLULAR NOVEL RAGE BINDING PROTEIN (EN-RAGE) AND USES THERE
; FILE REFERENCE: 0575/55873-B-PCT-US
; CURRENT APPLICATION NUMBER: US/09/826,589
; CURRENT FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Bovine
US-09-826-589-4

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RESULT 3
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; Sequence 11, Application US/09872185B
; Patent No. US20020122799A1
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Herold, Kevan
; APPLICANT: Yan, Shi Du
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Lamster, Ira
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATION
; FILE REFERENCE: 0575/64080
; CURRENT APPLICATION NUMBER: US/09/872,185B
; CURRENT FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 11
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Bovine
US-09-872-185B-11

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Query Match: 97.83% Indels: 0
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RESULT 4

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; Sequence 12, Application US/09872185B
; Patent No. US20020122799A1
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Herold, Kevan
; APPLICANT: Yan, Shi Du
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Lamster, Ira
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATION
; FILE REFERENCE: 0575/64080
; CURRENT APPLICATION NUMBER: US/09/872,185B
; CURRENT FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Bovine
US-09-872-185B-12

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Query Match: 97.83% Indels: 0
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RESULT 5

US-10-666-513-3
; Sequence 3, Application US/10666513
; Publication No. US20040043412A1
; GENERAL INFORMATION:
; APPLICANT: Stern, David
; APPLICANT: Schmidt, Ann Marie
; TITLE OF INVENTION: Extracellular No. US20040043412A1el RAGE Binding Protein (EN-RAGE)
; FILE REFERENCE: 0575/55873
; CURRENT APPLICATION NUMBER: US/10/666,513
; CURRENT FILING DATE: 2003-09-19
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Human
US-10-666-513-3

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Query Match: 97.83% Indels: 0
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RESULT 6

US-10-665-867-3
; Sequence 3, Application US/1065867
; Publication No. US20040121372A1
; GENERAL INFORMATION:
; APPLICANT: Stern, David
; APPLICANT: Schmidt, Ann Marie
; TITLE OF INVENTION: EXTRACELLULAR NOVEL RAGE BINDING PROTEIN (EN-RAGE) AND USES THERE
; FILE REFERENCE: 0575/55873-B-PCT-US
; CURRENT APPLICATION NUMBER: US/10/665,867
; CURRENT FILING DATE: 2003-09-17
; PRIOR FILING DATE: US/09/826,589
; PRIOR FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Bovine
US-10-665-867-3

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Query Match: 97.83% Indels: 0
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Db 21 ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40
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QY 184 GATCCGATAAAGACCGACCGCTGACCTTTGAGGAATTCGTAGTCTCGTGTGCCAGGTTG 243
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RESULT 7
US-10-665-867-4
; Sequence 4, Application US/10665867
; Publication No. US20040121372A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Ann Marie
; TITLE OF INVENTION: EXTRACELLULAR NOVEL RAGE BINDING PROTEIN (EN-RAGE) AND USES THERE
; FILE REFERENCE: 0575/5873-B-PCT-US
; CURRENT APPLICATION NUMBER: US/10/665,867
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US/09/826,589
; PRIOR FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 90
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US-10-665-867-4
Alignment Scores:
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RESULT 8
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; Sequence 5, Application US/09826589
; Patent No. US20020106726A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Ann Marie
; TITLE OF INVENTION: EXTRACELLULAR NOVEL RAGE BINDING PROTEIN (EN-RAGE) AND USES THERE
; FILE REFERENCE: 0575/5873-B-PCT-US
; CURRENT APPLICATION NUMBER: US/09/826,589
; CURRENT FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 5
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Human
US-09-826-589-5
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; Sequence 10, Application US/09872185B
; Patent No. US20020122799A1
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Herold, Kevan
; APPLICANT: Van, Shi Du
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Lamster, Ira
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATION
; FILE REFERENCE: 0575/64080
; CURRENT APPLICATION NUMBER: US/09/872,185B
; CURRENT FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Bovine
US-09-872-185B-10
Alignment Scores:
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Score: 18.00 Matches: 18
Percent Similarity: 100.00% Conservative: 0
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; Sequence 4, Application US/10666513
; Publication No. US20040043412A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Ann Marie
; TITLE OF INVENTION: Extracellular No. US20040043412A1el RAGE Binding Protein (EN-RAG
; FILE OF INVENTION: Uses Thereof
; FILE REFERENCE: 0575/5873
; CURRENT APPLICATION NUMBER: US/10/666,513
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/167,705B
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4

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; LENGTH: 18
; TYPE: PRT
; ORGANISM: Human
US-10-666-513-4

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Db 1 AspGlyAlaValSerPheGluGluPheValValLeuValSerArgValLeuLys 18

RESULT 11

US-10-665-867-5
; Sequence 5, Application US/10665867
; Publication No. US20040121372A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Ann Marie
; TITLE OF INVENTION: EXTRACELLULAR NOVEL RAGE BINDING PROTEIN (EN-RAGE) AND USES THERE
; FILE REFERENCE: 0575/55873-B-PCT-US
; CURRENT APPLICATION NUMBER: US/10/665,867
; PRIOR FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US/09/826,589
; PRIOR FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Human
US-10-665-867-5

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RESULT 12

US-09-826-589-2
; Sequence 2, Application US/09826589
; Patent No. US20020106726A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Ann Marie
; TITLE OF INVENTION: EXTRACELLULAR NOVEL RAGE BINDING PROTEIN (EN-RAGE) AND USES THERE
; FILE REFERENCE: 0575/55873-B-PCT-US
; CURRENT APPLICATION NUMBER: US/09/826,589
; CURRENT FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Human
; NAME/KEY: MISC_FEATURE

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; LOCATION: (47)..(47)
; OTHER INFORMATION: x=any amino acid
US-09-826-589-2

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US-09-910-208B-1 (1-276) x US-09-826-589-2 (1-50)

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RESULT 13

US-09-872-185B-9
; Sequence 9, Application US/09872185B
; Patent No. US20020122799A1
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Herold, Kevan
; APPLICANT: Yan, Shi Du
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Lamster, Ira
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATION
; FILE REFERENCE: 0575/64080
; CURRENT APPLICATION NUMBER: US/09/872,185B
; CURRENT FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Bovine
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (47)..(47)
; OTHER INFORMATION: Where Xaa = unknown
US-09-872-185B-9

Alignment Scores:
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US-09-910-208B-1 (1-276) x US-09-872-185B-9 (1-50)

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Db 15 HisGlnTyrSerValArgValGlyHisPheAspThrLeuAsnLys 29

RESULT 14

US-10-666-513-2
; Sequence 2, Application US/10666513
; Publication No. US20040043412A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Stern, David
; TITLE OF INVENTION: Extracellular No. US20040043412A1 RAGE Binding Protein (EN-RAGE)
; TITLE OF INVENTION: Uses Thereof
; FILE REFERENCE: 0575/55873
; CURRENT APPLICATION NUMBER: US/10/666,513
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/167,705B
; PRIOR FILING DATE: 1998-10-06
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; SEQ ID NO 2
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; TYPE: PRT
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; FEATURE:
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; LOCATION: (47)
; OTHER INFORMATION: Xaa at this position is unknown
US-10-666-513-2

Alignment Scores:
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US-09-910-208B-1 (1-276) x US-10-666-513-2 (1-50)
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Db 15 HisGIntyrSerValargValGlyHisPheAspThrLeuAsnLys 29

RESULT 15
US-10-665-867-2
; Sequence 2, Application US/10665867
; Publication No. US20040121372A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Ann Marie
; TITLE OF INVENTION: EXTRACELLULAR NOVEL RAGE BINDING PROTEIN (EN-RAGE) AND USES THERE
; FILE REFERENCE: 0575/55873-B-PCT-US
; CURRENT APPLICATION NUMBER: US/10/665,867
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US/09/826,589
; PRIOR FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 6
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; ORGANISM: Human
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; OTHER INFORMATION: x=any amino acid
US-10-665-867-2

Alignment Scores:
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117	6	6.5	13	1	US-08-466-285-6	Sequence 6, Appli	189	6	6.5	65	3	US-09-101-544-11	Sequence 11, Appl
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119	6	6.5	15	3	US-08-868-594-6	Sequence 6, Appli	191	6	6.5	65	3	US-09-101-544-12	Sequence 12, Appl
120	6	6.5	15	3	US-08-868-594-6	Sequence 6, Appli	192	6	6.5	65	4	US-08-467-602-414	Sequence 414, App
121	6	6.5	15	3	US-09-485-316A-3	Sequence 3, Appli	193	6	6.5	65	4	US-08-411-295F-53	Sequence 53, Appl
122	6	6.5	15	3	US-09-434-323-6	Sequence 6, Appli	194	6	6.5	65	4	US-08-411-295F-97	Sequence 97, Appl
123	6	6.5	15	4	US-09-947-372A-52	Sequence 52, Appl	195	6	6.5	66	4	US-09-248-796A-23693	Sequence 23693, A
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127	6	6.5	17	4	US-09-662-052-7	Sequence 7, Appli	199	6	6.5	72	2	US-08-738-975-21	Sequence 21, Appl
128	6	6.5	20	1	US-07-678-974D-35	Sequence 35, Appl	200	6	6.5	72	2	US-08-728-626-21	Sequence 21, Appl
129	6	6.5	20	2	US-08-821-355A-10	Sequence 10, Appl	201	6	6.5	72	3	US-08-808-599A-21	Sequence 21, Appl
130	6	6.5	20	2	US-08-945-168-40	Sequence 40, Appl	202	6	6.5	73	3	US-08-735-021-189	Sequence 189, App
131	6	6.5	20	2	US-09-003-687A-10	Sequence 10, Appl	c 203	6	6.5	73	4	US-09-252-919A-31444	Sequence 31444, A
132	6	6.5	20	2	US-09-136-605-10	Sequence 10, Appl	204	6	6.5	73	4	US-09-248-796A-27803	Sequence 27803, A
133	6	6.5	22	4	US-09-270-767-33351	Sequence 33351, A	205	6	6.5	75	1	US-07-987-272A-12	Sequence 12, Appl
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136	6	6.5	23	3	US-09-425-638A-83	Sequence 83, Appl	208	6	6.5	80	1	US-08-485-455D-55	Sequence 55, Appl
137	6	6.5	23	3	US-09-543-004-82	Sequence 82, Appl	209	6	6.5	80	2	US-08-482-130C-55	Sequence 55, Appl
138	6	6.5	23	4	US-09-543-004-83	Sequence 83, Appl	210	6	6.5	80	2	US-08-484-211C-55	Sequence 55, Appl
139	6	6.5	26	1	US-07-942-245-342	Sequence 342, App	211	6	6.5	80	3	US-08-906-769-55	Sequence 55, Appl
140	6	6.5	26	1	US-07-942-245-343	Sequence 343, App	212	6	6.5	80	3	US-08-906-616-55	Sequence 55, Appl
141	6	6.5	27	1	US-08-451-307-24	Sequence 24, Appl	213	6	6.5	80	3	US-08-817-795-55	Sequence 55, Appl
142	6	6.5	28	3	US-09-082-279B-97	Sequence 97, Appl	214	6	6.5	80	3	US-08-485-443B-55	Sequence 55, Appl
143	6	6.5	28	3	US-09-315-304B-97	Sequence 97, Appl	215	6	6.5	80	3	US-08-639-075A-55	Sequence 55, Appl
144	6	6.5	28	4	US-09-834-784-97	Sequence 97, Appl	216	6	6.5	80	3	US-09-012-431-55	Sequence 55, Appl
145	6	6.5	28	4	US-09-515-965A-97	Sequence 97, Appl	217	6	6.5	80	3	US-09-012-692-55	Sequence 55, Appl
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149	6	6.5	29	5	PCT-US94-05355-9	Sequence 9, Appli	c 221	6	6.5	80	4	US-09-545-433-4	Sequence 4, Appli
150	6	6.5	30	2	US-08-934-915-63	Sequence 63, Appl	c 222	6	6.5	80	4	US-09-545-433-5	Sequence 5, Appli
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152	6	6.5	30	6	5202239-9	Patent No. 5202239	c 224	6	6.5	80	4	US-09-545-433-7	Sequence 7, Appli
153	6	6.5	31	4	US-08-467-602-192	Sequence 192, App	c 225	6	6.5	80	4	US-09-248-796A-23275	Sequence 12, Appl
154	6	6.5	31	4	US-08-411-295F-316	Sequence 316, Appl	c 226	6	6.5	80	4	US-09-893-737-12	Sequence 12, Appl
155	6	6.5	34	3	US-08-817-335-3	Sequence 3, Appl	c 227	6	6.5	80	5	PCT-US95-14442A-55	Sequence 55, Appl
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157	6	6.5	34	3	US-08-467-602-188	Sequence 188, App	c 229	6	6.5	85	4	US-09-513-999C-7654	Sequence 7654, Ap
158	6	6.5	34	4	US-09-949-404-4	Sequence 4, Appli	c 230	6	6.5	85	4	US-09-902-540-12367	Sequence 12367, A
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c 233	6	6.5	87	4	US-09-191-468-45	Sequence 45, Appl	306	6	6.5	106	3	US-08-934-841-2	Sequence 2, Appl1
c 234	6	6.5	87	4	US-09-191-468-47	Sequence 47, Appl	307	6	6.5	106	3	US-09-393-409-2	Sequence 2, Appl1
c 235	6	6.5	87	4	US-09-191-468-49	Sequence 49, Appl	308	6	6.5	106	3	US-08-839-765-163	Sequence 163, App
c 236	6	6.5	87	4	US-09-191-468-51	Sequence 51, Appl	309	6	6.5	106	3	US-08-839-765-164	Sequence 164, App
c 237	6	6.5	87	4	US-09-191-468-53	Sequence 53, Appl	310	6	6.5	106	3	US-08-839-765-165	Sequence 165, App
c 238	6	6.5	88	2	US-08-391-916A-10	Sequence 10, Appl	311	6	6.5	106	3	US-09-136-389-163	Sequence 163, App
c 239	6	6.5	88	3	US-08-341-018-68	Sequence 68, Appl	312	6	6.5	106	3	US-09-136-389-164	Sequence 164, App
c 240	6	6.5	88	3	US-08-470-335-224	Sequence 224, App	313	6	6.5	106	3	US-09-136-389-165	Sequence 165, App
c 241	6	6.5	88	3	US-08-470-339-224	Sequence 224, App	314	6	6.5	106	3	US-08-484-537-1	Sequence 1, Appl1
c 242	6	6.5	88	4	US-08-467-602-418	Sequence 418, App	315	6	6.5	106	3	US-08-484-537-7	Sequence 7, Appl1
c 243	6	6.5	88	4	US-09-673-395A-332	Sequence 332, App	316	6	6.5	106	3	US-08-484-537-8	Sequence 8, Appl1
c 244	6	6.5	88	4	US-08-411-295F-61	Sequence 61, Appl	317	6	6.5	106	3	US-08-484-537-16	Sequence 16, Appl1
c 245	6	6.5	88	4	US-08-411-295F-101	Sequence 101, App	318	6	6.5	106	3	US-09-610-838-163	Sequence 163, App
c 246	6	6.5	91	4	US-09-484-577A-8	Sequence 8, Appl1	319	6	6.5	106	3	US-09-610-838-164	Sequence 164, App
c 247	6	6.5	92	4	US-09-252-991A-25401	Sequence 25401, A	320	6	6.5	106	3	US-09-610-838-165	Sequence 165, App
c 248	6	6.5	92	4	US-09-621-976-4576	Sequence 4576, Ap	321	6	6.5	106	4	US-09-252-991A-24846	Sequence 24846, A
c 249	6	6.5	94	4	US-09-252-991A-31208	Sequence 31208, A	322	6	6.5	106	4	US-09-711-485-163	Sequence 163, App
c 250	6	6.5	94	4	US-09-489-039A-9948	Sequence 9948, Ap	323	6	6.5	106	4	US-09-711-485-164	Sequence 164, App
c 251	6	6.5	94	4	US-09-270-767-60718	Sequence 60718, A	324	6	6.5	106	4	US-09-711-485-165	Sequence 165, App
c 252	6	6.5	95	2	US-08-467-046-25	Sequence 25, Appl	c 325	6	6.5	107	2	US-08-394-189B-24	Sequence 24, Appl
c 253	6	6.5	95	4	US-09-252-991A-29993	Sequence 29993, A	326	6	6.5	107	4	US-09-134-000C-4599	Sequence 4599, Ap
c 254	6	6.5	95	4	US-09-270-767-57388	Sequence 57388, A	327	6	6.5	109	1	US-07-987-272A-8	Sequence 8, Appl1
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c 256	6	6.5	96	4	US-09-489-039A-13145	Sequence 13145, A	c 329	6	6.5	109	3	US-09-425-638A-21	Sequence 21, Appl
c 257	6	6.5	97	3	US-09-902-540-16755	Sequence 16755, A	c 330	6	6.5	109	3	US-09-543-004-20	Sequence 20, Appl
c 258	6	6.5	99	3	US-09-199-637A-345	Sequence 345, App	c 331	6	6.5	109	3	US-09-543-004-21	Sequence 21, Appl
c 259	6	6.5	100	4	US-09-270-767-45993	Sequence 45993, A	332	6	6.5	109	4	US-09-252-991A-27588	Sequence 27588, A
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c 261	6	6.5	103	3	US-09-134-001C-3738	Sequence 3738, Ap	c 334	6	6.5	109	4	US-09-134-000C-5905	Sequence 5905, Ap
c 262	6	6.5	103	4	US-09-809-665A-85	Sequence 85, Appl	335	6	6.5	109	4	US-09-134-000C-6718	Sequence 6718, Ap
c 263	6	6.5	104	3	US-09-048-889-5	Sequence 5, Appl1	c 336	6	6.5	110	4	US-09-543-681A-7917	Sequence 7917, Ap
c 264	6	6.5	104	4	US-09-270-767-34088	Sequence 34088, A	c 337	6	6.5	110	4	US-09-513-999C-8073	Sequence 8073, Ap
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c 266	6	6.5	104	4	US-09-270-767-49305	Sequence 49305, A	339	6	6.5	111	3	US-09-500-654-4	Sequence 4, Appl1
c 267	6	6.5	105	4	US-09-270-767-53446	Sequence 53446, A	c 340	6	6.5	111	3	US-09-249-542-18	Sequence 18, Appl
c 268	6	6.5	105	4	US-09-270-767-59980	Sequence 59980, A	341	6	6.5	111	3	US-09-893-737-120	Sequence 120, App
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c 270	6	6.5	106	1	US-07-634-278-7	Sequence 7, Appl1	343	6	6.5	114	1	US-08-385-241-3	Sequence 3, Appl1
c 271	6	6.5	106	1	US-07-634-278-8	Sequence 8, Appl1	344	6	6.5	114	4	US-09-214-272-4	Sequence 4, Appl1
c 272	6	6.5	106	1	US-07-634-278-16	Sequence 16, Appl	345	6	6.5	114	4	US-09-806-382A-4	Sequence 4, Appl1
c 273	6	6.5	106	1	US-08-477-728-1	Sequence 1, Appl1	346	6	6.5	115	4	US-09-328-352-5509	Sequence 5509, Ap
c 274	6	6.5	106	1	US-08-477-728-7	Sequence 7, Appl1	347	6	6.5	115	4	US-09-800-729-126	Sequence 126, App
c 275	6	6.5	106	1	US-08-477-728-8	Sequence 8, Appl1	348	6	6.5	115	4	US-09-270-767-36954	Sequence 36954, A
c 276	6	6.5	106	1	US-08-477-728-16	Sequence 16, Appl	349	6	6.5	115	4	US-09-270-767-52171	Sequence 52171, A
c 277	6	6.5	106	1	US-08-474-040-1	Sequence 1, Appl1	350	6	6.5	116	4	US-09-071-035-422	Sequence 422, App
c 278	6	6.5	106	1	US-08-474-040-7	Sequence 7, Appl1	351	6	6.5	117	1	US-07-752-101A-37	Sequence 37, Appl
c 279	6	6.5	106	1	US-08-474-040-8	Sequence 8, Appl1	352	6	6.5	117	1	US-07-752-101A-40	Sequence 40, Appl
c 280	6	6.5	106	1	US-08-474-040-16	Sequence 16, Appl	353	6	6.5	117	1	US-07-752-101A-42	Sequence 42, Appl
c 281	6	6.5	106	1	US-08-487-200-1	Sequence 1, Appl1	354	6	6.5	117	4	US-09-634-238-369	Sequence 369, App
c 282	6	6.5	106	1	US-08-487-200-7	Sequence 7, Appl1	355	6	6.5	117	4	US-09-252-991A-23573	Sequence 23573, A
c 283	6	6.5	106	1	US-08-487-200-8	Sequence 8, Appl1	356	6	6.5	118	4	US-09-252-991A-18728	Sequence 18728, A
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c 285	6	6.5	106	1	US-08-488-113B-163	Sequence 163, App	358	6	6.5	121	4	US-09-248-796A-22471	Sequence 22471, A
c 286	6	6.5	106	1	US-08-488-113B-164	Sequence 164, App	c 359	6	6.5	123	4	US-09-583-110-4758	Sequence 4758, Ap
c 287	6	6.5	106	1	US-08-488-113B-165	Sequence 165, App	360	6	6.5	124	4	US-09-248-796A-27855	Sequence 27855, A
c 288	6	6.5	106	1	US-08-477-484B-163	Sequence 163, App	c 361	6	6.5	124	4	US-09-107-433-3739	Sequence 3739, Ap
c 289	6	6.5	106	1	US-08-477-484B-164	Sequence 164, App	362	6	6.5	126	1	US-07-634-278-21	Sequence 21, Appl
c 290	6	6.5	106	1	US-08-477-484B-165	Sequence 165, App	363	6	6.5	126	1	US-08-477-728-21	Sequence 21, Appl
c 291	6	6.5	106	1	US-08-107-669D-49	Sequence 49, Appl	364	6	6.5	126	1	US-08-474-040-21	Sequence 21, Appl
c 292	6	6.5	106	1	US-08-107-669D-50	Sequence 50, Appl	365	6	6.5	126	1	US-08-487-200-21	Sequence 21, Appl
c 293	6	6.5	106	1	US-08-107-669D-51	Sequence 51, Appl	366	6	6.5	126	3	US-08-484-537-21	Sequence 21, Appl
c 294	6	6.5	106	1	US-08-472-788A-50	Sequence 50, App	367	6	6.5	126	4	US-09-270-767-34641	Sequence 34641, A
c 295	6	6.5	106	1	US-08-472-788A-83	Sequence 83, Appl	368	6	6.5	126	4	US-09-270-767-49858	Sequence 49858, A
c 296	6	6.5	106	1	US-08-472-788A-84	Sequence 84, Appl	369	6	6.5	129	4	US-09-270-767-34801	Sequence 34801, A
c 297	6	6.5	106	2	US-08-477-531B-49	Sequence 49, Appl	c 370	6	6.5	129	4	US-09-270-767-50018	Sequence 50018, A
c 298	6	6.5	106	2	US-08-477-531B-50	Sequence 50, Appl	c 371	6	6.5	129	4	US-09-902-540-12686	Sequence 12686, A
c 299	6	6.5	106	2	US-08-477-531B-51	Sequence 51, Appl	c 372	6	6.5	129	4	US-09-902-540-15340	Sequence 15340, A
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c 301	6	6.5	106	2	US-08-646-360-164	Sequence 164, App	374	6	6.5	131	4	US-09-107-532A-4421	Sequence 4421, Ap
c 302	6	6.5	106	2	US-08-646-360-165	Sequence 165, App	c 375	6	6.5	131	4	US-09-489-039A-12400	Sequence 12400, A
c 303	6	6.5	106	2	US-08-082-842A-50	Sequence 50, Appl	c 376	6	6.5	131	4	US-09-540-236-2995	Sequence 2995, Ap
c 304	6	6.5	106	2	US-08-082-842A-83	Sequence 83, Appl	c 377	6	6.5	132	4	US-09-270-767-57697	Sequence 57697, A

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C 433 6 6.5 160 4 US-09-270-767-40290 Sequence 40290, A
C 434 6 6.5 160 4 US-09-270-767-55506 Sequence 55506, A
C 435 6 6.5 161 4 US-09-252-991A-24938 Sequence 24938, A
C 436 6 6.5 161 4 US-09-252-991A-32451 Sequence 32451, A
C 437 6 6.5 162 4 US-09-583-110-3532 Sequence 3532, Ap
C 438 6 6.5 163 3 US-09-188-930-143 Sequence 143, App
C 439 6 6.5 163 3 US-09-188-930-277 Sequence 277, App
C 440 6 6.5 163 4 US-09-312-283C-143 Sequence 143, App
C 441 6 6.5 163 4 US-09-312-283C-277 Sequence 277, App
C 442 6 6.5 163 4 US-09-583-110-4025 Sequence 4025, Ap
C 443 6 6.5 164 4 US-09-482-273-132 Sequence 132, App
C 444 6 6.5 164 4 US-09-252-991A-24260 Sequence 24260, A
C 445 6 6.5 164 4 US-09-270-767-35638 Sequence 35638, A
C 446 6 6.5 164 4 US-09-270-767-42021 Sequence 42021, A
C 447 6 6.5 164 4 US-09-270-767-50855 Sequence 50855, A
C 448 6 6.5 164 4 US-09-640-211A-1922 Sequence 1922, Ap
C 449 6 6.5 165 3 US-09-134-001C-3601 Sequence 3601, Ap
C 450 6 6.5 165 4 US-09-248-796A-33180 Sequence 33180, A

C 451 6 6.5 168 4 US-09-270-767-46662 Sequence 46662, A
C 452 6 6.5 168 4 US-09-248-796A-20919 Sequence 20919, A
C 453 6 6.5 168 4 US-09-949-016-10749 Sequence 10749, A
C 454 6 6.5 169 4 US-09-270-767-34124 Sequence 34124, A
C 455 6 6.5 169 4 US-09-270-767-49341 Sequence 49341, A
C 456 6 6.5 170 4 US-09-489-039A-7335 Sequence 7335, Ap
C 457 6 6.5 171 4 US-09-902-540-10737 Sequence 10737, A
C 458 6 6.5 172 4 US-09-252-991A-26947 Sequence 26947, A
C 459 6 6.5 173 4 US-08-467-602-240 Sequence 240, App
C 460 6 6.5 173 4 US-08-411-295P-166 Sequence 166, App
C 461 6 6.5 174 3 US-09-328-869-17 Sequence 17, Appl
C 462 6 6.5 174 3 US-09-629-774A-17 Sequence 17, Appl
C 463 6 6.5 175 4 US-09-248-796A-23209 Sequence 23209, A
C 464 6 6.5 175 4 US-09-902-540-14268 Sequence 14268, A
C 465 6 6.5 176 4 US-08-467-602-236 Sequence 236, App
C 466 6 6.5 176 4 US-08-459-260A-54 Sequence 54, Appl
C 467 6 6.5 176 4 US-09-252-991A-29512 Sequence 29512, A
C 468 6 6.5 176 4 US-08-488-446-54 Sequence 54, Appl
C 469 6 6.5 176 4 US-08-467-344A-54 Sequence 54, Appl
C 470 6 6.5 176 4 US-08-424-550B-54 Sequence 54, Appl
C 471 6 6.5 176 4 US-08-411-295P-162 Sequence 162, App
C 472 6 6.5 176 4 US-09-902-540-15758 Sequence 15758, A
C 473 6 6.5 177 4 US-09-252-991A-27881 Sequence 27881, A
C 474 6 6.5 177 4 US-09-252-991A-27957 Sequence 27957, A
C 475 6 6.5 177 4 US-09-662-052-4 Sequence 4, Appl
C 476 6 6.5 179 4 US-09-270-767-34964 Sequence 34964, A
C 477 6 6.5 179 4 US-09-270-767-50181 Sequence 50181, A
C 478 6 6.5 181 4 US-09-248-796A-15978 Sequence 15978, A
C 479 6 6.5 181 4 US-09-248-796A-16306 Sequence 16306, A
C 480 6 6.5 181 4 US-09-248-796A-18165 Sequence 18165, A
C 481 6 6.5 182 4 US-09-107-433-2657 Sequence 2657, Ap
C 482 6 6.5 182 4 US-09-248-796A-19145 Sequence 19145, A
C 483 6 6.5 182 4 US-09-248-796A-20866 Sequence 20866, A
C 484 6 6.5 183 4 US-09-902-540-14241 Sequence 14241, A
C 485 6 6.5 185 4 US-09-640-211A-820 Sequence 820, App
C 486 6 6.5 187 4 US-09-248-796A-15313 Sequence 15313, A
C 487 6 6.5 188 3 US-09-048-889-3 Sequence 3, Appl
C 488 6 6.5 189 4 US-09-252-991A-18969 Sequence 18969, A
C 489 6 6.5 189 4 US-09-902-540-14285 Sequence 14285, A
C 490 6 6.5 190 4 US-09-252-991A-17510 Sequence 17510, A
C 491 6 6.5 190 4 US-09-248-796A-27916 Sequence 27916, A
C 492 6 6.5 191 4 US-09-205-258-981 Sequence 981, App
C 493 6 6.5 192 4 US-09-540-236-3495 Sequence 3495, Ap
C 494 6 6.5 193 4 US-09-902-540-11605 Sequence 11605, A
C 495 6 6.5 194 4 US-09-248-796A-24122 Sequence 24122, A
C 496 6 6.5 194 4 US-09-252-991A-27440 Sequence 27440, A
C 497 6 6.5 195 4 US-09-270-767-43296 Sequence 43296, A
C 498 6 6.5 196 3 US-09-048-889-1 Sequence 1, Appl
C 499 6 6.5 196 4 US-08-467-602-244 Sequence 244, App
500 6 6.5 196 4 US-09-513-775B-8 Sequence 8, Appl

ALIGNMENTS

RESULT 1
US-08-568-310D-19
; Sequence 19, Application US/08568310D
; Patent No. 5976832
; GENERAL INFORMATION:
; APPLICANT: HITOMI, JIRO
; APPLICANT: YAMAGUCHI, KEN
; APPLICANT: YAMAMURA, TOKUJIRO
; APPLICANT: KIMURA, TATSUJI
; TITLE OF INVENTION: NOVEL CALCIUM-BINDING PROTEINS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WYATT, GERBER, MELLER & O'ROURKE
; STREET: 99 PARK AVENUE
; CITY: NEW YORK CITY
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016

COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH, 720 KB
MEDIUM TYPE: STORAGE
COMPUTER: IBM-PC COMPATIBLE
OPERATING SYSTEM: PC-DOS 6.2
SOFTWARE: WORDPERFECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/568,310D
FILING DATE: DECEMBER 6, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 7-70468 and 7-45564 (both Japan)
FILING DATE: 3/6/95 and 3/6/95, respectively
ATTORNEY/AGENT INFORMATION:
NAME: KLEIN, MILTON
REGISTRATION NUMBER: 27101
REFERENCE/DOCKET NUMBER: 3316
TELEPHONE: (212)953-3350
TELEFAX: (212)953-3352
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 92
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: cDNA
PUBLICATION INFORMATION:
RELEVANT RESIDUES IN SEQ ID NO: 19: FROM 1 TO 92

US-08-568-310D-19
Alignment Scores:
Pred. No.: 2,01e-82 Length: 92
Score: 92.00 Matches: 92
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-1 (1-276) x US-08-568-310D-19 (1-92)

QY	1	ATGACTAAGCTGGAAGATCACCTGGAGGAATCATCAACATCTTCCACCAGTACTCCGTT	60
Db	1	MetThrLysLeuGluAspHisLeuGluGlyIleleAsnIlePheHisGlnTyrSerVal	20
QY	61	CGGTGGGGGCATTTTCGACACCTCAACAGCTGAGCTGAAGCAGCTGATCAAAAGGAA	120
Db	21	ArgValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGlu	40
QY	121	CTTCCAAAACCTCCAGAACCCACCAAGATCAACCTACCATTCGACAAATATTTCCAGAC	180
Db	41	LeuProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAsp	60
QY	181	CTGGATGCCGATAAAGACGGAGCCGTCAGCTTTGAGGAATTCGTAGTCTCGTGTCCAGG	240
Db	61	LeuAspAlaAspLysAspGlyAlaValSerPheGluGluPheValValLeuValSerArg	80
QY	241	GTGCTGAAAACGCCACATAGATATCCCAAAGAG	276
Db	81	ValLeuLysThrAlaHisIleAspIleHisLysGlu	92

RESULT 2

US-09-270-455-19
Sequence 19, Application US/09270455
Patent No. 6313267
GENERAL INFORMATION:
APPLICANT: HITOMI, JIRO
APPLICANT: YAMAGUCHI, KEN
APPLICANT: YAMAMURA, TOKUJIRO
APPLICANT: KIMURA, TATSUJI
TITLE OF INVENTION: NOVEL CALCIUM-BINDING PROTEINS
NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:
ADDRESSEE: WYATT GERBER, MELLER & O'ROURKE
STREET: 99 PARK AVENUE
STREET: 6th FLOOR
CITY: NEW YORK CITY
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH, 720 KB
MEDIUM TYPE: STORAGE
COMPUTER: IBM-PC COMPATIBLE
OPERATING SYSTEM: PC-DOS 6.2
SOFTWARE: WORDPERFECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/270,455
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/568,310
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: KLEIN, MILTON
REGISTRATION NUMBER: 27101
REFERENCE/DOCKET NUMBER: 3316
TELEPHONE: (212)953-3350
TELEFAX: (212)953-3352
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 92
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: cDNA
PUBLICATION INFORMATION:
RELEVANT RESIDUES IN SEQ ID NO: 19: FROM 1 TO 92

US-09-270-455-19
Alignment Scores:
Pred. No.: 2,01e-82 Length: 92
Score: 92.00 Matches: 92
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-09-910-208B-1 (1-276) x US-09-270-455-19 (1-92)

QY	1	ATGACTAAGCTGGAAGATCACCTGGAGGAATCATCAACATCTTCCACCAGTACTCCGTT	60
Db	1	MetThrLysLeuGluAspHisLeuGluGlyIleleAsnIlePheHisGlnTyrSerVal	20
QY	61	CGGTGGGGGCATTTTCGACACCTCAACAGCTGAGCTGAAGCAGCTGATCAAAAGGAA	120
Db	21	ArgValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGlu	40
QY	121	CTTCCAAAACCTCCAGAACCCACCAAGATCAACCTACCATTCGACAAATATTTCCAGAC	180
Db	41	LeuProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAsp	60
QY	181	CTGGATGCCGATAAAGACGGAGCCGTCAGCTTTGAGGAATTCGTAGTCTCGTGTCCAGG	240
Db	61	LeuAspAlaAspLysAspGlyAlaValSerPheGluGluPheValValLeuValSerArg	80
QY	241	GTGCTGAAAACGCCACATAGATATCCCAAAGAG	276
Db	81	ValLeuLysThrAlaHisIleAspIleHisLysGlu	92

RESULT 3

US-09-263-312-3
Sequence 3, Application US/09263312
Patent No. 6555340

; Sequence 2, Application US/08568310D
; Patent No. 5976832
; GENERAL INFORMATION:
; APPLICANT: HITOMI, JIRO
; APPLICANT: YAMAGUCHI, KEN
; APPLICANT: YAMAMURA, TOKUJIRO
; APPLICANT: KIMURA, TATSUJI
; TITLE OF INVENTION: NOVEL CALCIUM-BINDING PROTEINS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WYATT GERBER, MELLER & O'ROURKE
; STREET: 99 PARK AVENUE
; STREET: 6th FLOOR
; CITY: NEW YORK CITY
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH, 720 Kb
; MEDIUM TYPE: STORAGE
; COMPUTER: IBM-PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS 6.2
; SOFTWARE: WORDPERFECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/568,310D
; FILING DATE: DECEMBER 6, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 7-70468 and 7-45564 (both Japan)
; FILING DATE: 3/6/95 and 3/6/95, respectively
; ATTORNEY/AGENT INFORMATION:
; NAME: KLEIN, MILTON
; REGISTRATION NUMBER: 27101
; REFERENCE/DOCKET NUMBER: 3316
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)953-3350
; TELEFAX: (212)953-3352
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 51
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; PUBLICATION INFORMATION:
; RELEVANT RESIDUES IN SEQ ID NO: 2:
; RELEVANT RESIDUES IN SEQ ID NO: FROM 1 TO 51

US-08-568-310D-2

Alignment Scores:
Pred. No.: 51
Score: 51.00
Length: 51
Matches: 51
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Query Match: 55.43%
Indels: 0
Gaps: 0

US-09-910-208B-1 (1-276) x US-08-568-310D-2 (1-51)

QY 4 ACTAAGCTGGAAGATCACCTGGAGGGAATCATCAACATCTTCCACGAGTACTCCGTTCCG 63
Db 1 ThrLysLeuGluAspHisLeuGluGlyIleIleAsnIlePheHisGlnTyrSerValArg 20
QY 64 GTGGGGCATTTTCGACACCCCTCAACAGCGTGAGCTGAAGCAGCTGATCACAAGGAACATT 123
Db 21 ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40
QY 124 CCCAAACCTCCAGAACACCAAGATCAACCT 156
Db 41 ProLysThrLeuGlnAsnThrLysAspGlnPro 51

RESULT 7

US-09-270-455-2
; Sequence 2, Application US/09270455

; Patent No. 6313267
; GENERAL INFORMATION:
; APPLICANT: HITOMI, JIRO
; APPLICANT: YAMAGUCHI, KEN
; APPLICANT: YAMAMURA, TOKUJIRO
; APPLICANT: KIMURA, TATSUJI
; TITLE OF INVENTION: NOVEL CALCIUM-BINDING PROTEINS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WYATT GERBER, MELLER & O'ROURKE
; STREET: 99 PARK AVENUE
; STREET: 6th FLOOR
; CITY: NEW YORK CITY
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH, 720 Kb
; MEDIUM TYPE: STORAGE
; COMPUTER: IBM-PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS 6.2
; SOFTWARE: WORDPERFECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/270,455
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/568,310
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: KLEIN, MILTON
; REGISTRATION NUMBER: 27101
; REFERENCE/DOCKET NUMBER: 3316
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)953-3350
; TELEFAX: (212)953-3352
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 51
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; PUBLICATION INFORMATION:
; RELEVANT RESIDUES IN SEQ ID NO: 2: FROM 1 TO 51

US-09-270-455-2

Alignment Scores:
Pred. No.: 51
Score: 51.00
Length: 51
Matches: 51
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Query Match: 55.43%
Indels: 0
Gaps: 0

US-09-910-208B-1 (1-276) x US-09-270-455-2 (1-51)

QY 4 ACTAAGCTGGAAGATCACCTGGAGGGAATCATCAACATCTTCCACGAGTACTCCGTTCCG 63
Db 1 ThrLysLeuGluAspHisLeuGluGlyIleIleAsnIlePheHisGlnTyrSerValArg 20
QY 64 GTGGGGCATTTTCGACACCCCTCAACAGCGTGAGCTGAAGCAGCTGATCACAAGGAACATT 123
Db 21 ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40
QY 124 CCCAAACCTCCAGAACACCAAGATCAACCT 156
Db 41 ProLysThrLeuGlnAsnThrLysAspGlnPro 51

RESULT 8

US-08-568-310D-6
; Sequence 6, Application US/08568310D
; Patent No. 5976832
; GENERAL INFORMATION:

APPLICANT: HITOMI, JIRO
APPLICANT: YAMAGUCHI, KEN
APPLICANT: YAMAMURA, TOKUJIRO
APPLICANT: KIMURA, TATSUJI
TITLE OF INVENTION: NOVEL CALCIUM-BINDING PROTEINS
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: WYATT GERBER, MELLER & O'ROURKE
STREET: 99 PARK AVENUE
CITY: NEW YORK CITY
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH, 720 Kb
MEDIUM TYPE: STORAGE
COMPUTER: IBM-PC COMPATIBLE
OPERATING SYSTEM: PC-DOS 6.2
SOFTWARE: WORDPERFECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/568,310D
FILING DATE: DECEMBER 6, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 7-70468 and 7-45564 (both Japan)
FILING DATE: 3/6/95 and 3/6/95, respectively
ATTORNEY/AGENT INFORMATION:
NAME: KLEIN, MILTON
REGISTRATION NUMBER: 27101
REFERENCE/DOCKET NUMBER: 3316
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)953-3350
TELEFAX: (212)953-3352
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 31
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
PUBLICATION INFORMATION:
RELEVANT RESIDUES IN SEQ ID NO: 6:
RELEVANT RESIDUES IN SEQ ID NO: FROM 1 TO 31
US-08-568-310D-6

Alignment Scores:
Pred. No.: 3178-22 Length: 31
Score: 31.00 Matches: 31
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 33.70% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-1 (1-276) x US-08-568-310D-6 (1-31)
QY 121 CTTCCCAAAACCTCCAGAACCAAGATCAACCTACCATGACAAATATTCACAGAC 180
Db 1 LeuProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAsp 20
QY 181 CTGGATGCCGATAAGACGCGCGTCAGCTTT 213
Db 21 LeuAspAlaAspLysAspGlyAlaValSerPhe 31

RESULT 9
US-09-270-455-6
Sequence 6, Application US/09270455
Patent No. 6313267
GENERAL INFORMATION:
APPLICANT: HITOMI, JIRO
APPLICANT: YAMAGUCHI, KEN
APPLICANT: YAMAMURA, TOKUJIRO
APPLICANT: KIMURA, TATSUJI
TITLE OF INVENTION: NOVEL CALCIUM-BINDING PROTEINS

NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: WYATT GERBER, MELLER & O'ROURKE
STREET: 99 PARK AVENUE
CITY: NEW YORK CITY
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH, 720 Kb
MEDIUM TYPE: STORAGE
COMPUTER: IBM-PC COMPATIBLE
OPERATING SYSTEM: PC-DOS 6.2
SOFTWARE: WORDPERFECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/270,455
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/568,310
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: KLEIN, MILTON
REGISTRATION NUMBER: 27101
REFERENCE/DOCKET NUMBER: 3316
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)953-3350
TELEFAX: (212)953-3352
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 31
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
PUBLICATION INFORMATION:
RELEVANT RESIDUES IN SEQ ID NO: 6:
FROM 1 TO 31
US-09-270-455-6

Alignment Scores:
Pred. No.: 3178-22 Length: 31
Score: 31.00 Matches: 31
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 33.70% Indels: 0
DB: 3 Gaps: 0

US-09-910-208B-1 (1-276) x US-09-270-455-6 (1-31)
QY 121 CTTCCCAAAACCTCCAGAACCAAGATCAACCTACCATGACAAATATTCACAGAC 180
Db 1 LeuProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAsp 20
QY 181 CTGGATGCCGATAAGACGCGCGTCAGCTTT 213
Db 21 LeuAspAlaAspLysAspGlyAlaValSerPhe 31

RESULT 10
US-08-568-310D-7
Sequence 7, Application US/08568310D
Patent No. 5976832
GENERAL INFORMATION:
APPLICANT: HITOMI, JIRO
APPLICANT: YAMAGUCHI, KEN
APPLICANT: YAMAMURA, TOKUJIRO
APPLICANT: KIMURA, TATSUJI
TITLE OF INVENTION: NOVEL CALCIUM-BINDING PROTEINS
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: WYATT GERBER, MELLER & O'ROURKE
STREET: 99 PARK AVENUE
CITY: NEW YORK CITY

STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH, 720 KB
MEDIUM TYPE: STORAGE
COMPUTER: IBM-PC COMPATIBLE
OPERATING SYSTEM: PC-DOS 6.2
SOFTWARE: WORDPERFECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/568,310D
FILING DATE: DECEMBER 6, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 7-70468 and 7-45564 (both Japan)
FILING DATE: 3/6/95 and 3/6/95, respectively
ATTORNEY/AGENT INFORMATION:
NAME: KLEIN, MILTON
REGISTRATION NUMBER: 27101
REFERENCE/DOCKET NUMBER: 3316
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)953-3350
TELEFAX: (212)953-3352
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 40
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
PUBLICATION INFORMATION:
RELEVANT RESIDUES IN SEQ ID NO: 7:
FROM 1 TO 20

US-08-568-310D-7

Alignment Scores:
Pred. No.: 2,33e-11 Length: 20
Score: 20.00 Matches: 20
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 21.74% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-1 (1-276) x US-08-568-310D-7 (1-20)

QY 217 GAATTCGTAGTCCTGCTCCAGGCTGCTGAAACAGCCCATAGATATCCACAAGAG 276
Db 1 GluPheValValLeuValSerArgValLeuLysThrAlaHisIleAspIleHisLysGlu 20

RESULT 11
US-09-270-455-7
Sequence 7, Application US/09270455
Patent No. 6313267
GENERAL INFORMATION:
APPLICANT: HITOMI, JIRO
APPLICANT: YAMAGUCHI, KEN
APPLICANT: YAMAMURA, TOKUJIRO
APPLICANT: KIMURA, TATSUJI
TITLE OF INVENTION: NOVEL CALCIUM-BINDING PROTEINS
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: WYATT, GERBER, MELLER & O'ROURKE
STREET: 99 PARK AVENUE
STREET: 6th FLOOR
CITY: NEW YORK CITY
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH, 720 KB
MEDIUM TYPE: STORAGE
COMPUTER: IBM-PC COMPATIBLE
OPERATING SYSTEM: PC-DOS 6.2
SOFTWARE: WORDPERFECT 6.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/270,455
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/568,310
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: KLEIN, MILTON
REGISTRATION NUMBER: 27101
REFERENCE/DOCKET NUMBER: 3316
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)953-3350
TELEFAX: (212)953-3352
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
PUBLICATION INFORMATION:
RELEVANT RESIDUES IN SEQ ID NO: 7:
FROM 1 TO 20

US-09-270-455-7

Alignment Scores:
Pred. No.: 2,33e-11 Length: 20
Score: 20.00 Matches: 20
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 21.74% Indels: 0
DB: 3 Gaps: 0

US-09-910-208B-1 (1-276) x US-09-270-455-7 (1-20)

QY 217 GAATTCGTAGTCCTGCTCCAGGCTGCTGAAACAGCCCATAGATATCCACAAGAG 276
Db 1 GluPheValValLeuValSerArgValLeuLysThrAlaHisIleAspIleHisLysGlu 20

RESULT 12
US-08-794-000-2
Sequence 2, Application US/08794000
Patent No. 6087123
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Metal-Containing Ribonucleotide Polypeptides
NUMBER OF SEQUENCES: 4
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/794,000
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DE96/01337
FILING DATE: 17-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 195 25 992.0
FILING DATE: 17-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 195 30 500.0
FILING DATE: 18-AUG-1995
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 91 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-794-000-2
Alignment Scores:

Pred. No.: 1.98e-11 Length: 91
Score: 20.00 Matches: 20
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 21.74% Indels: 0
DB: 3 Gaps: 0

US-09-910-208B-1 (1-276) x US-08-794-000-2 (1-91)

Qy 4 ACTAAGCTGGAAGATCACCTGGAGGAATCATCAATCTTCCACAGTACTCCGTTGG 63
Db 1 ThrLysLeuGluAspHisLeuGluGlyIleIleAsnIlePheHisGlnTyrSerValArg 20

RESULT 13
US-09-646-651C-1
; Sequence 1, Application US/09646651C
; Patent No. 6770455
; GENERAL INFORMATION:
; APPLICANT: Klesewetter, Stefan
; APPLICANT: Kuhn, Ekehard
; APPLICANT: Koch-Pelster, Brigitte
; APPLICANT: Brunner, Herwig
; TITLE OF INVENTION: METAL-CONTAINING RIBONUCLEOTIDE POLYPEPTIDES
; FILE REFERENCE: 206579
; CURRENT APPLICATION NUMBER: US/09/646,651C
; CURRENT FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: PCT/EP98/07722
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: DE 198 11 047.2
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (..) {}
; OTHER INFORMATION: Angiotropin-related protein
US-09-646-651C-1

Alignment Scores:
Pred. No.: 1.98e-11 Length: 91
Score: 20.00 Matches: 20
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 21.74% Indels: 0
DB: 4 Gaps: 0

US-09-910-208B-1 (1-276) x US-09-646-651C-1 (1-91)

Qy 4 ACTAAGCTGGAAGATCACCTGGAGGAATCATCAATCTTCCACAGTACTCCGTTGG 63
Db 1 ThrLysLeuGluAspHisLeuGluGlyIleIleAsnIlePheHisGlnTyrSerValArg 20

RESULT 14
US-09-263-312-4
; Sequence 4, Application US/09263312
; Patent No. 655340
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Stern, David
; TITLE OF INVENTION: Extracellular No. 6555340el RAGE Binding Protein (EN-RAGE) and
; TITLE OF INVENTION: Uses thereof
; FILE REFERENCE: 0575/55873-A
; CURRENT APPLICATION NUMBER: US/09/263,312
; CURRENT FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 18
; TYPE: PRT

; ORGANISM: Human
US-09-263-312-4

Alignment Scores:
Pred. No.: 2.21e-09 Length: 18
Score: 18.00 Matches: 18
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 19.57% Indels: 0
DB: 4 Gaps: 0

US-09-910-208B-1 (1-276) x US-09-263-312-4 (1-18)

Qy 196 GACGAGCCGTCAGCTTTGAGGAATTCGTAGTCCTGTCAGGTCGCTGAAA 249
Db 1 AspGlyAlaValSerPheGluGluPheValValSerArgValLeuLys 18

RESULT 15
US-09-826-589-5
; Sequence 5, Application US/09826589
; Patent No. 6670136
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Stern, David
; TITLE OF INVENTION: EXTRACELLULAR NOVEL RAGE BINDING PROTEIN (EN-RAGE) AND USES THERE
; FILE REFERENCE: 0575/55873-B-PCT-US
; CURRENT APPLICATION NUMBER: US/09/826,589
; CURRENT FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Human
US-09-826-589-5

Alignment Scores:
Pred. No.: 2.21e-09 Length: 18
Score: 18.00 Matches: 18
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 19.57% Indels: 0
DB: 4 Gaps: 0

US-09-910-208B-1 (1-276) x US-09-826-589-5 (1-18)

Qy 196 GACGAGCCGTCAGCTTTGAGGAATTCGTAGTCCTGTCAGGTCGCTGAAA 249
Db 1 AspGlyAlaValSerPheGluGluPheValValSerArgValLeuLys 18

Search completed: February 23, 2005, 11:50:02
Job time : 36 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: February 23, 2005, 12:01:38 ; Search time 27 Seconds
(without alignments)
1967.098 Million cell updates/sec

Title: US-09-910-208B-12
Perfect score: 477
Sequence: 1 atgacaaaactgaagagca.....attaccacaccacaagaag 276

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+n2p.model -DEV=xlp
-O=/cgn2.1/USPTO/spool_p/HADDAD-09-910208B/runat_23022005_101934_15302/app_query.fasta_1
-DB=PIR79 -QFMT=fastan -SUFFIX=rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blsum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=spt -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=HADDAD-09-910208B @CGN 1.1 63 @runat_23022005_101934_15302 -NCPU=6
-ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THRSADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	468	98.1	92	JC4712	S-100 calcium-bind
2	332	69.6	91	A5406	calgranulin c - pi
3	226.5	47.5	122	A42628	calgranulin B - bo
4	214.5	45.0	114	B31848	calgranulin B [val
5	194	40.7	95	S24145	S-100 protein p -
6	190	39.8	92	A48015	S-100 protein beta
7	189	39.6	92	BCHUIB	S-100 protein beta
8	187	39.2	92	A26557	S-100 protein beta
9	185	38.8	91	BCHOIB	S-100 protein beta
10	180.5	37.8	113	JN0686	calgranulin B - ra
11	178.5	37.4	113	S68242	calgranulin B - mo
12	177.5	37.2	95	S35985	S-100 protein alph
13	169.5	35.5	101	S06207	calvasculin - mous
14	168	35.2	591	A45135	profilaggrin - hum

15	167	35.0	102	1	JQ1300	calgizzarin - rabb
16	166.5	34.9	101	2	S01759	calvasculin - rat
17	162.5	34.1	94	1	BCBOIA	S-100 protein alph
18	161.5	33.9	94	1	BCHUIA	S-100 protein alph
19	158	33.1	93	1	BCHUCF	calgranulin A [val
20	157.5	33.0	101	2	A48219	calvasculin - huma
21	157	32.9	105	1	I37080	calgizzarin - huma
22	156	32.7	306	2	A48118	major epidermal ca
23	154	32.3	89	1	I56163	calgranulin A - mo
24	153.5	32.2	98	2	A41988	S-100 calcium-bind
25	152.5	32.0	100	2	A53217	placental calcium-
26	149	31.2	89	1	JN0685	calgranulin A - ra
27	147.5	30.9	90	1	BCHUY	calgizzarin - huma
28	147.5	30.9	97	2	A30129	S-100 protein, lun
29	146	30.6	110	2	B48219	S-100 calcium-bind
30	144.5	30.3	217	2	JF0330	26-kDa Ca2+-bindi
31	142.5	29.9	89	2	A54314	calgizzarin - mouse
32	142.5	29.9	90	1	S27011	calgizzarin - rabbit
33	139.5	29.2	90	2	B28363	calgizzarin - rat
34	139	29.1	99	2	S20342	calcium-binding pr
35	137.5	28.8	98	2	JC5064	S-100 calcium-bind
36	136	28.5	65	2	A41004	calgizzarin - chic
37	127.5	26.7	95	1	LUPG10	calpactin I light
38	127.5	26.7	97	1	JH0663	calpactin I light
39	127.5	26.7	97	2	JC1139	calpactin I light
40	127.5	26.7	97	2	B28489	calpactin I light
41	126.5	26.5	97	2	A28489	calpactin I light
42	124	26.0	79	1	KLBOI	calcium-binding pr
43	123.5	25.9	95	2	A31373	calpactin I light
44	122.5	25.7	79	1	KLPGI	calcium-binding pr
45	121.5	25.5	79	1	JN0246	calcium-binding pr

ALIGNMENTS

RESULT 1

JC4712
S-100 calcium-binding protein A12 - human
N:Alternate names: calcium-binding amniotic fluid protein 1 (CAAF1); calgranulin C; cal-
utrophil protein
C:Species: Homo sapiens (man)
C:Date: 10-May-1996 #sequence revision 19-Jul-1996 #text_change 09-Jul-2004
C:Accession: JC4712; JC4717; JC4891; S56113
R:Yamamura, T.; Hitomi, J.; Nagasaki, K.; Suzuki, M.; Takahashi, E.; Saito, S.; Tsukada,
Biochem. Biophys. Res. Commun. 221, 356-360, 1996
A:Title: Human CAAF1 gene - molecular cloning, gene structure, and chromosome mapping.
A:Reference number: JC4712; MUID:96192053; PMID:8619860
A:Accession: JC4712
A:Molecule type: mRNA
A:Residues: 1-92 <YAM>
A:Cross-references: UNIPROT:P80511; DBJ:D83657; NID:G1502284; PIDN:BAAL2030.1; PID:G150
R:Marti, T.; Ertmann, K.D.; Gallin, M.Y.
Biochem. Biophys. Res. Commun. 221, 454-458, 1996
A:Title: Host-parasite interaction in human onchocerciasis: Identification and sequence
A:Reference number: JC4717; MUID:96192069; PMID:8619876
A:Accession: JC4717
A:Molecule type: protein
A:Residues: 2-92 <MAR>
A:Experimental source: Onchocerca volvulus infecting human tissue
R:Rig, E.C.; Troxler, H.; Buerigisser, D.M.; Kuster, T.; Markert, M.; Guignard, F.; Hunz
Biochem. Biophys. Res. Commun. 225, 146-150, 1996
A:Title: Amino acid sequence determination of human S100 A12 (P6, Calgranulin C, CGRP, c
A:Reference number: JC4891; MUID:96332419; PMID:8769108
A:Accession: JC4891
A:Molecule type: protein
A:Residues: 2-92 <ILG>
R:Guignard, F.; Maue, J.; Markert, M.
Biochem. J. 309, 395-401, (1995)
A:Title: Identification and characterization of a novel human neutrophil protein relate
A:Reference number: S56113; MUID:95351965; PMID:7626002
A:Accession: S56113
A>Status: preliminary
A:Molecule type: protein

A;Residues: 'XX',4-14,'X',16-17,'XXXX' <GUI1>
 A;Experimental source: isoform 6a

A;Accession: S56114

A;Status: preliminary

A;Molecule type: protein

A;Residues: 2-21 <GUI2>

A;Experimental source: isoform 6b

C;Comment: This protein is released by activated neutrophils in the course of inflammation

C;Genetics:

A;Gene: GDB:S100A12; p6; MRP6; CGRP; CAAFI

A;Cross-references: GDB:S218374

A;Map position: 1q21-1q21

C;Complex: monomer

C;Superfamily: S-100 protein; calmodulin repeat homology

F;2-92/Product: S-100 calcium-binding protein A12 #status experimental <MAT>

F;6-39/Domain: calmodulin repeat homology <EF1>

F;49-81/Domain: calmodulin repeat homology <EF2>

F;86-90/Region: zinc binding #status predicted

Alignment Scores:

Pred. No.: 1.45e-43 Length: 92

Score: 468.00 Matches: 92

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 98.11% Indels: 0

DB: 2 Gaps: 0

US-09-910-208B-12 (1-276) x JC4712 (1-92)

```

QY 1 ATGCAAAACTTGAAGACATCTGAGGGAATTGTCAATATCTTCCACCAATCTCAGTT 60
DB 1 MetThrLysLeuGluGluHisLeuGluGlyLeuValAsnIlePheHisGlnTyrSerVal 20

QY 61 CGAAGGGGCATTTTGACACCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTACAAAGAG 120
DB 21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGlu 40

QY 121 CTTCACACACATCAAGAAATATCAAGATAAAGTGTCTATGATGAATAATTCAGGC 180
DB 41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60

QY 181 CTGGATGCTAATCAAGATGAACAGCTGCACCTTCAAGAAATTCATATCCTCGTAGCCATT 240
DB 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80

QY 241 CGCTGAAGGTGCCATTACACACCCACAAAGAG 276
DB 81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92
  
```

RESULT 2

A55406

calgranulin c - pig

C;Species: Sus scrofa domestica (domestic pig)

C;Date: 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 09-Jul-2004

C;Accession: A55406

R;Dell'Angelica, E.C.; Schleicher, C.H.; Santome, J.A.

J. Biol. Chem. 269, 28929-28936, 1994

A;Title: Primary structure and binding properties of calgranulin C, a novel S100-like cal-

A;Reference number: A55406; MUID:95050708; PMID:7961855

A;Accession: A55406

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-91

A;Cross-references: UNIPROT:P80310

C;Superfamily: S-100 protein; calmodulin repeat homology

C;Keywords: calcium binding; EF hand

F;48-80/Domain: calmodulin repeat homology <EF2>

Alignment Scores:

Pred. No.: 1.61e-28 Length: 91

Score: 332.00 Matches: 64

Percent Similarity: 81.32% Conservative: 10

Best Local Similarity: 70.33% Mismatches: 17
 Query Match: 69.60% Indels: 0
 DB: 2 Gaps: 0

US-09-910-208B-12 (1-276) x A55406 (1-91)

```

QY 4 ACAAACCTTGAAGACATCTGAGGGAATTGTCAATATCTTCCACCAATCTCAGTTCCG 63
DB 1 ThrLysLeuGluAspHisLeuGluGlyIleAsnIlePheHisGlnTyrSerValArg 20

QY 64 AAGGGCATTGTGACACCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTACAAAGAGCTT 123
DB 21 LeuGlyHisTyrAspThrLeuIleLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40

QY 124 GCAACACCATCAAGATATCAAGATAAAGCTGTCTATGATGAATAATTCAGAGGCTG 183
DB 41 ProAsnThrLeuLysAsnThrLysAspGlnGlyThrIleAspLysIlePheGlnAsnLeu 60

QY 184 GATGCTAATCAAGATGAACAGGTGCGACTTTCAAGAATTCATATCCTCTGGTAGCCATTGCG 243
DB 61 AspAlaAsnGlnAspGluGlnValSerPheLysGluPheValValLeuValThrAspVal 80

QY 244 CTGAAGCTCCCCATTACACACCCACAAAGAG 276
DB 81 LeuIleThrAlaHisAspAsnIleHisLysGlu 91
  
```

RESULT 3

A42628

calgranulin B - bovine (fragment)

N;Alternate names: calcium-binding protein MRP-14; macrophage migration inhibitory factor in 2

C;Species: Bos primigenius taurus (cattle)

C;Date: 30-Sep-1993 #sequence_revision 23-May-1997 #text_change 23-May-1997

C;Accession: B22309; A42628

R;Tang, T.K.; Hong, T.M.; Lin, C.Y.; Lai, M.L.; Liu, C.H.L.; Lo, H.J.; Wang, M.E.; Chen,

submitted to the Protein Sequence Database, July 1992

A;Reference number: A22309

A;Accession: B22309

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-122 <TAN>

R;Dianoux, A.C.; Stasia, M.J.; Garin, J.; Gagnon, J.; Vignais, P.V.

Biochemistry 31, 5898-5905, 1992

A;Title: The 23-kilodalton protein, a substrate of protein kinase C, in bovine neutrophil

A;Reference number: A42628; MUID:92304974; PMID:1610833

A;Accession: A42628

A;Molecule type: protein

A;Residues: 4-32,'F',34-56 <DIA>

C;Complex: heterodimer and higher complexes with calgranulin A

C;Superfamily: S-100 protein; calmodulin repeat homology

C;Keywords: blocked amino end; calcium binding; EF hand; heterodimer; inflammation; phos

F;6-40/Domain: calmodulin repeat homology <EF1>

F;50-82/Domain: calmodulin repeat homology <EF2>

Alignment Scores:

Pred. No.: 7.74e-17 Length: 122

Score: 226.50 Matches: 47

Percent Similarity: 70.33% Conservative: 17

Best Local Similarity: 51.65% Mismatches: 26

Query Match: 47.48% Indels: 1

DB: 1 Gaps: 1

US-09-910-208B-12 (1-276) x A42628 (1-122)

```

QY 1 ATGCAAAACTTGAAGACATCTGAGGGAATTGTCAATATCTTCCACCAATCTCAGTT 60
DB 1 MetSerGlnMetGluSerSerIleGluThrIleAsnIlePheHisGlnTyrSerVal 20

QY 61 CGAAGGGCATTGTGACACCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTACAAAGAG 120
DB 21 ArgLeuGlyHisTyrAspThrLeuIleGlnLysGluSerLysGlnLeuValGlnLysGlu 40

QY 121 CTGCAAAACCAATC---AAGAATATCAAAAGATAAAGCTGTCTATGATGAATAATTTCCA 177
  
```


Db 41 LeuProAsnPhLeuLysGlnLysLysAsnGluAlaAlaAlaAsnGluileMetGlu 60
 QY 178 GSCCTGGTCTAATCAAGACGAGCTCGACTTTCAGAAATTCATATCCTCGTAGCC 237
 Db 61 AspLeuAspThrAsnValAspLysGlnLeuSerPheGluGluPheileMetLeuValAla 80
 QY 238 ATTGCGCTGAAGGCTGCCATTACCACACCCAC 270
 Db 81 ArgLeuThrValAlaSerHisGluGluMetHis 91
 RESULT 4
 B31848
 calgranulin B [validated] - human
 N:Alternate names: calcium-binding protein MRP-14; cystic fibrosis-associated antigen (C
 (MRP-14); MIF-related 14K protein; S-100 calcium-binding protein A9 (S100A9)
 C:Species: Homo sapiens (man)
 C:Date: 21-May-1990 #sequence_revision 23-May-1997 #text_change 09-Jul-2004
 C:Accession: B31848; S00667; A33819; B60911; B61082; D54327
 R:LAGasse, E.; Clerc, R.G.
 Mol. Cell. Biol. 8, 2402-2410, 1988
 A:Title: Cloning and expression of two human genes encoding calcium-binding proteins tha
 A:Reference number: A93102; MUID:88302148; PMID:3405210
 A:Accession: B31848
 A:Molecule type: DNA
 A:Residues: 1-114 <LAG>
 A:Cross-references: UNIPROT:P06702; GB:M21064; NID:G188689; PIDN:AAA36326.1; PID:G386958
 R:Odink, K.; Carletti, N.; Brueggen, J.; Clerc, R.G.; Tarceay, L.; Zwadlo, G.; Gerhards,
 Nature 330, 80-84, 1987
 A:Title: Two calcium-binding proteins in infiltrate macrophages of rheumatoid arthritis.
 A:Reference number: S00667; MUID:88039099; PMID:3313057
 A:Accession: S00667
 A:Molecule type: mRNA
 A:Residues: 1-114 <ODI>
 A:Cross-references: EMBL:X06233; NID:G34770; PIDN:CAA29579.1; PID:G34771
 A:Note: Parts of this sequence were confirmed by protein sequencing
 R:Murao, S.; Collart, F.R.; Huberman, E.
 J. Biol. Chem. 264, 8356-8360, 1989
 A:Title: A protein containing the cystic fibrosis antigen is an inhibitor of protein kin
 A:Reference number: A33819; MUID:89255276; PMID:3656677
 A:Accession: A33819
 A:Molecule type: protein
 A:Residues: 39-42, 'X', 44-50:64-77, 'X', 79:84, 'X', 86-90, 'X', 92-94, 'X', 96-98 <AND>
 R:Tobe, T.; Murakami, K.; Tomita, M.; Nozawa, R.
 Chem. Pharm. Bull. 37, 1576-1580, 1989
 A:Title: Amino acid sequences of 60B8 antigens induced in HL-60 cells by 1,25-dihydroxyv
 A:Reference number: A61082; MUID:89376638; PMID:2776242
 A:Accession: B61082
 A:Molecule type: protein
 A:Residues: 5-77;80-90, 'A', 92-114 <TOB>
 A:Note: The blocked amino end of the mature protein is identified as 2-Thr; residue 91-H
 R:Madson, P.; Rasmussen, H.H.; Leffers, H.; Honore, B.; Dejgaard, K.; Olsen, E.; Kiil, J
 E. Invest. Dermatol. 97, 701-712, 1991
 A:Title: Molecular cloning, occurrence, and expression of a novel partially secreted pro
 A:Reference number: A54327; MUID:92043866; PMID:1940442
 A:Accession: D54327
 A:Molecule type: protein
 A:Residues: 11-19;26-38;94-105, 'X', 107 <MAD>
 A:Note: In several peptide samples no PTH was detected for 95-His but in one peptide PTH
 C:Comment: This protein appears to be expressed only in cells of myeloid origin actively
 C:Comment: The presence of 3'-methylhistidine at position 105, corresponding to 107-His
 C:Genetics:
 A:Gene: GDB:S100A9; 60B8AG; CAGB; CFAG; LIAG; MAC387; MIF; MRP14; NIF; P14

A:Cross-references: GDB:120570; OMIM:123886
 A:Map position: 1q21-1q21
 A:Introns: 50/3
 A:Note: the first intron occurs before the initiator codon
 C:Complex: heterodimer and higher complexes with calgranulin A (see PIR:BCHUCF)
 C:Superfamily: S-100 protein; calmodulin repeat homology
 C:Keywords: blocked amino end; calcium binding; EF hand; heterodimer; inflammation; pho
 F:2-114/Product: calgranulin B #status experimental <MAT>
 F:10-44/Domain: calmodulin repeat homology <EF1>
 F:54-86/Domain: calmodulin repeat homology <EF2>
 F:2/Modified site: blocked amino end (Thr) (in mature form) (probably acetylated) #stat
 F:113/Binding site: phosphate (Thr) (covalent) #status predicted
 Alignment Scores:
 Pred. No.: 1.64e-15 Length: 114
 Score: 214.50 Matches: 43
 Percent Similarity: 70.65% Conservative: 22
 Best Local Similarity: 46.74% Mismatches: 26
 Query Match: 44.97% Indels: 1
 DB: 1 Gaps: 1
 US-09-910-208B-12 (1-276) x B31848 (1-114)
 QY 1 ATGCAAACTTGAAGACATCTGGAGGAATTGTCAATATCTTCACCAATACTCAGTT 60
 Db 5 MetSerGlnLeuGluArgAsnIleGluThrIleAsnThrPheHisGlnTyrSerVal 24
 QY 61 CGGAGGGGCGATTTTGACACCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTACAAAGGAG 120
 Db 25 LysLeuGlyHisProAspThrLeuAsnGlnGluPheLysGluLeuValArgLysAsp 44
 QY 121 CTTCGAAACACCATC---AAGAAATATCAAGATAAAGCTGTCATTGATGATAATATTCCAA 177
 Db 45 LeuGlnAsnPhLeuLysLysGluAsnLysAsnGluValIleGluHisIleMetGlu 64
 QY 178 GGCCTGGATCTAATCAAGATGACAGCTGCAGCTTTTCAAGAAATTCATATCCTCGTAGCC 237
 Db 65 AspLeuAspThrAsnAlaAspLysGlnLeuSerPheGluGluPheIleMetLeuMetAla 84
 QY 238 ATTGCGCTGAAGGCTGCCATTACCACACCCACCAA 273
 Db 85 ArgLeuThrTrpAlaSerHisGluLysMethHisGlu 96
 RESULT 5
 S24146
 S-100 protein P - human
 C:Species: Homo sapiens (man)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
 C:Accession: S24146; PS0340
 R:Becker, T.; Gerke, V.; Kube, E.; Weber, K.
 Eur. J. Biochem. 207, 541-547, 1992
 A:Title: S100P, a novel Ca(2+)-binding protein from human placenta. cDNA cloning, recom
 A:Reference number: S24146; MUID:92339442; PMID:1633809
 A:Accession: S24146
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-95 <BEC>
 A:Cross-references: UNIPROT:P25815; EMBL:X65614; NID:G36177; PIDN:CAA46566.1; PID:G3617
 R:Emoto, Y.; Kobayashi, R.; Akatsuka, H.; Hidaka, H.
 Biochem. Biophys. Res. Commun. 182, 1246-1253, 1992
 A:Title: Purification and characterization of a new member of the S-100 protein family
 A:Reference number: PS0340; MUID:92171935; PMID:1540168
 A:Accession: PS0340
 A:Molecule type: protein
 A:Residues: 1-31, 'T', 33-84, 'X', 86-91 <EMO>
 A:Experimental source: placenta
 C:Genetics:
 A:Gene: GDB:S100P
 A:Cross-references: GDB:134405; OMIM:600614
 A:Map position: 4p16-4p16
 C:Superfamily: S-100 protein; calmodulin repeat homology
 C:Keywords: calcium binding; EF hand; placenta
 F:6-40/Domain: calmodulin repeat homology <EF1>

F;49-81/Domain: calmodulin repeat homology <EF2>

Alignment Scores:

Pred. No.: 3e-13 Length: 95
Score: 194.00 Matches: 41
Percent Similarity: 63.74% Conservatives: 17
Best Local Similarity: 45.05% Mismatches: 33
Query Match: 40.67% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-12 (1-276) x S24146 (1-95)

QY 1 ATGACAAACTTGAGAGCATCTGGAGGAATGTCATATATCTCCACCAATCTCAGTT 60
DB 1 MetThrGluLeuGluThrAlaMetGlyMetIleAspValPheSerArgTySerGly 20
QY 61 CGGAGGGGCATTGTGACACCTCTCTAAGGCTGAGCTGAAGCAGCTGCTTACAAAGGAG 120
DB 21 SerGluGlySerThrGlnThrLeuThrLysGlyGluLeuLysValLeuMetGluLysGlu 40
QY 121 CTGTCAACACCATCAAGATATCAAGATATAAGCTGTCAATTGATGAATAATTCACAGGC 180
DB 41 LeuProGlyPheLeuGlnSerGlyLysAspLysAspAlaValAspLysLeuLysAsp 60
QY 181 CTGGATGCTAATCAAGATCAAGCTGCACCTTCAGATTCATATCCCTGGTAGCCATT 240
DB 61 LeuAspAlaAsnGlyAspAlaGlnValAspPheSerGluPheIleValPheValAlaAla 80
QY 241 CGCGTGAAGGTCGCCATTCACACCCACCAAA 273
DB 81 IleThrSerAlaCysHisLysTyPheGluLys 91

RESULT 6

A48015
S-100 protein beta chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 09-Jul-2004
C:Accession: A48015
R:Jiang, H.; Shah, S.; Hilt, D.C.
J. Biol. Chem. 268, 20502-20511, 1993
A:Title: Organization, sequence, and expression of the murine S100beta gene. Transcript
A:Reference number: A48015; MUID:93388628; PMID:8376406
A:Accession: A48015
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-92 <JIA>
A:Cross-references: UNIPROT:P50114; GB:L22144; NID:G404768; PID:G404769
C:Genetics:
A:Introns: 46/3
C:Superfamily: S-100 protein; calmodulin repeat homology
C:Keywords: acetylated amino end; calcium binding; EF hand
F:2-92/Product: S-100 protein beta chain #status predicted <MAT>
F:6-40/Domain: calmodulin repeat homology <EF1>
F:49-81/Domain: calmodulin repeat homology <EF2>
F:20,22,24,27,32/Binding site: calcium (Gly, Glu, Asp, Lys, Glu) #status predicted
F:62,64,66,68,70,73/Binding site: calcium (Asp, Asp, Glu, Asp, Glu) #status predicted

Alignment Scores:

Pred. No.: 8.29e-13 Length: 92
Score: 190.00 Matches: 34
Percent Similarity: 69.77% Conservatives: 26
Best Local Similarity: 39.53% Mismatches: 26
Query Match: 39.83% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-12 (1-276) x A48015 (1-92)

QY 1 ATGACAAACTTGAGAGCATCTGGAGGAATGTCATATCTCCACCAATCTCAGTT 60
DB 1 MetSerGluLeuGluLysAlaMetValAlaLeuIleAspValPheHisGlnTySerGly 20
QY 61 CGGAGGGGCATTGTGACACCTCTCTAAGGCTGAGCTGAAGCAGCTGCTTACAAAGGAG 120

DB 21 ArgGluGlyAspLysHisLysLeuLysSerGluLeuLysGluLeuLeuAsnAsnGlu 40
QY 121 CTGTCAACACCATCAAGATATCAAGATATAAGCTGTCAATTGATGAATAATTCACAGGC 180
DB 41 LeuSerHisPheLeuGluGluLeuLysGluGlnGluValValAspLysValMetGluThr 60
QY 181 CTGGATGCTAATCAAGATCAAGCTGCACCTTCAGATTCATATCCCTGGTAGCCATT 240
DB 61 LeuAspGluAspGlyAspGlyGluCysAspPheGlnGluPheMetAlaPheValAlaMet 80
QY 241 CGCGTGAAGGTCGCCCAT 258
DB 81 ValThrThrAlaCysHis 86

RESULT 7

BCHUIB
S-100 protein beta chain [validated] - human
N:Alternate names: neural S-100 calcium-binding protein beta
C:Species: Homo sapiens (man)
C:Date: 04-Dec-1986 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C:Accession: A38364; A92972; A03076
R:Allore, R.J.; Friend, W.C.; O'Hanlon, D.; Neilson, K.M.; Baumal, R.; Dunn, R.J.; Marks
J. Biol. Chem. 265, 15537-15543, 1990
A:Title: Cloning and expression of the human S100beta gene.
A:Reference number: A38364; MUID:90368757; PMID:2394738
A:Accession: A38364
A:Molecule type: DNA
A:Residues: 1-92 <ALL>
A:Cross-references: UNIPROT:P04271; GB:J05600; GB:M59486; NID:G337726; GB:M59487; NID:G3
J:Jensen, R.; Marshak, D.R.; Anderson, C.; Lukas, T.J.; Watterson, D.M.
J. Neurochem. 45, 700-705, 1985
A:Title: Characterization of human brain S100 protein fraction: amino acid sequence of S
A:Reference number: A92972; MUID:85291729; PMID:4031854
A:Accession: A92972
A:Molecule type: protein
A:Residues: 2-92 <JEN>
R:Baudier, J.; Glasser, N.; Haglid, K.; Gerard, D.
Biochim. Biophys. Acta 790, 164-173, 1984
A:Title: Purification, characterization and ion binding properties of human brain S100b
A:Reference number: A90853; MUID:85023393; PMID:6487634
A:Contents: annotation; metal ion-binding properties
C:Comment: This protein binds p53, tubulin and many other proteins at physiological conc
C:Comment: S-100 is an intracellular protein that binds calcium. It binds zinc more tigh
different affinities exist for both ions on each monomer. Physiological concentrations
nding sites.
C:Comment: This protein is expressed predominantly in brain tissue by astroglial cells.
C:Comment: The homodimer contains disulfide bonds, but the bond pattern has not been det
C:Genetics:
A:Gene: GDB:S100B
A:Cross-references: GDB:I20360; OMIM:176990
A:Map position: 21q22.3-21q22.3
A:Introns: 46/3
A:Note: the first intron occurs before the initiator codon
C:Complex: homodimer; heterodimer with S-100 protein alpha chain (see PIR:BCHUIA)
C:Superfamily: S-100 protein; calmodulin repeat homology
C:Keywords: blocked amino end; brain; calcium binding; EF hand; heterodimer; homodimer;
F:2-92/Product: S-100 protein beta chain #status experimental <MAT>
F:6-40/Domain: calmodulin repeat homology <EF1>
F:49-81/Domain: calmodulin repeat homology <EF2>
F:2/Modified site: blocked amino end (Ser) (in mature form) (probably acetylated) #statu
F:19,22,24,27,32/Binding site: calcium (Ser, Glu, Asp, Lys, Glu) #status predicted
F:62,64,66,68,73/Binding site: calcium (Asp, Asp, Glu, Asp, Glu) #status predicted

Alignment Scores:
Pred. No.: 1.07e-12 Length: 92
Score: 189.00 Matches: 24
Percent Similarity: 69.77% Conservatives: 26
Best Local Similarity: 39.53% Mismatches: 26
Query Match: 39.62% Indels: 0
DB: 1 Gaps: 0

US-09-910-208B-12 (1-276) x BCHUIB (1-92)

```
QY 1 ATGACAAAATTGAAGAGCATCTGGAGGAATGTCAATATCTTCCACCAATACTCAGTT 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MetSerGluLeuGluLysAlaMetValAlaLeuLeuAspValPheHisGlnTyrSerGly 20
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 CGGAGGGGCATTTTGACACCCCTCTCTAAGGTGAGCTGAAGCAGCTGCTTACAAGGAG 120
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 21 ArgGluGlyAspLysHisLysLeuLysSerGluLeuLysGluLeuLeuAsnGlu 40
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 121 CTTCGAAACACCATCAAGATATCAAGATAAAGCTGTCTCATGATGAATATTCACAGGC 180
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 41 LeuSerHisPheLeuGluGluLeuLysGluGlnGluValValAspLysValMetGluThr 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 181 CTGGATGCTTAATCAGATCAAGAGTCGACTTTTCAAGATTCATATCCCTGGTAGCCATT 240
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 LeuAspAsnAspGlyAspGlyGluCysAspPheGlnGluPheMetAlaPheValAlaMet 80
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 241 CGCCTGAAGCTGCCCAT 258
|||:|||||:
Db 81 ValThrThrAlaCysHis 86
|||:|||||:

RESULT 8
A26557
S-100 protein beta chain - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 25-Mar-1988 #sequence revision 04-Nov-1994 #text_change 09-Jul-2004
C:Accession: A60046; S07357; A26557
R:Maeda, T.; Usui, H.; Araki, K.; Kuwano, R.; Takahashi, Y.; Suzuki, Y.
Brain Res. Mol. Brain Res. 10, 193-202, 1991
A:Title: Structure and expression of rat S-100 beta subunit gene.
A:Reference number: A60046; MUID:91359841; PMID:1653388
A:Accession: A60046
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-92 <MAE>
A:CROSS-references: UNIPROT:P04631; GB:SS3527
R:Kuwano, R.; Usui, H.; Maeda, T.; Fukui, T.; Yamanari, N.; Ohtsuka, E.; Ikehara, M.; Ta
Nucleic Acids Res. 12, 7455-7465, 1984
A:Title: Molecular cloning and the complete nucleotide sequence of cDNA to mRNA for S-10
A:Reference number: S07357; MUID:85037924; PMID:6093041
A:Accession: S07357
A:Molecule type: mRNA
A:Residues: 1-92 <KUN>
A:CROSS-references: ENBL:X01090; NID:G57174; PIDN:CAA25567.1; PID:G57175
R:Dunn, R.; Landry, C.; O'Hanlon, D.; Dunn, J.; Allore, R.; Brown, I.; Marks, A.
J. Biol. Chem. 262, 3562-3566, 1987
A:Title: Reduction in S100 protein Beta-subunit mRNA in C6 rat glioma cells following tr
A:Reference number: A26557; MUID:87137848; PMID:3818655
A:Accession: A26557
A:Molecule type: mRNA
A:Residues: 6-92 <DUN>
A:CROSS-references: GB:M15705
A:Comment: S-100 protein occurs as alpha-beta heterodimers, alpha-alpha heterodimers, an
C:Genetics:
A:Introns: 46/3
C:Superfamily: S-100 protein; calmodulin repeat homology
C:Keywords: brain; calcium binding; dimer; EF hand; zinc
P:2-92/Product: S-100 protein beta chain #status predicted <MAT>
P:6-40/Domain: calmodulin repeat homology <EPI>

Alignment Scores:
Pred. No.: 1.78e-12 Length: 92
Score: 187.00 Matches: 33
Percent Similarity: 69.77% Conservative: 27
Best Local Similarity: 38.37% Mismatches: 26
Query Match: 39.20% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-12 (1-276) x A26557 (1-92)
```

```
QY 61 CGGAGGGGCATTTTGACACCCCTCTCTAAGGTGAGCTGAAGCAGCTGCTTACAAGGAG 120
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 21 ArgGluGlyAspLysHisLysLeuLysSerGluLeuLysGluLeuLeuAsnGlu 40
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 121 CTTCGAAACACCATCAAGATATCAAGATAAAGCTGTCTCATGATGAATATTCACAGGC 180
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 41 LeuSerHisPheLeuGluGluLeuLysGluGlnGluValValAspLysValMetGluThr 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 181 CTGGATGCTTAATCAGATCAAGAGTCGACTTTTCAAGATTCATATCCCTGGTAGCCATT 240
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 LeuAspGluAspGlyAspGlyCysAspPheGlnGluPheMetAlaPheValSerMet 80
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 241 CGCCTGAAGCTGCCCAT 258
|||:|||||:
Db 81 ValThrThrAlaCysHis 86
|||:|||||:

RESULT 9
BC01B
S-100 protein beta chain - bovine
N:Alternate names: neurocalcin delta-binding protein S100-beta
C:Species: Bos primigenius taurus (cattle)
C:Date: 31-May-1979 #sequence revision 14-Nov-1983 #text_change 09-Jul-2004
C:Accession: A91254; B91110; A90075; S54348; A03077
R:Isobe, T.; Okuyama, T.
Eur. J. Biochem. 89, 379-388, 1978
A:Title: The amino-acid sequence of S-100 protein (PAP-I-b protein) and its relation to
A:Reference number: A91254; MUID:79045265; PMID:710399
A:Accession: A91254
A:Molecule type: protein
A:Residues: 'ESEL', 5-91 <ISO>
A:CROSS-references: UNIPROT:P02638
A:Experimental source: brain
A:Note: this sequence has since been revised in reference A91110
R:Isobe, T.; Okuyama, T.
Eur. J. Biochem. 116, 79-86, 1981
A:Title: The amino-acid sequence of the alpha subunit in bovine brain S-100 a protein.
A:Reference number: A91110; MUID:81236562; PMID:7250124
A:Accession: B91110
A:Molecule type: protein
A:Residues: 1-91 <IS2>
R:Saudier, J.; Gerard, D.
Biochemistry 22, 3360-3369, 1983
A:Title: Ions binding to S100 proteins: structural changes induced by calcium and zinc
A:Reference number: A90471; MUID:84000339; PMID:6615778
A:Contents: annotation; metal ion-binding properties
A:Note: annotation; metal ion-binding properties
R:Marshall, D.R.; Umekawa, H.; Watterson, D.M.; Hidaka, H.
Arch. Biochem. Biophys. 240, 777-780, 1985
A:Title: Structural characterization of the calcium binding protein S100 from adipose t
A:Reference number: A90075; MUID:85278169; PMID:4026304
A:Accession: A90075
A:Molecule type: protein
A:Residues: 1-91 <MAR>
A:Experimental source: adipose tissue
R:Okazaki, K.; Obata, N.H.; Inoue, S.; Hidaka, H.
Biochem. J. 306, 551-555, 1995
A:Title: S100-beta is a target protein of neurocalcin delta, an abundant isoform in gli
A:Reference number: S54343; MUID:95194333; PMID:7887910
A:Accession: S54348
A:Molecule type: protein
A:Residues: 56-61, 'N', 63-79, 'V' <OKA>
C:Comment: The S-100 protein is composed of two related polypeptide chains, alpha and beta
brain proteins, S-100 is also found in a variety of other tissues.
C:Comment: S-100 is an intracellular protein that weakly binds calcium. It binds zinc v
es with different affinities exist for both ions on each monomer. Physiological concentr
cium-binding sites.
C:Superfamily: S-100 protein; calmodulin repeat homology
C:Keywords: blocked amino end; brain; calcium binding; EF hand; zinc
P:5-39/Domain: calmodulin repeat homology <EPI>
P:48-80/Domain: calmodulin repeat homology <EF2>
P:1/Modified site: blocked amino end (Ser) (probably acetylated) #status experimental
P:18,21,23,26,31/Binding site: calcium (Ser, Glu, Asp, Lys, Glu) #status predicted
P:61,63,65,67,72/Binding site: calcium (Asp, Asp, Glu, Glu) #status predicted
```

Alignment Scores:

Pred. No.: 2,96e-12 Length: 91
Score: 185.00 Matches: 33
Percent Similarity: 70.59% Conservative: 27
Best Local Similarity: 38.82% Mismatches: 25
Query Match: 38.78% Indels: 0
DB: 1 Gaps: 0

US-09-910-208B-12 (1-276) x BCBOIB (1-91)

Qy 4 ACAAACTTGAAGCATCTGGAGGAATTCCTCAATATCTTCCACCAATACTCAGTTCGG 63
Db 1 SerGluLeuGluLysAlaValAlaLeuileAspValPheHisGlnTyrSerGlyArg 20
Qy 64 AAGGGCATTTTGACACCCCTCTTAAGGTCAGCTGAGCAGCTGCTTACAAAGGAGCTT 123
Db 21 GluGlyAspLysHisLysLysSerGluLeuLysGluLeuLysAlaAsnGluLeu 40
Qy 124 GCAAACACCATCAAGATATCAAGATCAAGCTCTCATTTCAAGAATTCATATCCCTGGTAGCCATTCG 183
Db 41 SerHisPheLeuGluGluLeuLysGluGlnGluValValAspLysValMetGluThrLeu 60
Qy 184 GATGCTAATCAAGTCAAGCATCTGACCTTTCAAGAATTCATATCCCTGGTAGCCATTCG 243
Db 61 AspSerAspGlyAspGlyGluCysAspPheGlnGluPheMetAlaPheValAlaMetIle 80
Qy 244 CTGAAGGCTGCCAT 258
Db 81 ThrThrAlaCysHis 85

RESULT 10

UN0686
calgranulin B - rat
N;Alternate names: calcium-binding protein MRP-14; macrophage migration inhibitory factor
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-May-1994 #sequence_revision 23-May-1997 #text_change 09-Jul-2004
C;Accession: JN0686
R;Imamichi, T.; Uchida, I.; Wahl, S.M.; McCartney-Francis, N.
Biochem. Biophys. Res. Commun. 194, 819-825, 1993
A;Title: Expression and cloning of migration inhibitory factor-related protein (MRP) 8 and
A;Reference number: JN0685; MUID:93343942; PMID:8343166
A;Accession: JN0686
A;Molecule type: mRNA
A;Residues: 1-113 <I>A>
A;Cross-references: UNIPROT:P50116; GB:L18948; NID:9488156; PIDN:AAA18214.1; PID:9488157
C;Genetics:
A;Gene: MRP14
C;Complex: heterodimer and higher complexes with calgranulin A
C;Superfamily: S-100 protein; calmodulin repeat homology
C;Keywords: acetylated amino end; calcium binding; EF hand; heterodimer; inflammation; P

F;2-113/Product: calgranulin B #status predicted <MAT>
F;11-45/Domain: calmodulin repeat homology <EF1>
F;55-87/Domain: calmodulin repeat homology <EF2>
F;2/Modified site: acetylated amino end (Ala) (in mature form) #status predicted
F;80-91/Disulfide bonds: #status predicted

Alignment Scores:
Pred. No.: 9.45e-12 Length: 113
Score: 180.50 Matches: 35
Percent Similarity: 64.84% Conservative: 24
Best Local Similarity: 38.46% Mismatches: 31
Query Match: 37.84% Indels: 1
DB: 1 Gaps: 1

US-09-910-208B-12 (1-276) x JN0686 (1-113)

Qy 4 ACAAACTTGAAGCATCTGGAGGAATTCCTCAATATCTTCCACCAATACTCAGTTCGG 63
Db 7 SerGlnLeuGluArgSerIleThrIleLeuValPheHisGlnTyrSerArgLys 26
Qy 64 AAGGGCATTTTGACACCCCTCTTAAGGTCAGCTGAGCAGCTGCTTACAAAGGAGCTT 123

Db 27 TyrGlyHisProAspThrLeuAsnLysAlaGluPheLysGluMetValAsnLysAspLeu 46
Qy 124 GCAAACACCATCAAGATATCAAA--GATAAAGCTGTCATTGATGAATATTCACAGGC 180
Db 47 ProAsnPheLysArgGluLysArgAsnGluAsnLeuLeuArgAspIleMetGluAsp 66
Qy 181 CTGGATGCTTAATCAAGTCAAGCTGACCTTTCAAGAATTCATATCCCTGGTAGCCATT 240
Db 67 LeuAspThrAsnGlnAspAsnGlnLeuSerPheGluGluCysMetMetLeuMetGlyLys 86
Qy 241 GCGTGAAGCTGCCATTACACACCCACAAA 273
Db 87 LeuIlePheAlaCysHisGluLysLeuHisGlu 97

RESULT 11

S68242
calgranulin B - mouse
N;Alternate names: calcium-binding protein MRP-14; macrophage migration inhibitory factor
C;Species: Mus musculus (house mouse)
C;Date: 06-Sep-1996 #sequence_revision 23-May-1997 #text_change 09-Jul-2004
C;Accession: S68242; S68272
R;Lagasse, E.; Weissman, I.L.
submitted to the EMBL Data Library, February 1992
A;Description: Mouse MRP8 and MRP14, two intracellular calcium-binding proteins associat
A;Reference number: S68242
A;Accession: S68242
A;Molecule type: mRNA
A;Residues: 1-113 <I>AG>
A;Cross-references: UNIPROT:P31725; EMBL:M83219; NID:gl99807; PIDN:AAB07228.1; PID:gl998
R;Raftery, M.J.; Harrison, C.A.; Alewood, P.; Jones, A.; Geczy, C.L.
Biochem. J. 316, 285-293, 1996
A;Title: Isolation of the murine S100 protein MRP14 (14 kDa migration-inhibitory-factor-
ding:
A;Reference number: S68272; MUID:96235204; PMID:8645219
A;Accession: S68272
A;Molecule type: protein
A;Residues: 2-10;95-109 <RAP>
A;Note: 107-His is identified as 3'-methylhistidine; the authors' source for the referen
ylhistidine
C;Genetics:
A;Gene: MRP14
C;Complex: heterodimer and higher complexes with calgranulin A
C;Superfamily: S-100 protein; calmodulin repeat homology
C;Keywords: acetylated amino end; calcium binding; EF hand; heterodimer; inflammation; m
F;2-113/Product: calgranulin B #status predicted <MAT>
F;11-45/Domain: calmodulin repeat homology <EF1>
F;55-87/Domain: calmodulin repeat homology <EF2>
F;2/Modified site: acetylated amino end (Ala) (in mature form) #status experimental
F;80-91/Disulfide bonds: #status experimental
F;103,105,107/Binding site: zinc (His) #status predicted
F;107/Modified site: 3'-methylhistidine (His) #status experimental

Alignment Scores:
Pred. No.: 1.57e-11 Length: 113
Score: 178.50 Matches: 36
Percent Similarity: 67.03% Conservative: 25
Best Local Similarity: 39.56% Mismatches: 29
Query Match: 37.42% Indels: 1
DB: 1 Gaps: 1

US-09-910-208B-12 (1-276) x S68242 (1-113)

Qy 4 ACAAACTTGAAGCATCTGGAGGAATTCCTCAATATCTTCCACCAATACTCAGTTCGG 63
Db 7 SerGlnMetGluArgSerIleThrIleLeuAspThrPheHisGlnTyrSerArgLys 26
Qy 64 AAGGGCATTTTGACACCCCTCTTAAGGTCAGCTGAGCAGCTGCTTACAAAGGAGCTT 123
Db 27 GluGlyHisProAspThrLeuSerLysLysGluPheArgGlnMetValGluAlaGlnLeu 46
Qy 124 GCAAACACCATCAAGATATCAAA--GATAAAGCTGTCATTGATGAATATTCACAGGC 180
Db 47 AlaThrPheMetLysLysGluLysArgAsnGluAlaLeuIleAsnAspIleMetGluAsp 66

R;Tulchinsky, E.M.; Grigorian, M.S.; Ebraldize, A.K.; Milshina, N.I.; Lukanidin, E.M. Gene 87, 219-223, 1990

A;Title: Structure of gene mtsl, transcribed in metastatic mouse tumor cells.

A;Reference number: JH0097; MUID:90236313; PMID:2332170

A;Accession: JH0097

A;Molecule type: DNA

A;Residues: 1-101 <TUL>

A;Cross-references: GB:M36578; GB:M36579

A;Experimental source: liver

R;Tulchinsky, B.

submitted to the EMBL Data Library, August 1989

A;Reference number: S07981

A;Accession: S07981

A;Molecule type: DNA

A;Residues: 1-47, 'VSGSGFNG', 56-57, 'RTDEAA', <TU2>

A;Cross-references: EMBL:X16094; NID:G53249; PIDN:CAA34224.1; PID:G53250

R;Jackson-Grueby, L.L.; Swiergiel, J.; Linzer, D.I.H.

Nucleic Acids Res. 15, 6677-6890, 1987

A;Title: A growth-related mRNA in cultured mouse cells encodes a placental calcium bind

A;Reference number: A26803; MUID:87316927; PMID:3628004

A;Accession: A26803

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-101 <TUL>

A;Cross-references: GB:X05835; NID:G50310; PIDN:CAA29282.1; PID:G50311

R;Goto, K.; Endo, H.; Fujiyoshi, T.

J. Biochem. 103, 48-53, 1988

J. Biochem. 103, 48-53, 1988
A:Title: Cloning of the sequences expressed abundantly in established cell lines: identification of a novel protein-coding gene.
A:Reference number: A41411; MUID:88198109; PMID:3162911
A:Accession: A41411
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-101 <GOT>
A:Cross-references: GB:D00208; NID:G220569; PID:BAA00148.1; PID:G220570
R:Rulchinsky, E.; Kramerov, D.; Ford, H.L.; Reshetnyak, E.; Lukanidin, E.; Zain, S. Oncogene 8, 79-86, 1993
A:Title: Characterization of a positive regulatory element in the *mts1* gene.

A;Title: Characterization of a positive regulatory element in the mts1 gene.
A;Reference number: I48674; MUID:93141279; PMID:8423998
A;Accession: I48674
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-47; 'VSGSXPNQ', 48-54 <RES>
A;Cross-references: EMBL:X16034; NID:G53249; PIDN:CAA34234.1; PID:G53250
C;Comment: Gene mts1 is expressed in metastatic cells.
C;Genetics:
A;Gene: mts1
A;Introns: 47/3
C;Superfamily: S-100 protein; calmodulin repeat homology
C;Keywords: calcium binding; cancer; EF hand
F;7-41/Domain: calmodulin repeat homology <EF1>
F;50-82/Domain: calmodulin repeat homology <EF2>

Alignment Scores:	
Pred. No.:	1.55e-10
Score:	169.50
Percent Similarity:	63.54%
Best Local Similarity:	41.67%
Query Match:	35.53%
DB:	2
	2
	Length: 101
	Matches: 40
	Conservative: 21
	Mismatches: 28
	Indels: 8
	Gaps: 2
US-09-910-208B-12 (1-276) x S06207 (1-101)	

Qy 10 CTTGAAGAGCATCTGGAGGAAATTGTCAATATATCTCCACCAATACTCAGTTCGGAAGGGG 69
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5 LeuGlulAlalLeuAspValIleValSerThrPheHisLysTySerGlyLysGluGly 24
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 70 CATTTTGACACCCTCTCTTAAGGGTAGCTGAAGAGCGTCTTCAAAGGAGCTTGC AAAC 129
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 25 AspLysPheLysLeuAsnLysThrGluLeuLysGluLeuLeuthrArgGluLeuProSer 44
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 130 ACCATCAAGAATATCAAAGATAAAGCTGTCATTGATGAANAATATTC CAAGCGCTGATGCT 189
::: ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 45 PheLeuGluLysArgThrAspGluAlaAlaPheGlnLysValMetSerAsnLeuAspSer 64
::: ||||| ||||| ||||| ||||| ||||| ||||| |||||

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: February 23, 2005, 11:50:07 ; Search time 116.5 Seconds
(without alignments)
2426.332 Million cell updates/sec

Title: US-09-910-208B-12
Perfect score: 477
Sequence: 1 atgacaaactgaagagca.....attaccacacccacaaagag 276

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp
-O=/cpn2.1/USPTO spool_p/HADAD-09-910208B/runat 23022005 101933 15291/app_query.fasta.1
-DB=UniProt_03 -QFMT=fasten -SUFFIX=rup -MINMATCH=0.1 -LOOPEL=0 -LOOPEX=10
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pco -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=HADAD-09-910208B @CNC 1.1.244 @runat 23022005 101933 15291 -NCPU=6
-ICPU=3 -NO MMAP -LARGEOVERLY -NEG SCORES=0 -WAIT -DSFBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : UniProt 03.*

1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	463	97.1	91	1 S112 HUMAN	P80511 homo sapien
2	332	69.6	91	1 S112_PIG	P80310 sus scrofa
3	314	65.8	91	1 S112_BOVIN	P79105 bos taurus
4	273	57.2	81	1 S112_RABIT	O77791 cryptotlagus
5	248	52.0	70	2 Q9TR16	Q9tr16 bos taurus
6	228.5	47.9	122	1 S109_BOVIN	P28783 bos taurus
7	218	45.7	119	2 Q6PRV2	Q6prv2 coturnix co
8	214.5	45.0	114	1 S109_HUMAN	P06702 homo sapien
9	210.5	44.0	119	1 M126_CHICK	P28318 gallus gall
10	201.5	42.2	118	1 S109_RABIT	P50117 cryptotlagus
11	198	41.5	100	2 Q7ZVA4	Q7zva4 brachydanio
12	194	40.7	95	1 S10P_HUMAN	P25815 homo sapien
13	190.5	39.9	99	2 Q8AVJ2	Q8avj2 squalus aca
14	189	39.6	92	2 Q6YNR6	Q6ynr6 cryptotlagus
15	189	39.6	92	2 Q925T3	Q925t3 cricetus
16	189	39.6	101	2 Q93395	Q93395 salvelinus

17	188	39.4	92	1 S10I ICTPU	Q91061 ictalurus p
18	186	39.0	92	2 Q9PSF6	Q9psf6 ictalurus p
19	185	38.8	91	1 S10B_BOVIN	P02638 bos taurus
20	185	38.8	91	1 S10B_MOUSE	P50114 mus musculu
21	184	38.6	91	1 S10B_HUMAN	P04271 homo sapien
22	183.5	38.5	95	2 Q5XG62	Q5xg62 brachydanio
23	182	38.2	91	1 S10B_RAT	P04631 rattus norv
24	180.5	37.8	111	2 Q761U7	Q761u7 rattus norv
25	180.5	37.8	112	1 S109_RAT	P50116 rattus norv
26	178.5	37.4	112	1 S109_MOUSE	P31725 mus musculu
27	177.5	37.2	95	1 S10A_MISFO	Q71zt1 misgurnus f
28	173.5	36.4	95	2 Q5DGT8	Q5dgt8 brachydanio
29	169.5	35.5	101	1 S104_MOUSE	P07091 mus musculu
30	169.5	35.5	102	2 Q68ET4	Q68et4 brachydanio
31	168.5	35.3	98	1 S10Z_HUMAN	Q8wxg8 homo sapien
32	168	35.2	591	2 Q01720	Q01720 homo sapien
33	168	35.2	687	2 Q9H4U2	Q9h4u2 homo sapien
34	167	35.0	102	1 S111_RABIT	P24480 cryptotlagus
35	166.5	34.9	101	1 S104_RAT	P05942 rattus norv
36	164.5	34.5	93	1 S10A_RAT	P35467 rattus norv
37	164	34.4	101	1 S111_CHICK	P24479 gallus gall
38	163	34.2	148	2 Q8BLX1	Q8blx1 mus musculu
39	163	34.2	2496	1 HORN_MOUSE	Q8vhd8 mus musculu
40	162.5	34.1	93	1 S10A_BOVIN	P02639 bos taurus
41	161.5	33.9	93	1 S10A_HUMAN	P23297 homo sapien
42	161.5	33.9	501	2 Q8CIU0	Q8ciu0 rattus norv
43	161	33.8	2850	1 HORN_HUMAN	Q86yz3 homo sapien
44	158	33.1	93	1 S108_HUMAN	P05109 h calgranul
45	158	33.1	1218	2 Q05331	Q05331 homo sapien

ALIGNMENTS

RESULT 1
S112_HUMAN
ID S112_HUMAN STANDARD; PRT; 91 AA.
AC P80511; P83219;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE 25-OCT-2004 (Rel. 45, Last annotation update)
DE Calgranulin C (CAGC) (GGRP) (Neutrophil S100 protein) (Calcium-binding protein in amniotic fluid 1) (CAAF1) (p6) [Contains: Calcitermin].
GN Name=S100A12;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97138564; PubMed=8985590; DOI=10.1016/S0143-4160(96)90087-1; Wicki R., Marenholz I., Mischke D., Schaefer B.W., Heizmann C.W.; "Characterization of the human S100A12 (calgranulin C, p6, CAAF1, GGRP) gene, a new member of the S100 gene cluster on chromosome 1q21."; Cell Calcium 20:459-464 (1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96192053; PubMed=8619860; DOI=10.1006/bbrc.1996.0600; Yamamura T., Hitomi J., Nagasaki K., Suzuki M., Takahashi E., Saito S., Tsukada T., Yameguchi K.; "Human CAAF1 gene -- molecular cloning, gene structure, and chromosome mapping."; Biochem. Biophys. Res. Commun. 221:356-360 (1996).
RN [3]
RP SEQUENCE.
RX MEDLINE=96192069; PubMed=8619876; DOI=10.1006/bbrc.1996.0616; Marti T., Ertmann K.D., Gallin M.Y.; "Host-parasite interaction in human onchocerciasis: identification and sequence analysis of a novel human calgranulin."; Biochem. Biophys. Res. Commun. 221:454-458 (1996).
RN [4]
RP SEQUENCE.
RX TISSUE=Neutrophils;

RX MEDLINE=963332419; PubMed=8769108; DOI=10.1006/bbrc.1996.1144;
 RA Ilg E.C., Troxler H., Buergisser D.M., Kuster T., Markert M.,
 RA Guignard F., Hunsicker P., Birchler N., Heilmann C.W.;
 RT "Amino acid sequence determination of human S100A12 (p6, calgranulin
 C, CGRP, CAAFI) by tandem mass spectrometry.";
 RL Biochem. Biophys. Res. Commun. 225:146-150(1996).
 RN [5]
 RP SEQUENCE OF 1-20.
 RX MEDLINE=95351965; PubMed=7626002;
 RA Guignard F., Maue J., Markert M.;
 RA "Identification and characterization of a novel human neutrophil
 RT protein related to the S100 family.";
 RL Biochem. J. 309:395-401(1995).
 RN [6]
 RP SEQUENCE OF 77-91, ANTIMICROBIAL ACTIVITY, AND MASS SPECTROMETRY.
 RC TISSUE=Nasal mucus;
 RX MEDLINE=21413725; PubMed=11522286; DOI=10.1016/S0014-5793(01)02731-4;
 RA Cole A.M., Kim Y.-H., Tahk S., Hong T., Weiss P., Waring A.J., Ganz T.;
 RA "Callictermin, a novel antimicrobial peptide isolated from human airway
 RT secretions.";
 RL FEBS Lett. 504:5-10(2001).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (1.95 ANGSTROMS).
 RX MEDLINE=21065388; PubMed=11134923; DOI=10.1107/S090744490001458X;
 RA Moroz O.V., Anton A.A., Murshudov G.N., Maitland N.J., Dodson G.G.,
 RA Wilson K.S., Skibshoj I., Lukandin E.M., Bronstein I.B.;
 RT "The three-dimensional structure of human S100A12.";
 RL Acta Crystallogr. D 57:20-29(2001).
 CC -!- FUNCTION: Callictermin possesses antifungal activity against
 CC C. albicans and is also active against E.coli and P.aeruginosa but
 CC not L.monocytogenes and S.aureus.
 CC -!- SUBUNIT: Homodimer.
 CC -!- TISSUE SPECIFICITY: Monocytes and lymphocytes.
 CC -!- MASS SPECTROMETRY: MW=10444; METHOD=Electrospray; RANGE=1-91;
 CC NOTE=Ref.6.
 CC -!- MASS SPECTROMETRY: MW=1688.9; METHOD=MALDI; RANGE=77-91;
 CC NOTE=Ref.6.
 CC -!- SIMILARITY: Belongs to the S-100 family.
 CC -!- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
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 CC or send an email to license@isb-sib.ch).
 CC
 CC -----
 CC EMBL; X97859; CAA66453.1; -;
 CC EMBL; X98288; CAA66934.1; -;
 CC EMBL; X98289; CAA66934.1; JOINED.
 CC EMBL; X98290; CAA66934.1; JOINED.
 CC EMBL; X98289; CAB94792.1; -;
 CC EMBL; X98290; CAB94792.1; JOINED.
 CC EMBL; D49549; BAA08497.1; -;
 CC EMBL; D83664; BAA12036.1; -;
 CC EMBL; D83657; BAA12030.1; -;
 CC PIR; JC4712; JC4712.
 CC PDB; 1B8A; X-ray; A/B=1-91.
 CC PDB; 1Q0M; X-ray; A/B/C/D/E/F/G/H/I/J/K/L=1-91.
 CC PDB; 1QDB; X-ray; A/B/C/D/E/F=1-91.
 CC Genew; HGNC:10489; S100A12.
 CC MIM; 603112; -;
 CC GO; GO:0005829; Cytosol; TAS.
 CC GO; GO:0005826; C-insoluble fraction; TAS.
 CC GO; GO:0005509; F:calcium ion binding; TAS.
 CC GO; GO:0006954; P:inflammatory response; TAS.
 CC InterPro; IPR001751; CaBP S100.
 CC InterPro; IPR002048; EF-hand.
 CC InterPro; IPR010983; EF-hand.
 CC Pfam; PF00036; ehand; I.
 CC Pfam; PF01023; S_100; I.
 CC ProDom; PD003407; CaBP_S100; 1.

DR PROSITE; PS00018; EF HAND; FALSE NEG.
 DR PROSITE; PS00303; S100 CABP; 1
 KW 3D-structure; Antibiotic; Calcium-binding; Direct protein sequencing;
 KW Fungicide; Metal-binding; Zinc.
 FT INIT MET 0 0
 FT PEPTIDE 77 91 Callictermin.
 FT CA_BIND 18 31 EF-hand 1; low affinity (By similarity).
 FT CA_BIND 61 72 EF-hand 2; high affinity (By similarity).
 FT HELIX 2 18
 FT TURN 19 19
 FT TURN 24 25
 FT STRAND 26 27
 FT HELIX 29 39
 FT TURN 41 43
 FT TURN 45 48
 FT HELIX 50 60
 FT TURN 62 63
 FT STRAND 68 69
 FT HELIX 70 85
 SQ SEQUENCE 91 AA; 10444 MW; 325685EA8695F6B7 CRC64;
 Alignment Scores:
 Pred. NO.: 5.54e-41 Length: 91
 Score: 463.00 Matches: 91
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 97.06% Indels: 0
 DB: 1 Gaps: 0
 US-09-910-208B-12 (1-276) x S112_HUMAN (1-91)
 QY 4 ACAAACCTGAAGAGCATCTGGAGGAATTGTCAATATCTTCCACCAATACTCAGTTCCG 63
 Db 1 ThrLysLeuGluHisLeuGluGlyIleValAsnIlePheHisGlnTyrSerValArg 20
 QY 64 AAGGGCATTTGACACCCCTCTCTAAGGTCAGCTGAAGCAGCTGCTTACAAGAGAGCTT 123
 Db 21 LysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGluLeu 40
 QY 124 GCAACACCATCAGATATCAAGATCAAGCTGCTCATTTGATGAATATTCACAGGCTG 183
 Db 41 AlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGlyLeu 60
 QY 184 GATCCTAATCAAGATCAAGCTGCTGCTTCAAGATTCATATCCCTGGTAGCATTGCG 243
 Db 61 AspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIleAla 80
 QY 244 CTGAAGGCTGCCATTTACCAACCCACACCCACAAAGAG 276
 Db 81 LeuLysAlaAlaHisTyrHisThrHisLysGlu 91
 RESULT 2
 S112_PIG
 ID S112_PIG STANDARD; PRT; 91 AA.
 AC P80310;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Calgranulin C (CAGC).
 GN Name=S100A12;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa;
 OC Mammalia; Eutheria;
 OC Cetartiodactyla; Suina; Suidae; Sus.
 ON NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Granulocyte;
 RX MEDLINE=95050708; PubMed=7961855;
 RA Dell'Angelica E.C., Schleicher C.H., Santome J.A.;
 RT "Primary structure and binding properties of calgranulin C, a novel
 FT S100-like calcium-binding protein from pig granulocytes.";
 RL J. Biol. Chem. 269:28929-28936(1994).
 CC -!- TISSUE SPECIFICITY: Found essentially in granulocytes with small

CC amounts found in lymphocytes.
 CC -!- MISCELLANEOUS: In the absence of zinc binds one calcium ion per
 CC molecule, in the presence of zinc binds two calcium ions per
 CC molecule.
 CC -!- SIMILARITY: Belongs to the S-100 family.
 CC -!- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
 DR PIR; A55406; A55406.
 DR HSSP; P80511; 1E8A.
 DR InterPro; IPR001751; CaBP_S100.
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR010983; EF_Hand_Like.
 DR Pfam; PF00036; ehand; 1.
 DR Pfam; PF01023; S_100; 1.
 DR ProDom; PD003407; CaBP_S100; 1.
 DR ProSITE; PS00018; EF_HAND; FALSE_NEG.
 DR ProSITE; PS00303; S100_CABP; 1.
 KW Calcium-binding; Direct protein sequencing; Metal-binding; Zinc.
 FT CA_BIND 18 31 EF-hand 1; low affinity (By similarity).
 FT CA_BIND 61 72 EF-hand 2; high affinity (By similarity).
 SQ SEQUENCE 91 AA; 10614 MW; B4204461432D7FCE CRC64;
 Alignment Scores:
 Pred. No.: 7 22e-27 Length: 91
 Score: 332.00 Matches: 64
 Percent Similarity: 81.32% Conservative: 10
 Best Local Similarity: 70.33% Mismatches: 17
 Query Match: 69.60% Indels: 0
 DB: 1 Gaps: 0
 US-09-910-208B-12 (1-276) x S112_PIG (1-91)
 QY 4 ACAAACTTGAAGAGCATCTGAGGGAATTGTCAATATCTTCCACCAATCTCAGTTCGG 63
 Db 1 ThrLysLeuGluAspHisLeuGluGlylleAenllePheHisGlnTyrSerValarg 20
 QY 64 AAGGGCATTGACACCTCTCTAAGGGTGAGCTGAGCAGCTGCTTACAAAGAGCTT 123
 Db 21 LeuGlyHisTyrAspThrLeuLeuLysArgGluLeuLysGlnLeuLeuThrLysGluLeu 40
 QY 124 GCAACACCATCAAGAATATCAAGATTAAGCTGTCATTGATGAATATTCACAGGCTG 183
 Db 41 ProAenThrLeuLysAsnThrLysAspGlnGlyThrIleAspLysIlePheGlnAsnLeu 60
 QY 184 GATGCTAATCAAGATCAACAGCTGACCTTCAAGAAATTCATATCCCTGCTAGCCATTGCG 243
 Db 61 AspAlaAsnGlnAspGluGlnValSerPheLysGluPheValValLeuValThrAspVal 80
 QY 244 CTGAAGGCTGCCATTACACACCCACAAAGAG 276
 Db 81 LeuIleThrAlaHisAspAsnIleHisLysGlu 91
 RESULT 3
 S112_BOVIN
 ID S112_BOVIN STANDARD; PRT; 91 AA.
 AC P79105;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Calgranulin C (CAGC) (Calcium-binding protein in amniotic fluid 1)
 DE (CAAF1) (PAGE binding protein).
 GN Name=S100A12; Synonyms=CAAF1;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Oesophagus;
 RX MEDLINE=96298783; PubMed=8718672;
 RA Hitomi J., Yamaguchi K., Kikuchi Y., Kimura T., Maruyama K.,
 RA Nagasaki K.;
 RT "A novel calcium-binding protein in amniotic fluid, CAAF1: its

RT molecular cloning and tissue distribution.";
 RL J. Cell Sci. 109:805-815(1996).
 RN [2]
 RC SEQUENCE FROM N.A.
 RX TISSUE=Lung;
 RX MEDLINE=99325504; PubMed=10399917; DOI=10.1016/S0092-8674(00)80801-6;
 RA Hofmann M.A., Drury S., Fu C., Qu W., Taguchi A., Lu Y., Avila C.,
 RA Kambham N., Bierhaus A., Nawroth P., Neurath M.F., Slattery T.,
 RA Beach D., McClary J., Nagashima M., Morser J., Stern D., Schmidt A.M.;
 RT "RAGE mediates a novel proinflammatory axis: a central cell surface
 RT receptor for S100/calgranulin polypeptides.";
 RL Cell 97:889-901(1999).
 CC -!- SIMILARITY: Belongs to the S-100 family.
 CC -!- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
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 CC or send an email to license@isb-sib.ch).
 CC EMBL; D49548; BAA08496.1; -.
 DR EMBL; AF011757; AAB65423.1; -.
 DR HSSP; P80511; 1GQM.
 DR InterPro; IPR001751; CaBP_S100.
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR010983; EF_Hand_Like.
 DR Pfam; PF00036; ehand; 1.
 DR Pfam; PF01023; S_100; 1.
 DR ProDom; PD003407; CaBP_S100; 1.
 DR ProSITE; PS00018; EF_HAND; 1.
 DR ProSITE; PS00303; S100_CABP; 1.
 KW Calcium-binding; Metal-binding; Zinc.
 FT INIT_MET 0 0 By similarity.
 FT CA_BIND 18 31 EF-hand 1; low affinity (By similarity).
 FT CA_BIND 61 72 EF-hand 2; high affinity (By similarity).
 SQ SEQUENCE 91 AA; 10554 MW; 66FBC3C1B0354482 CRC64;
 Alignment Scores:
 Pred. No.: 6 28e-25 Length: 91
 Score: 314.00 Matches: 60
 Percent Similarity: 80.22% Conservative: 13
 Best Local Similarity: 65.93% Mismatches: 18
 Query Match: 65.83% Indels: 0
 DB: 1 Gaps: 0
 US-09-910-208B-12 (1-276) x S112_BOVIN (1-91)
 QY 4 ACAAACTTGAAGAGCATCTGAGGGAATTGTCAATATCTTCCACCAATCTCAGTTCGG 63
 Db 1 ThrLysLeuGluAspHisLeuGluGlylleAenllePheHisGlnTyrSerValarg 20
 QY 64 AAGGGCATTGACACCTCTCTAAGGGTGAGCTGAGCAGCTGCTTACAAAGAGCTT 123
 Db 21 ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuLeuThrLysGluLeu 40
 QY 124 GCAACACCATCAAGAATATCAAGATTAAGCTGTCATTGATGAATATTCACAGGCTG 183
 Db 41 ProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAspLeu 60
 QY 184 GATGCTAATCAAGATCAACAGCTGACCTTCAAGAAATTCATATCCCTGCTAGCCATTGCG 243
 Db 61 AspAlaAspLysAspGlyAlaValSerPheGluGluPheValValLeuValSerargVal 80
 QY 244 CTGAAGGCTGCCATTACACACCCACAAAGAG 276
 Db 81 LeuLysThrAlaHisIleAspIleHisLysGlu 91
 RESULT 4
 S112_RABIT
 ID S112_RABIT STANDARD; PRT; 81 AA.

AC 077791;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Calgranulin C (CAGC) (Fragment).
 GN Name=S100A12;
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC STRAIN=New Zealand white; TISSUE=Neutrophils;
 RX MEDLINE=96355278; PubMed=8702688; DOI=10.1074/jbc.271.33.19802;
 RA Yang Z., Devere M.J., Gardiner E.E., Devenish R.J., Handley C.J.,
 RA Underwood J.R., Robinson H.C.;
 RT "Rabbit polymorphonuclear neutrophils form 35S-labeled S-sulfo-
 calgranulin C when incubated with inorganic [35S] sulfate.";
 RL J. Biol. Chem. 271:19802-19809(1996).
 CC -1- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
 CC -----
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 CC or send an email to license@ebi.ac.uk).
 CC -----
 DR EMBL; AF091848; AAC61770.1; --
 DR HSP; P80511; 1E8A.
 DR InterPro; IPR001751; CaBP_S100.
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR010983; EF_Hand_like.
 DR Pfam; PF00036; ehand; 1.
 DR Pfam; PF01023; S_100; 1.
 DR ProDom; PD003407; CaBP_S100; 1.
 DR PROSITE; PS00018; EF_HAND; 1.
 DR PROSITE; PS00303; S100_CaBP; 1.
 KW Calcium-binding; Direct protein sequencing.
 FT NON_TER 1
 FT CA_BIND 8 21 EF-hand 1; low affinity (By similarity).
 FT CA_BIND 51 62 EF-hand 2; high affinity (By similarity).
 SQ SEQUENCE 81 AA; 9401 MW; 95B67A209180CB66 CRC64;
 Alignment Scores:
 Pred. No.: 1.64e-20 Length: 81
 Score: 273.00 Matches: 52
 Percent Similarity: 79.01% Conservative: 12
 Best Local Similarity: 64.20% Mismatches: 17
 Query Match: 57.23% Indels: 0
 DB: 1 Gaps: 0
 US-09-910-208B-12 (1-276) x S112_RABIT (1-81)
 QY 34 GTCATATCTCCACCAATCTAGTTCGGAGGGGCAATTTGACACCCCTCTTAAGGGT 93
 Db 1 IleAenillePheHisGlnTyrSerValArgThrGlyHisTyrAspThrLeuSerLysCys 20
 QY 94 GAGCTGAAGCAGCTCTCTTACAAAGGAGCTTGCACACACCATCAAGATATCAAGATAAA 153
 Db 21 GluLeuLysLysLeuIleThrThrGluLeuValAenThrIleLysAenThrLysAspGln 40
 QY 154 GCTGTCAATGTAATATTCACAGCTGATGCTAATCAAGATGAACAGCTGCACTTT 213
 Db 41 AlaThrValAspArgIlePheArgAspLeuAspGluAspGlyAspHisGlnValAspPhe 60
 QY 214 CAAGATTCATATCCCTGAGCCATTCGCTGAGGCTGCCATTACACACCCACAAA 273
 Db 61 LysGluPheLeuSerLeuAlaSerValLeuValThrAlaHisGluAenlleHisLys 80
 QY 274 GAG 276

Db 81 Glu 81
 RESULT 5
 Q9TR16
 ID Q9TR16 PRELIMINARY; PRT; 70 AA.
 AC Q9TR16;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE CORNEA-associated antigen, CO-AG-CALGRANULIN C homolog.
 DE Bos taurus (Bovine).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=96181454; PubMed=8603881;
 RA Liu S.H., Gottsch J.D.;
 RT "Amino acid sequence of an immunogenic corneal stromal protein.";
 RL Invest. Ophthalmol. Vis. Sci. 37:944-948(1996).
 CC -1- SIMILARITY: Belongs to the S-100 family.
 DR HSP; P80511; 1E8A.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR InterPro; IPR001751; CaBP_S100.
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR010983; EF_Hand_like.
 DR Pfam; PF01023; S_100; 1.
 DR ProDom; PD003407; CaBP_S100; 1.
 SQ SEQUENCE 70 AA; 8134 MW; 7D52BEA97A4D53A5 CRC64;
 Alignment Scores:
 Pred. No.: 8.12e-18 Length: 70
 Score: 248.00 Matches: 48
 Percent Similarity: 82.86% Conservative: 10
 Best Local Similarity: 68.57% Mismatches: 12
 Query Match: 51.99% Indels: 0
 DB: 2 Gaps: 0
 US-09-910-208B-12 (1-276) x Q9TR16 (1-70)
 QY 4 ACAAACCTGAAGAGCATCTCGAGGGAATTTGCAATATCTTCCACCAATCTCAGTTGG 63
 Db 1 ThrLysLeuGluAspHisLeuGluGlyIleAenlleHisGlnTyrSerValArg 20
 QY 64 AAGGGCATTGTGACACCTCTCTTAAGGGTGAAGCTGCTGCTTACAAAGGAGCTT 123
 Db 21 ValGlyHisPheAspThrLeuAenLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40
 QY 124 GCAACACCATCAAGATATCAAGATAAAGCTGTCTATTGATGAATATTCCAAGGCTG 183
 Db 41 ProLysThrLeuGlnAenThrLysAspGlnProThrIleAspLysIlePheGlnAspLeu 60
 QY 184 GATGCTAATCAAGATGAACAGCTGCTGACTTT 213
 Db 61 AspAlaAspLysLysGlyAlaValPhe 70
 RESULT 6
 S109_BOVIN
 ID S109_BOVIN STANDARD; PRT; 122 AA.
 AC P28783;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Calgranulin B (Neutrophil cytosolic 23 kDa protein) (P23) (BEE22)
 DE (Fragment).
 GN Name=S100A9;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OX NCBI_TaxID=9913;

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RN RP SEQUENCE.
RC TISSUE=Oesophageal epithelium;
RX MEDLINE=93280230; PubMed=8505358;
RA Tang T.K., Hong T.-M., Lin C.-Y., Lai M.-L., Liu C.H.-L., Lo H.-J.,
RA Wang M.-E., Chen L.B., Chen W.-T., Ip W., Lin D.C., Lin J.J.-C.,
RA Lin S., Sun T.-T., Wang E., Wang J.L., Wu R., Wu C.-W., Chien S.;
RT "Nuclear proteins of the bovine esophageal epithelium. I. Monoclonal
RT antibody W2 specifically reacts with condensed nuclei of
RT differentiated superficial cells.";
RL J. Cell Sci. 104:237-247(1993).
RN [2]
RP SEQUENCE OF 4-56.
RC TISSUE=Neutrophils;
RX MEDLINE=92304974; PubMed=1610833;
RA Dianoux A.-C., Stasia M.-J., Garin J., Gagnon J., Vignais P.V.;
RT "The 23-kilodalton protein, a substrate of protein kinase C, in bovine
RT neutrophil cytosol is a member of the S100 family.";
RL Biochemistry 31:5998-5903(1992).
CC -!- SUBUNIT: Disulfide linked heterodimer of a 7/11 kDa and a 22/23
CC kDa subunits.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic; loosely associated to the
CC cytoskeleton.
CC -!- TISSUE SPECIFICITY: Found essentially in phagocytic cells.
CC -!- PTM: Phosphorylated by protein kinase C.
CC -!- SIMILARITY: Belongs to the S-100 family.
CC -!- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
DR HSP; P06703; IIRJ.
DR InterPro: IPR001751; CabP S100.
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR010983; EF_Hand_like.
DR Pfam: PF00036; ehand; 1.
DR ProDom: PD003407; CabP S100; 1.
DR PROSITE; PS00018; EF_HAND; PARTIAL.
DR PROSITE; PS00303; S100_CABP; 1.
KW Calcium-binding; Direct protein sequencing; Phosphorylation.
FT NON_TER 1
FT CA_BIND 19 32 EF-hand 1; low affinity (Potential).
FT CA_BIND 63 74 EF-hand 2; high affinity (Potential).
FT SEQUENCE 122 AA; 13673 MW; F3C8C48806BECD CRC64;
SQ SEQUENCE 122 AA; 13673 MW; F3C8C48806BECD CRC64;

Alignment Scores:
Pred. No.: 1,03e-15 Length: 122
Score: 228.50 Matches: 47
Percent Similarity: 70.33% Conservative: 17
Best Local Similarity: 51.65% Mismatches: 26
Query Match: 47.90% Indels: 1
DB: 1 Gaps: 1

US-09-910-208b-12 (1-276) x S109_BOVIN (1-122)
QY 1 ATGCAAAACTTCAGAGCATCTGGAGGAATGTCAATATCTTCCACCAACTACTCAGTT 60
Db 1 MetSerGlnMetGluSerSerIleGluThrIleAseNilePheHisGlnTyrSerVal 20
QY 61 CGGAAGGGCATTCTTACACACCTCTCTAAGGCTGAGCTGAAGCAGCTGCTTCAAAAGGAG 120
Db 21 ArgLeuGlyHisTyrAspThrLeuIleGlnLysGluPheLysGlnLeuValGlnLysGlu 40
QY 121 CTTGCAAAACACCATC---AAGAAATCAAAAGATAAGCTGTGTCATGATGAATATTCCAA 177
Db 41 LeuProAsnPheLeuLysLysGlnLysLysAsnGluAlaIleAsnGluIleMetGlu 60
QY 178 GCCTCGGCTGAATCAAGATGACAGCTCGACTTTCAGAAATTCATATCCCTGGTAGCC 237
Db 61 AspLeuAspThrAsnValAspLysGlnLeuSerPheGluGluPheIleMetLeuValAla 80
QY 238 ATTGCGCTGAAGCTGCCCATACCAACACCCAC 270
Db 81 ArgLeuThrValAlaSerHisGluGluMetHis 91

RESULT 7

US-09-910-208b-12 (1-276) x Q6PRV2 (1-119)
QY 1 ATGCAAAACTTCAGAGCATCTGGAGGAATGTCAATATCTTCCACCAACTACTCAGTT 60
Db 11 LeuSerGluLeuGluLysAlaMetAspThrIleIleAspValPheHisGlnTyrSerArg 30
QY 61 CGGAAGGGCATTCTTACACACCTCTCTAAGGCTGAGCTGAAGCAGCTGCTTCAAAAGGAG 120
Db 31 ArgGluGlyAspAsnAspThrLeuThrLysLysGluLeuLysLeuLeuIleGluLysGln 50
QY 121 CTTGCAAAACACCATCAAGAATATCAAGATCAAGCTGTGTCATGATGAATATTCCAAAGGC 180
Db 51 LeuAlaAsnTyrLeuLysHisValLysAsnGlnValSerIleAspGlnIlePheLysAsp 70
QY 181 CTGGATGCTAATCAAGATGACAGCTCGACTTTCAGAAATTCATATCCCTGGTAGCCATT 240
Db 71 LeuAspGlyAsnLysAspGlnGlnLysSerPheGlyGluValMetLeuLeuIleArg 90
QY 241 GCGCTGAAGCTGCCCATACCAACCCAC 270
Db 91 ValIleIleAlaThrHisGluHisLeuHis 100

RESULT 8
S109_HUMAN
ID S109_HUMAN STANDARD; PRT; 114 AA.
AC P06702; Q9NMY0; Q9UCJ1;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Calgranulin B (Migration inhibitory factor-related protein 14) (MRP-
DE 14) (P14) (Leukocyte L1 complex heavy chain) (S100 calcium-binding
DE protein A9) (Calprotectin L1H subunit).
GN Name=S100A9; Synonyms=CAGB, MRP14;
OS Homo sapiens (Human).

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Q6PRV2
ID Q6PRV2 PRELIMINARY; PRT; 119 AA.
AC Q6PRV2;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE MRP protein.
GN Name=MRP;
OS Coturnix coturnix japonica (Japanese quail).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Coturnix.
OX NCBI_TaxID=93934;
RN [1]
RP SEQUENCE FROM N.A.
RA Hartl M., Bister K.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the S-100 family.
DR EMBL; AY583752; AAT01286.1; -.
DR HSP; P04631; IB4C.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro: IPR001751; CabP S100.
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR010983; EF_Hand_like.
DR Pfam: PF00036; ehand; 1.
DR ProDom: PD003407; CabP S100; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
DR PROSITE; PS00303; S100_CABP; 1.
SQ SEQUENCE 119 AA; 14012 MW; 00DFB09902DC5CFB CRC64;

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Alignment Scores:
Pred. No.: 1,39e-14 Length: 119
Score: 218.00 Matches: 40
Percent Similarity: 73.33% Conservative: 26
Best Local Similarity: 44.44% Mismatches: 24
Query Match: 45.70% Indels: 0
DB: 2 Gaps: 0

US-09-910-208b-12 (1-276) x Q6PRV2 (1-119)

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88030999; PubMed=3313057; DOI=10.1038/330080a0;
 RA Odink K., Cerletti N., Bruggen J., Clerc R.G., Tarcsay L., Zwaldo G.,
 RA Gerhards G., Schlegel R., Sorg C.;
 RT "Two calcium-binding proteins in infiltrate macrophages of rheumatoid
 RT arthritis";
 RL Nature 330:80-82(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88302148; PubMed=3405210;
 RA Lagasse E., Clerc R.G.;
 RT "Cloning and expression of two human genes encoding calcium-binding
 RT proteins that are regulated during myeloid differentiation";
 RL Mol. Cell. Biol. 8:2402-2410(1988).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89255276; PubMed=2656677;
 RA Murao S., Collart F.R., Huberman E.;
 RT "A protein containing the cystic fibrosis antigen is an inhibitor of
 RT protein kinases";
 RL J. Biol. Chem. 264:9356-9360(1989).
 RN [4]
 RP SEQUENCE FROM N.A.; AND VARIANT ARG-20.
 RA Wang M., Xu X., Cai Y., Xu H., Han Y., Xu Z., Wu M.;
 RT "Human gene for migration inhibitory factor-related protein 14
 RT (MRP14), variant allele";
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBSJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.H.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalius D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [6]
 RP SEQUENCE OF 84-114, AND PHOSPHORYLATION SITE THR-113.
 RX MEDLINE=90044075; PubMed=2478889; DOI=10.1038/342189a0;
 RA Edgeworth J., Freeman P., Hogg N.;
 RT "Ionomycin-regulated phosphorylation of the myeloid calcium-binding
 RT protein p14";
 RL Nature 342:189-192(1989).
 RN [7]
 RP SEQUENCE OF 11-19; 26-37 AND 94-107.
 RC TISSUE=Keratinocytes;
 RX MEDLINE=93162043; PubMed=1286667;
 RA Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E.,
 RA Vandekerckhove J.;
 RT "Microsequences of 145 proteins recorded in the two-dimensional gel
 RT protein database of normal human epidermal keratinocytes";
 RL Electrophoresis 13:960-969(1992).
 RN [8]
 RP SEQUENCE OF 5-34.

RX MEDLINE=93139333; PubMed=8423249;
 RA Miyasaki K.T., Bodeau A.L., Murthy A.R., Lehrer R.I.;
 RT "In vitro antimicrobial activity of the human neutrophil cytosolic S-
 RT 100 protein complex, calprotectin, against Capnocytophaga sputigena";
 RL J. Dent. Res. 72:517-523(1993).
 CC -!- FUNCTION: Expressed by macrophages in acutely inflamed tissues
 CC and in chronic inflammations. Seem to be an inhibitor of protein
 CC kinases. Also expressed in epithelial cells constitutively or
 CC induced during dermatoses. May interact with components of the
 CC intermediate filaments in monocytes and epithelial cells.
 CC -!- MISCELLANEOUS: Has been shown to bind calcium.
 CC -!- SIMILARITY: Belongs to the S-100 family.
 CC -!- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; X06233; CAA29579.1; -
 CC EMBL; M21064; AAA36326.1; -
 CC EMBL; M26311; AAA68480.1; -
 CC EMBL; AF237581; AAF62536.1; -
 CC EMBL; AF237582; AAF62537.1; -
 CC EMBL; AF237582; AAF62537.1; -
 CC EMBL; A12029; CAA01002.1; -
 CC EMBL; A12032; CAA01004.1; -
 CC EMBL; BC047681; AAH47681.1; -
 CC PIR; B31848; B31848.
 CC PDB; 1IRJ; X-ray; A/B/C/D/E/F/G/H=2-114.
 CC SWISS-2DPAGE; P06702; HUMAN
 CC Aarhus/Ghent-2DPAGE; 5007; IEF.
 CC Aarhus/Ghent-2DPAGE; 6010; IEF.
 CC Aarhus/Ghent-2DPAGE; 6017; IEF.
 CC Aarhus/Ghent-2DPAGE; 7013; IEF.
 CC OGP; P06702; -
 CC PMMA-2DPAGE; P06702; -
 CC Genew; HGNC:10499; S100A9.
 CC MIM; 123886; -
 CC GO; GO:0005509; F:calcium ion binding; TAS.
 CC GO; GO:0004871; P:signal transducer activity; TAS.
 CC GO; GO:0007267; P:cell-cell signaling; TAS.
 CC GO; GO:0006954; P:inflammatory response; TAS.
 CC InterPro; IPR001751; CaBP_S100.
 CC InterPro; IPR002048; EF-hand.
 CC InterPro; IPR010983; EF_Hand_like.
 CC Pfam; PF00036; efhand; 1.
 CC Pfam; PF01023; S_100; 1.
 CC ProDom; PD03407; CaBP_S100; 1.
 CC PROSITE; PS00018; EF_HAND; 1.
 CC PROSITE; PS00303; S100_CaBP; 1.
 CC 3D-structure; Calcium-Binding; Direct protein sequencing; Macrophage;
 CC Phosphorylation; Polymorphism.
 KW CA_BIND 23 36 EF-hand 1; low affinity (Potential).
 FT CA_BIND 67 78 EF-hand 2; high affinity (Potential).
 FT MOD_RES 113 113 Phosphothreonine.
 FT VARIANT 20 20 H->R.
 FT
 FT CONFLICT 6 6 /FTID=VAR_013008.
 FT CONFLICT 25 25 S->H (in Ref. 8).
 FT CONFLICT 28 28 K->F (in Ref. 8).
 FT CONFLICT 7 7 H->L (in Ref. 8).
 FT HELIX 23 23
 FT TURN 24 24
 FT TURN 29 30
 FT STRAND 32 32
 FT HELIX 34 44
 FT TURN 46 51
 FT HELIX 52 54
 FT HELIX 56 66
 FT TURN 68 69
 FT TURN 74 74
 FT STRAND 74

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FT HELIX 76 80
FT HELIX 81 85
SQ SEQUENCE 114 AA; 13242 MW; C3BE19729E14C078 CRC64;

Alignment Scores:
Pred. No.: 3,31e-14 Length: 114
Score: 214.50 Matches: 43
Percent Similarity: 70.65% Conservative: 22
Best Local Similarity: 46.74% Mismatches: 26
Query Match: 44.97% Indels: 1
DB: 1 Gaps: 1

US-09-910-208B-12 (1-276) x S109_HUMAN (1-114)
QY 1 ATGACAAAACCTTGAAGAGCATCTGGAGGGAATGTCAATATCTTCCACCAATCTCAGTT 60
Db 5 MetSerGlnLeuGluArgAsnIleGluThrIleAsnThrPheHisGlnTyrSerVal 24
QY 61 CGAAGGGGCATTTGACACCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTCAAGAGGAG 120
Db 25 LysLeuGlyHisProAspThrLeuAsnGlnGlyGluPheLysGluLeuValArgLysAsp 44
QY 121 CTTCGAACACCATC---AAGATATCAAGATAAGCTGTTCATTCATCAATATTCGAA 177
Db 45 LeuGlnAsnPheLeuLysLysGluAsnLysAsnGluLysValIleGluHisIleMetGlu 64
QY 178 GCGCTGGATGCTAATCAAGATCAAGAGTGGAGTCTTCAAGATTCATATCCCTGGTAGCC 237
Db 65 AspLeuAspThrAsnAlaAspLysGlnLeuSerPheGluGluPheIleMetLeuMetAla 84
QY 238 ATTGCGCTGAAGCTGCCCATTTACCACACCCCAAA 273
Db 85 ArgLeuThrTyrAlaSerHisGluLysMetHisGlu 96

RESULT 9
M126_CHICK STANDARD; PRT; 119 AA.
ID M126_CHICK
AC P28318;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein MRP-126.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=White leghorn; TISSUE=Bone marrow;
RX MEDLINE=92195690; PubMed=1549365;
RA Nakano T., Graf T.;
RT "Identification of genes differentially expressed in two types of v-
myb-transfected avian myelomonocytic cells.";
RL Oncogene 7:527-534(1992).
CC -!- TISSUE SPECIFICITY: Expressed in v-myb-transformed myelomonocytic
cells.
CC -!- SIMILARITY: Belongs to the S-100 family.
CC -!- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
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-----
CC EMBL; X61200; -; NOT_ANNOTATED_CDS.
CC HSP; P25815; IJ55.
CC InterPro; IPR001751; CaBP_S100.
CC InterPro; IPR002048; EF-hand.
CC InterPro; IPR010983; EF_Hand_like.

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DR Pfam; PF00036; ehand; 1.
DR Pfam; PF01023; S_100; 1.
DR ProDom; PD003407; CaBP_S100; 1.
DR PROSITE; PS00018; EF_HAND; 1.
DR PROSITE; PS00303; S100_CABP; 1.
KW Calcium-binding.
FT CA BIND 29 42 EF-hand 1; low affinity (Potential).
FT CA BIND 72 83 EF-hand 2; high affinity (Potential).
SQ SEQUENCE 119 AA; 14065 MW; 2D268DAF6309AD7A CRC64;

Alignment Scores:
Pred. No.: 1.01e-13 Length: 119
Score: 210.00 Matches: 39
Percent Similarity: 72.22% Conservative: 26
Best Local Similarity: 43.33% Mismatches: 25
Query Match: 44.03% Indels: 0
DB: 1 Gaps: 0

US-09-910-208B-12 (1-276) x M126_CHICK (1-119)
QY 1 ATGACAAAACCTTGAAGAGCATCTGGAGGGAATGTCAATATCTTCCACCAATCTCAGTT 60
Db 11 LeuSerGluLeuGluLysAlaIleAspValIleIleAspValPheHisGlnTyrSerArg 30
QY 61 CGAAGGGGCATTTTGCACACCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTCAAGAGGAG 120
Db 31 ArgGluGlyAspLysAspThrLeuThrArgLysGluLeuLysLeuLeuIleGluLysGln 50
QY 121 CTTCGAACACCATCAAGATATCAAGATAAGCTGTTCATTCATCAATATTCGAA 180
Db 51 LeuAlaAsnTyrLeuLysHisValLysAsnGlnValSerIleAspGlnIlePheLysAsp 70
QY 181 CTGGATGCTAATCAAGATCAAGAGTGGAGTCTTCAAGATTCATATCCCTGGTAGCCATT 240
Db 71 LeuAspAsnAsnLysAspGlnLeuSerPheGlyGluValMetLeuLeuIleLeuArg 90
QY 241 GCGCTGAAGGCTGCCCATTTACCACACCCAC 270
Db 91 ValThrValAlaThrHisGluHisLeuHis 100

RESULT 10
S109_RABBIT STANDARD; PRT; 118 AA.
ID S109_RABBIT
AC P50117;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Calgranulin B (Migration inhibitory factor-related protein 14) (MRP-
14) (Fragment).
GN Name=S100A9; Synonyms=MRP-14;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=New Zealand white; TISSUE=Neutrophils;
RX MEDLINE=96355278; PubMed=8702688; DOI=10.1074/jbc.271.33.19802;
RA Yang Z., de Veer M.J., Gardiner E.E., Devenish R.J., Handley C.J.,
RA Underwood J.R., Robinson H.C.;
RT "Rabbit polymorphonuclear neutrophils form 35S-labeled S-sulfo-
calgranulin C when incubated with inorganic [35S] sulfate.";
RL J. Biol. Chem. 271:19802-19809(1996).
RN [2]
RP SEQUENCE OF 45-82 FROM N.A.
RC STRAIN=New Zealand white;
RX MEDLINE=94198229; PubMed=8148323;
RA Mori S., Goto K., Goto F., Mutakami K., Ohkawara S., Yoshinaga M.;
RT "Dynamic changes in mRNA expression of neutrophils during the course
of acute inflammation in rabbits.";
RL Int. Immunol. 6:149-156(1994).
CC -!- SIMILARITY: Belongs to the S-100 family.
CC -!- SIMILARITY: Contains 2 EF-hand calcium-binding domains.

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CC or send an email to license@isb-sib.ch)
CC -----
DR EMBL; AF091849; AAC61771.1; -.
DR EMBL; D17404; BAA04227.1; -.
DR PIR; I46861; I46861.
DR HSSP; P06702; 1IRJ.
DR InterPro; IPR001751; CaBP_S100.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR010983; EF_Hand_like.
DR Pfam; PF00036; ehand; 1.
DR Pfam; PF01023; S_100; 1.
DR ProDom; PD003407; CaBP_S100; 1.
DR PROSITE; PS00018; EF HAND; 1.
DR PROSITE; PS00303; S100 CABP; 1.
KW Calcium-binding; Repeat.
FT NON TER 1
FT CA BIND 9 22 EF-hand 1; low affinity (Potential).
FT CA BIND 53 64 EF-hand 2; high affinity (Potential).
FT DOMAIN 103 118 2 X 8 AA tandem repeats of G-H-G-H-G-H-S-
FT REPEAT 103 110 1.
FT REPEAT 111 118 2.
FT SEQUENCE 118 AA; 13292 MW; 7496118E21AD5C41 CRC64;
Alignment Scores:
Pred. No.: 8 32e-13 Length: 118
Score: 201.50 Matches: 41
Percent Similarity: 70.73% Conservative: 17
Best Local Similarity: 50.00% Mismatches: 23
Query Match: 42.24% Indels: 1
DB: 1 Gaps: 1
US-09-910-208B-12 (1-276) x S109_RABIT (1-118)
QY 31 ATTGTCATATCTCCACCAATCTAGTTCGGAAGGGGCAATTTTGACACCTCTCTAAG 90
Db 1 lilelleAsnillePheHisGlnIyrSerValArgValGlyProArgAspSerLeuSerGln 20
QY 91 GGTGAGCTGAACACGCTGTTACAAAGAGCTTGCAACACCATC--AAGAATATCAAA 147
Db 21 LysGluPheLysGlnLeuValGlnLysGlnLeuHisAsnPhLeuLysGlnAlaArg 40
QY 148 GATAAGCTGTCATTGATGAATATTTCCAAAGCCCTGGATGCTTAATCAAGATGAACAGTGC 207
Db 41 AspGluLysAlaAlaAsnAspIleMetGluAspLeuAspThrAsnGlnAspLysGlnLeu 60
QY 208 GACTTTCAGAAATTCATATCCCTGAGCAGTTCGCTGAGGCTGCCCATTCACACACC 267
Db 61 SerPheGluGluPheValIleLeuMetAlaArgLeuValHisAlaSerHisGlnGluMet 80
QY 268 CACAAA 273
Db 81 HisLys 82
RESULT 11
Q7ZVA4
ID Q7ZVA4 PRELIMINARY; PRT; 100 AA.
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ZGC:56142.
GN ORFNames=zgc:56142;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

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OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole body;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M., Soares M.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Peters G.J., Abramson R.D., Mullany S.J.,
RA Raba S.A., Loquellano N.A., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Bosak S.A., McEwan P.J., Hales S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalón D.K., Muzny D.M., Kettman M., Madan A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Madan A., Young A.C., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Smailus D.S., Schnerch A., Schein J.E.,
RA Krzywinski M.I., Skalska U., Jones S.J., Marra M.A.;
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole body;
RA Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the S-100 family.
DR EMBL; BC045941; AAH45941.1; -.
DR HSSP; P35467; 1K2H.
DR ZFIN; ZDB-GENE-040426-1937; zgc:56142.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR001751; CaBP_S100.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR010983; EF_Hand_like.
DR Pfam; PF00036; ehand; 1.
DR Pfam; PF01023; S_100; 1.
DR ProDom; PD003407; CaBP_S100; 1.
DR PROSITE; PS00018; EF HAND; UNKNOWN.1.
DR PROSITE; PS00303; S100 CABP; 1.
SQ SEQUENCE 100 AA; 11157 MW; DAB81814E54CB8C8 CRC64;
Alignment Scores:
Pred. No.: 1 98e-12 Length: 100
Score: 198.00 Matches: 38
Percent Similarity: 76.00% Conservative: 19
Best Local Similarity: 50.67% Mismatches: 18
Query Match: 41.51% Indels: 0
DB: 2 Gaps: 0
US-09-910-208B-12 (1-276) x Q7ZVA4 (1-100)
QY 10 CTTGAAGAGCATCTGGAGGGGAATTTGCAATATCTTCCACCAATCTCAGTTCGGAAGGG 69
Db 5 LeuGluArgAlaMetGluThrLeuIleThrValPheHisArgTyrSerGlyAlaGluGly 24
QY 70 CATTGTCACACCTCTCTAAGGGTGGAGTGAAGCAGCTGCTTACAAGGAGCTTGCACAA 129
Db 25 AsnSerSerThrLeuSerArgGluLeuLysGlnLeuMetGluLysGluLeuAlaSer 44
QY 130 ACCATCAAGATATCAAGATAAAGCTCTCATTGTAATATTTCCAAAGGCTTGATGCT 189
Db 45 PheLeuLysSerGlnLysAspProAlaValAspLysIleMetLysAspLeuAspAla 64
QY 190 AATCAAGATGAACAGGTCGACCTTTCAAGAAATTCATATCCCTGGTA 234
Db 65 AsnGlyAspGlyGluValAsnPhGluPheValSerLeuVal 79
RESULT 12

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S10P_HUMAN
ID S10P_HUMAN STANDARD; PRT; 95 AA.
AC P25815;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE S-100P protein.
GN Name=S100P; Synonyms=S100E;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=92339442; PubMed=1633809;
RA Becker T., Gerke V., Kube E., Weber K.;
RT "S100P, a novel Ca(2+)-binding protein from human placenta. cDNA
cloning, recombinant protein expression and Ca2+ binding properties.";
RL Eur. J. Biochem. 207:541-547(1992).
RN [2]
RP SEQUENCE FROM N.A.
RA Jin G., Wang S., Chen J.;
RT "Cloning, expression and characterization of a novel human calcium-
binding S100 gene.";
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan B., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stableton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.J., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP SEQUENCE OF 1-91.
RC TISSUE=Placenta;
RX MEDLINE=92171935; PubMed=1540168;
RA Emoto Y., Kobayashi R., Akatsuka H., Hidaka H.;
RT "Purification and characterization of a new member of the S-100
protein family from human placenta.";
RL Biochem. Biophys. Res. Commun. 182:1246-1253(1992).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX PubMed=12507480; DOI=10.1016/S0022-2836(02)01278-0;
RA Zhang H., Wang G., Ding Y., Wang Z., Barracough R., Rudland P.S.,
RA Fernig D.G., Rao Z.;
RT "The crystal structure at 2A resolution of the Ca2+ -binding protein
S100P.";
RL J. Mol. Biol. 325:785-794(2003).
CC -!- SUBUNIT: Homodimer. Interacts with S100Z.
CC -!- MISCELLANEOUS: This protein binds two calcium ions.
CC -!- SIMILARITY: Belongs to the S-100 family.
CC -!- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
CC
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DR EMBL; X65614; CAA46366.1; -;
DR EMBL; AF539739; AA041114.1; -;
DR EMBL; BC006819; AAH06819.1; -;
DR PIR; S24146; S24146.
DR PDB; 1J55; X-ray; Asl-95.
DR Genew; HGNC:10504; S100P.
DR H-InvDB; HIX0004067; -;
DR MIM; 600614; -;
DR GO; GO:0005509; F:calcium ion binding; TAS.
DR GO; GO:0005515; F:protein binding; TAS.
DR InterPro; IPR001751; CABP_S100.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR010983; EF_Hand_like.
DR Pfam; PF00036; ehand; 1.
DR Pfam; PF01023; S100; 1.
DR ProDom; PD003407; CABP_S100; 1.
DR PROSITE; PS00018; EF_HAND; FALSE_NEG.
DR PROSITE; PS00303; S100_CABP; 1.
KW 3D-structure; Calcium-binding; Direct protein sequencing; Placenta.
FT CA BIND 19 32 EF-hand 1; low affinity.
FT CA BIND 62 73 EF-hand 2; high affinity.
FT CONFLICT 32 32 E -> T (in Ref. 4).
FT CONFLICT 44 44 F -> E (in Ref. 4).
FT HELIX 3 18
FT TURN 19 20
FT TURN 25 26
FT STRAND 27 28
FT HELIX 30 40
FT TURN 42 43
FT HELIX 53 61
FT STRAND 69 70
FT HELIX 71 92
FT TURN 93 93
SQ SEQUENCE 95 AA; 10400 MW; 786E6E3F3EACC6C1 CRC64;

Alignment Scores:

Pred. No.: 5.35e-12 Length: 95
Score: 194.00 Matches: 41
Percent Similarity: 63.74% Conservative: 17
Best Local Similarity: 45.05% Mismatches: 33
Query Match: 40.67% Indels: 0
DB: 1 Gaps: 0

US-09-910-208B-12 (1-276) x S10P_HUMAN (1-95)

QY 1 ATGACAACTTGAGAGCATCTGGAGGAATTGTCATATCTTCCACCAATACTCAGTT 60
DB 1 MetThrGluLeuGluThrAlaMetGlyMetIleAspValPheSerArgTyrSerGly 20
QY 61 CGGAGGGGCGCATTTTGACACCTCTCTAAGGCTGAGCTGAAGCAGCTGCTTACAAGAGGAG 120
DB 21 SerGluGlySerThrGlnThrLeuThrLysGlyGluLeuLysValLeuMetGluLysGlu 40
QY 121 CTTCACAAACACCATCAAGAATATCAAGATAAAGCTGTCTATTGATGAATAATTCACAGGC 180
DB 41 LeuProGlyPheLeuGlnSerGlyLysAspLysAspAlaValAspLysLeuLysAsp 60
QY 181 CTGATGCTATCAAGATGAACAGCTCGACTTCAGATTCATTCAGATTCATTCCTGGTAGCCATT 240
DB 61 LeuAspAlaAsnGlyAspAlaGlnValAspPheSerGluPheIleValPheValAlaAla 80
QY 241 CGCTGAAGGCTGCCCATTTACACACCCACCAAAA 273
DB 81 IleThrSerAlaCysHisLysTyrPheGluLys 91

RESULT 13
QBAYJ2

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ID Q8AYJ2 PRELIMINARY; PRT; 99 AA.
AC Q8AYJ2;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE S-100 calcium-binding protein A1.
OS Squalus acanthias (Spiny dogfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squalia; Hymnosqualia; Squaliformes; Squaloidei;
OC Squalidae; Squalus.
OX NCBI_TaxID=7797;
RN [1]_TaxID=7797;
RP SEQUENCE FROM N.A.
RA Wang C., Callard G.V.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the S-100 family.
DR EMBL; AF421551; AAN63527.1; -.
DR HSP; P35467; IK2H.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR001751; CaBP_S100.
DR InterPro; IPR002048; EF_Hand.
DR InterPro; IPR010983; EF_Hand_like.
DR Pfam; PF00036; ehand; 1.
DR Pfam; PF01023; S100; 1.
DR ProDom; PD003407; CaBP_S100; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
DR PROSITE; PS00303; S100_CaBP; 1.
SQ SEQUENCE 99 AA; 11050 MW; BA62D8190A4A3693 CRC64;

Alignment Scores:
Pred. No.: 1,27e-11 Length: 99
Score: 190.50 Matches: 40
Percent Similarity: 69.41% Conservative: 19
Best Local Similarity: 47.06% Mismatches: 25
Query Match: 39.94% Indels: 1
DB: 2 Gaps: 1

US-09-910-208B-12 (1-276) x Q8AYJ2 (1-99)
QY 1 ATGACAAACTTGAAGAGCATCTGGAGGAATGTCAATATCTTCCACCAATACTCAGTT 60
Db 1 MetThrGluLeuGluSerAlaMetAlaGlyIleIleGlyValPheArgLysIleSergly 20
QY 61 CGGAGGGGCATTTTGACACCTCTCTAAGGCTGAGCTGAACGACGCTGCTTACAAAGGAG 120
Db 21 LysGluGlyAspLysTyrSerLeuSerAsnAenGluMetValAspLeuLeuLysAlaGlu 40
QY 121 CTTCGAAACACCATCAAGATATCAAGATAAAGCTGCTCATTTGATGAATATTTCCAAAGGC 180
Db 41 LeuProAsnPheLeuLysSerGlnLysAspLysAlaAlaValAspLysIleMetLysAsp 60
QY 181 CTGGATGCTAATCAAGATGAACAGGTCGACTTTCAGATTCATATCCCTGGTAGCCATT 240
Db 61 LeuAspArgAsnLysAspGlyGluLeuAspPheGlnGluPheValValleuIleAla--- 79
QY 241 GCGCTGAAGGCTGCC 255
Db 80 AlaLeuAlaAlaAla 84

RESULT 14
Q6YNR6 PRELIMINARY; PRT; 92 AA.
ID Q6YNR6;
AC Q6YNR6;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE S-100 calcium-binding protein beta subunit.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]_TaxID=9986;
RP SEQUENCE FROM N.A.

TISSUE=Cerebellum;
Qian Z., Barmack N.H.;
Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
-!- SIMILARITY: Belongs to the S-100 family.
EMBL; AY050568; AAL12231.1; -.
DR HSP; P04631; IB4C.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR001751; CaBP_S100.
DR InterPro; IPR002048; EF_Hand.
DR InterPro; IPR010983; EF_Hand_like.
DR Pfam; PF00036; ehand; 1.
DR Pfam; PF01023; S100; 1.
DR ProDom; PD003407; CaBP_S100; 1.
DR SMART; SM00054; EFb_1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
DR PROSITE; PS00303; S100_CaBP; 1.
SQ SEQUENCE 92 AA; 10713 MW; 43815AC212A3AD6B CRC64;

Alignment Scores:
Pred. No.: 1,85e-11 Length: 92
Score: 189.00 Matches: 34
Percent Similarity: 69.77% Conservative: 26
Best Local Similarity: 39.53% Mismatches: 26
Query Match: 39.62% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-12 (1-276) x Q6YNR6 (1-92)
QY 1 ATGACAAACTTGAAGAGCATCTGGAGGAATGTCAATATCTTCCACCAATACTCAGTT 60
Db 1 MetSerGluLeuGluLysAlaMetValAlaLeuIleAspValPheHisGlnTyrSerGly 20
QY 61 CGGAGGGGCATTTTGACACCTCTCTAAGGCTGAGCTGAAGCAGCTGCTTACAAAGGAG 120
Db 21 ArgGluGlyAspLysHisLysLysLysSerGluLeuLysGluLeuIleAsnAsnGlu 40
QY 121 CTTCGAAACACCATCAAGATATCAAGATAAAGCTGCTCATTTGATGAATATTTCCAAAGGC 180
Db 41 LeuSerHisPheLeuGluGluLeuLysGluGlnValValAspLysValMetGluThr 60
QY 181 CTGGATGCTAATCAAGATGAACAGGTCGACTTTCAGATTCATATCCCTGGTAGCCATT 240
Db 61 LeuAspAsnAspGlyAspGlyGluCysAspPheGlnGluPheMetAlaPheValAlaMet 80
QY 241 GCGCTGAAGGCTGCCCAT 258
Db 81 ValThrThrAlaCysHis 86

RESULT 15
Q925T3 PRELIMINARY; PRT; 92 AA.
ID Q925T3;
AC Q925T3;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE S100B.
OS Cricetus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetulus.
OX NCBI_TaxID=10029;
RN [1]_TaxID=10029;
RP SEQUENCE FROM N.A.
RA Kuse O., Yamakawa Y., Nishijima M.;
RT "Enhancement of transport-dependent decarboxylation of phosphatidylserine by S100B protein in permeabilized Chinese hamster ovary cells.";
RL J. Biol. Chem. 0:0-0(2001).
CC -!- SIMILARITY: Belongs to the S-100 family.
DR EMBL; AB056121; BAB43945.1; -.
DR HSP; P04631; IB4C.
DR GO; GO:0005737; Cytoplasm; ISS.
DR GO; GO:0005576; Extracellular; ISS.

```


DR GO: 0005509; F: calcium ion binding; ISS.
 DR GO: 0019210; F: kinase inhibitor activity; ISS.
 DR GO: 0042803; F: protein homodimerization activity; ISS.
 DR GO: 0048155; F: S100 alpha binding; ISS.
 DR GO: 0048154; F: S100 beta binding; ISS.
 DR GO: 0048156; F: tau protein binding; ISS.
 DR GO: 0008270; F: zinc ion binding; ISS.
 DR GO: 0048143; P: astrocyte activation; ISS.
 DR GO: 0007409; P: axonogenesis; ISS.
 DR GO: 0006874; P: calcium ion homeostasis; ISS.
 DR GO: 0006112; P: energy reserve metabolism; ISS.
 DR GO: 0048151; P: hyperphosphorylation; ISS.
 DR GO: 0008917; P: induction of apoptosis; ISS.
 DR GO: 0007611; P: learning and/or memory; ISS.
 DR GO: 0045917; P: positive regulation of complement activation; ISS.
 DR GO: 0042035; P: regulation of cytokine biosynthesis; ISS.
 DR GO: 0048169; P: regulation of long-term neuronal synaptic p. . .; ISS.
 DR Pfam: PF00016; ehand, 1.
 DR Pfam: PF01023; S100, 1.
 DR ProDom: PD003407; CaBP_S100; 1.
 DR PROSITE: PS00018; EF_HAND; UNKNOWN_1.
 DR PROSITE: PS00303; S100_CaBP; 1.
 SQ SEQUENCE 92 AA; 10749 MW; AF50107EC2BEDF6B CRC64;

Alignment Scores:

Pred. No.:	Score:	Length:	Matches:
1	189.00	92	35
Percent Similarity:	67.39%	Conservative:	27
Best Local Similarity:	38.04%	Mismatches:	30
Query Match:	39.62%	Indels:	0
DB:	2	Gaps:	0

US-09-910-208B-12 (1-276) x Q925T3 (1-92)

QY	1	ATGCAAAACTTGAAGAGCATCTGGAGGGAATTGTCAATATCTCCACCAATACTCAGTT	60
Db	1	MetSerGluLeuGluLysAlaMetValAlaLeuIleAspIlePheHisGlnTyrSerGly	20
QY	61	CGGAAGGGGCATTTTGACACCCCTCTTAAGGGTGAGCTGAAGCAGCTGCTTACAAAGGAG	120
Db	21	ArgGluGlyAspLysHisLysLeuLysLysSerGluLeuLysGluLeuIleAsnAsnGlu	40
QY	121	CTTGCAAAACCATCAAGAATATCAAGATAAAGCTGTCATTGATGAATATTCGAAGGC	180
Db	41	LeuSerHisPheLeuGluGluIleLysGluGlnGluValValAspLysValMetGluThr	60
QY	181	CTGGATGCTAATCAAGATGAAGCTCGACTTTCAGATTTCATATCCCTGGTAGCCATT	240
Db	61	LeuAspGluAspGlyAspGlyGluCysAspPheGlnGluPheMetAlaPheValSerMet	80
QY	241	GGCTGAAGGCTGCCCATTTACCACACCCCAAGAG	276
Db	81	ValThrAlaCysHisGluPheGluGlnGlu	92

Search completed: February 23, 2005, 12:12:58
 Job time : 118.5 secs

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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: February 23, 2005, 11:49:17; Search time 114 seconds

(without alignments)

1872.734 Million cell updates/sec

Title: US-09-910-208B-12

Perfect score: 477

Sequence: 1 atgacaaaactgaagagca.....attaccacacccacaagaag 276

Scoring table: BLOSUM62

Xgapop 10.0, Xgapext 0.5

Ygapop 10.0, Ygapext 0.5

Fgapop 6.0, Fgapext 7.0

Delop 6.0, Delext 7.0

Searched: 1105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 4211384

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp

-Q/cn2_1/USPTO spool_p/HADDAD-09-910208B/runat_23022005_101933_15284/app_query.fasta.1

-DB=A Genesep 16Dec04 -QMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPCL=0

-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi

-LIST=45 -DOALIGN=200 -THR SCORE=ptc -THR MAX=100 -THR MIN=0 -ALIGN=15

-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000

-USER=HADDAD-09-910208B @CGN 1.1.224 @runat_23022005_101933_15284 -NCPU=6

-ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG

-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6

-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A Genesep 16Dec04:*

1: Genesep1980s:*

2: Genesep1990s:*

3: Genesep2000s:*

4: Genesep2001s:*

5: Genesep2002s:*

6: Genesep2003as:*

7: Genesep2003bs:*

8: Genesep2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	468	98.1	92	AAW03564	Calcium b
2	468	98.1	92	AAW24137	Human che
3	468	98.1	92	AAW45542	Human S10
4	468	98.1	92	AAW31911	Amino aci
5	468	98.1	92	AAW31907	Amino aci
6	468	98.1	92	AAW31908	Amino aci
7	468	98.1	92	ADA93649	Human cal
8	468	98.1	92	ADN04192	Antipsori
9	468	98.1	92	ADN19540	Human PRO
10	468	98.1	92	ADR14333	Human NF-

11	468	98.1	92	ADP23921	PRO polyp
12	468	98.1	92	ADS74331	PRO polyp
13	463	97.1	91	AAW31909	Amino aci
14	442	92.7	95	ABG27582	Novel hum
15	332	69.6	91	AAW01826	Component
16	332	69.6	91	AAW93819	Angiotrop
17	319	66.9	92	AAW03563	Calcium b
18	309	64.8	90	AAW90765	Bovine CA
19	309	64.8	90	AAW90764	Bovine co
20	234	49.1	46	ABB43183	Peptide #
21	234	49.1	46	AAW37021	Peptide #
22	234	49.1	46	ABB26281	Protein #
23	234	49.1	46	AAW76914	Human bon
24	234	49.1	46	AAW64093	Human bra
25	234	49.1	46	ABG58579	Human liv
26	234	49.1	46	ABG46027	Human pep
27	224	47.0	363	ABG27581	Novel hum
28	214.5	45.0	114	AAW17062	Human mul
29	214.5	45.0	114	AAW60178	Human cal
30	214.5	45.0	114	AAW48615	Human bre
31	214.5	45.0	114	AAW87637	Human cal
32	214.5	45.0	114	AAW45539	Human S10
33	214.5	45.0	114	ABB44613	Human wou
34	214.5	45.0	114	AAW31905	Amino aci
35	214.5	45.0	114	ABB82712	Human MRP
36	214.5	45.0	114	ADB17567	Human mye
37	214.5	45.0	114	ADE57110	Human Pro
38	214.5	45.0	114	ADE34548	Human mig
39	214.5	45.0	114	ADP09358	Human cal
40	214.5	45.0	114	ADL83164	Human PRO
41	214.5	45.0	114	ADN03968	Antipsori
42	214.5	45.0	114	ADQ30562	Pancreas
43	214.5	45.0	114	ADR14329	Human NF-
44	214.5	45.0	114	ABW80144	Tumour-as
45	214.5	45.0	114	ADP23562	PRO polyp

ALIGNMENTS

RESULT 1

AAW03564

ID AAW03564 standard; protein; 92 AA.

XX

AC AAW03564;

DT 01-MAY-1997 (first entry)

XX

DE Calcium binding protein CAAFL1.

XX

KW Calcium binding protein; human; amniotic fluid; S100 protein family;
KW intracellular signal transduction; squamous epithelial cell; neutrophil;
KW macrophage; cancer; cancerous lesion; inflammation; neoplasia; cervix;
KW squamous cell carcinoma; skin; oesophagus; CAAFL1; lung; blood disease.

OS Homo sapiens.

XX

PN EP731166-A2.

XX

PD 11-SEP-1996.

XX

PF 04-DEC-1995; 95EP-00119045.

XX

PR 06-MAR-1995; 95JP-00045564.

XX

PR 06-MAR-1995; 95JP-00070468.

XX

PA (TOFU) TONEN CORP.

XX

PA (HITO/) HITOMI J.

XX

PI Hitomi J, Yamaguchi K, Yamamura T, Kimura T;

XX

DR WPI; 1996-403989/41.

XX

DR N-PSDB; AAT39346.

XX

PT New human or bovine calcium binding protein and related nucleic acid - is
 PT a marker for inflammation, neoplasia, skin and blood diseases.

XX
 PS Claim 1; Page 24; 36pp; English.

XX This sequence represents the CAAFI calcium-binding protein isolated from
 CC human amniotic fluid. CAAFI belongs to the S100 protein family, which
 CC includes calyculin, MRP8, and MRP14. Intracellular calcium ion
 CC concentration is one of the key factors for intracellular signal
 CC transduction. The calcium signals are transduced by various calcium-
 CC binding proteins, such as this protein. CAAFI is normally expressed in
 CC squamous epithelial cells, neutrophils and macrophages, but atypical
 CC epithelial cells are negative for CAAFI and overexpression is observed in
 CC several types of cancer cells and neutrophils/macrophages infiltrating
 CC cancerous lesions. Detection of CAAFI (using antibodies in usual
 CC immunosays) can be used to diagnose (or monitor) inflammation,
 CC neoplasia (particularly squamous cell carcinoma of the skin, oesophagus,
 CC lung and cervix), and skin and blood diseases

XX Sequence 92 AA;

Alignment Scores:
 Pred. No.: 4,066-49 Length: 92
 Score: 468.00 Matches: 92
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 98.11% Indels: 0
 DB: 2 Gaps: 0

US-09-910-208B-12 (1-276) x AAW03564 (1-92)

QY 1 ATGCAAACTTGAAGAGCATCTGGAGGAATTGTCAATATCTTCCACCAATCTCAGTT 60
 Db 1 MetThrLysLeuGluGluHisLeuGluGlyLeuValAsnIlePheHisGlnTyrSerVal 20
 QY 61 CGGAAGGGGCATTTTGACACCCCTCTTAAGGGTGAGCTCAAGCAGCTGCTTACAAAGGAG 120
 Db 21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuThrLysGlu 40
 QY 121 CTTCGAAACACCATCAAGATATCAAGATAAAGCTGTCATGTGATGAATATTCGAAGGC 180
 Db 41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60
 QY 181 CTGGATGCTAATCAAGATGAACAGCTCGACTTTCAAGAATTCATATCCCTGGTAGCCATT 240
 Db 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80
 QY 241 GCGCTGAAGGTCGCCATTACACACCCACCAAGAG 276
 Db 81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92

RESULT 2

AAW24137

ID AAW24137 standard; protein; 92 AA.

XX

XX AAW24137;

XX AC

XX 28-JAN-1998 (first entry)

XX Human chemotactic cytokine I.

XX Chemotactic cytokine; tumour; autoimmune disease; antagonist; agonist.

XX Homo sapiens.

XX OS

XX PN W09723640-A1.

XX XX

XX 03-JUL-1997.

XX XX

XX 26-DEC-1995; 95WO-US016871.

XX XX

XX 26-DEC-1995; 95WO-US016871.

XX XX

XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX Ni J, Yu G, Alfonso P, Gentz R, Su JY;

XX WPI; 1997-351075/32.

DR N-PSDB; AAT85774.

XX DNA encoding chemotactic cytokine I - used to treat, e.g. tumours,

XX chronic infection, leukaemia, etc.

XX Claim 12; Page 48-49; 64pp; English.

XX This is a human chemotactic cytokine I polypeptide. The encoding
 CC polynucleotide, along with a vector and a host cell can be used for the
 CC recombinant production of the chemotactic cytokine. Cytokine agonists and
 CC antagonists can be used for the treatment of a patient requiring a
 CC chemotactic cytokine I and for the treatment of a patient requiring the
 CC inhibition of a chemotactic cytokine I polypeptide, respectively. The
 CC chemotactic cytokine is used to treat tumours, chronic infection,
 CC leukaemia and T-cell mediated autoimmune diseases

XX Sequence 92 AA;

Alignment Scores:
 Pred. No.: 4,066-49 Length: 92
 Score: 468.00 Matches: 92
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 98.11% Indels: 0
 DB: 2 Gaps: 0

US-09-910-208B-12 (1-276) x AAW24137 (1-92)

QY 1 ATGCAAACTTGAAGAGCATCTGGAGGAATTGTCAATATCTTCCACCAATCTCAGTT 60
 Db 1 MetThrLysLeuGluGluHisLeuGluGlyLeuValAsnIlePheHisGlnTyrSerVal 20
 QY 61 CGGAAGGGGCATTTTGACACCCCTCTTAAGGGTGAGCTCAAGCAGCTGCTTACAAAGGAG 120
 Db 21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuThrLysGlu 40
 QY 121 CTTCGAAACACCATCAAGATATCAAGATAAAGCTGTCATGTGATGAATATTCGAAGGC 180
 Db 41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60
 QY 181 CTGGATGCTAATCAAGATGAACAGCTCGACTTTCAAGAATTCATATCCCTGGTAGCCATT 240
 Db 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80
 QY 241 GCGCTGAAGGTCGCCATTACACACCCACCAAGAG 276
 Db 81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92

RESULT 3

AAW45542

ID AAW45542 standard; protein; 92 AA.

XX

XX AAW45542;

XX AC

XX 22-FEB-2001 (first entry)

XX Human S100A12 protein.

XX S100 protein; human; treatment; cardiomyopathy; cardiac insufficiency;

XX calcium-binding protein; calcium homeostasis; cardiac muscle;

XX pumping capacity; myocardial cell; systolic calcium ion release;

XX sarcoplasmic reticulum; cardiac disease; hypertension; rhythm disorder;

XX valve defect.

XX Homo sapiens.

XX OS

XX PN DE19915485-A1.

XX XX

XX

PD 19-OCT-2000;
XX
XX
PF 07-APR-1999; 99DE-01015485.
XX
XX
PR 07-APR-1999; 99DE-01015485.
XX
XX
XX (KATU/) KATUS H A.
PA (REMP/) REMPPIS A.
XX
XX Katus HA, Remppis A;
XX
XX WPI; 2000-673510/66.
DR N-PSDB; AAC81812.
XX
XX Composition containing S100 protein, corresponding nucleic acid or
PT vector, useful for treating cardiomyopathy and cardiac insufficiency.
PT
PT
XX
XX Claim 35; Page 20; 36pp; German.
XX
XX This invention describes a novel composition for treating primary or
CC secondary cardiomyopathy or cardiac insufficiency contains at least one
CC S100 protein (I) or nucleic acid (II) encoding (I), or their mutants or
CC fragments, or a gene transfer vector containing (II), optionally
CC formulated with auxiliaries and/or carriers. (I) are calcium-binding
CC proteins involved in calcium homeostasis, so their overexpression in
CC cardiac muscle will improve pumping capacity (and overall capacity) of
CC the heart. In cultured myocardial cells they increase the contraction and
CC relaxation rates associated with increased systolic calcium ion release
CC from the sarcoplasmic reticulum (SR) and calcium re-uptake by SR. (I) are
CC used to treat cardiomyopathy (CMP) where inherited or caused by
CC spontaneous mutations and ischemic CMP caused by arteriosclerosis,
CC dilative CMP caused by toxic/infectious disease, cardiac disease caused
CC by pulmonary and/or arterial hypertension, and structural disease caused
CC by rhythm disorders or valve defects, generally any condition associated
CC with reduced contractile force. Unlike calmodulin, which is expressed
CC ubiquitously, (I) show tissue-specific expression and treat the
CC underlying defect in the sarcoplasmic reticulum (SR) that causes cardiac
CC disease
XX
XX Sequence 92 AA;
SQ
Alignment Scores:
Pred. No.: 4,06e-49 Length: 92
Score: 468.00 Matches: 92
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.11% Indels: 0
DB: 3 Gaps: 0
US-09-910-208B-12 (1-276) x AAB45542 (1-92)
QY 1 ATGACAAAACCTTGAAGAGCATCTGAGGGAATTGTCAATATCTTCCACCAATCTCAGTT 60
Db 1 MetThrLysLeuGluHisLeuGluGlyLeuValAsnIlePheHisGlnTyrSerVal 20
QY 61 CGGAAGGGGCATTGACACCCCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTACAAAGGAG 120
Db 21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGlu 40
QY 121 CTTGCAAAACCATCATCAAGATATCAAGATTAAGCTGCTCAATGATGAATATTCGAAGGC 180
Db 41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60
QY 181 CTGGATGCTAATCAAGATGAACAGGTCGACTTTCAGAGATTCATATCCCTGGTAGCCATT 240
Db 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80
QY 241 GCCTGAAGCTGCCCATTTACCAACCCACCAAGAG 276
Db 81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92
RESULT 4
AAB31911

ID AAB31911 standard; protein; 92 AA.
XX
XX AAB31911;
XX
XX 15-MAY-2001 (first entry)
XX
XX Amino acid sequence of a human protein.
XX
XX Human; perlecan; retinol-binding plasma protein; calgranulin B; vaccine;
KW ganglioside GM2 activator; saposin B; degenerative disease; glial cell;
KW neurological disease; auto-immune disease; multiple sclerosis; toxicity;
KW Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;
KW rheumatoid polyarthritis; lupus erythematosus; gene therapy.
XX
XX Homo sapiens.
XX
XX WO200105422-A2.
XX
XX 25-JAN-2001.
XX
XX 17-JUL-2000; 2000WO-FR002057.
XX
XX 15-JUL-1999; 99FR-00009372.
XX
XX (INNR) BIOMERIEUX STELHYS.
XX
XX Roecklin D, Kolbe H, Charles M, Malcus C, Santoro L, Perron H;
XX WPI; 2001-159475/16.
XX
XX Detecting, preventing and treating degenerative, neurological and
PT autoimmune diseases, particularly multiple sclerosis, using specified
PT polypeptides or related nucleic acid or ligand.
XX
XX Claim 1; Page 168; 209pp; French.
XX
XX The present sequence represents a human protein, which is used in the
CC method of the invention. The specification describes a method which uses
CC at least one polypeptide or polynucleotide sequence belonging to the
CC perlecan, precursor of the retinol-binding plasma protein, precursor of
CC the ganglioside GM2 activator, calgranulin B or saposin B protein
CC families. The method is used for detecting, preventing or treating a
CC degenerative, neurological and/or auto-immune disease. The
CC polynucleotides and polypeptides are used for diagnosis, prognosis,
CC prevention and treatment of multiple sclerosis (in its various forms and
CC phases). They may also be useful in cases of e.g. Alzheimer's and
CC Parkinson's diseases, amyotrophic lateral sclerosis, rheumatoid
CC polyarthritis and lupus erythematosus, including use as vaccines and in
CC gene therapy (expression of sense or antisense sequences). They can also
CC be used to assess efficacy of potential therapeutic agents, particularly
CC compounds that reduce or inhibit toxicity towards glial cells
XX
XX Sequence 92 AA;
SQ
Alignment Scores:
Pred. No.: 4,06e-49 Length: 92
Score: 468.00 Matches: 92
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.11% Indels: 0
DB: 4 Gaps: 0
US-09-910-208B-12 (1-276) x AAB31911 (1-92)
QY 1 ATGACAAAACCTTGAAGAGCATCTGAGGGAATTGTCAATATCTTCCACCAATCTCAGTT 60
Db 1 MetThrLysLeuGluHisLeuGluGlyLeuValAsnIlePheHisGlnTyrSerVal 20
QY 61 CGGAAGGGGCATTGACACCCCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTACAAAGGAG 120
Db 21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGlu 40
QY 121 CTTGCAAAACCATCATCAAGATATCAAGATTAAGCTGCTCAATGATGAATATTCGAAGGC 180
XX

```

DB      41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60
QY      181 CTGGATGCTTAATCAAGATGAACAGGTCGACTTTCAAGAATTTCATATCCCTGGTAGCCATT 240
DB      61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80
QY      241 GCGCTGAAGGCTGCCATTACACACCCACCAAGAG 276
DB      81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92

RESULT 5
AAB31907
ID  AAB31907 standard; protein; 92 AA.
AC  AAB31907;
XX
XX
DT  15-MAY-2001 (first entry)
XX
XX  Amino acid sequence of a human protein.
DE  Human; perlecan; retinol-binding plasma protein; calgranulin B; vaccine;
KW  ganglioside GM2 activator; saposin B; degenerative disease; glial cell;
KW  neurological disease; auto-immune disease; multiple sclerosis; toxicity;
KW  Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;
KW  rheumatoid polyarthritis; lupus erythematosus; gene therapy.
XX
XX  Homo sapiens.
XX
XX  WO200105422-A2.
XX
XX  25-JAN-2001.
XX
XX  17-JUL-2000; 2000WO-FR002057.
XX
XX  15-JUL-1999; 99FR-00009372.
XX
XX  (INNR ) BIOMERIEUX STELHYS.
XX
XX  Roecklin D, Kolbe H, Charles M, Malcus C, Santoro L, Perron H;
XX  WPI; 2001-159475/16.
XX
XX  Detecting, preventing and treating degenerative, neurological and
XX  autoimmune diseases, particularly multiple sclerosis, using specified
XX  polypeptides or related nucleic acid or ligand.
XX
XX  Claim 1; Page 166-167; 209pp; French.
XX
XX  The present sequence represents a human protein, which is used in the
XX  method of the invention. The specification describes a method which uses
XX  at least one polypeptide or polynucleotide sequence belonging to the
XX  perlecan, precursor of the retinol-binding plasma protein, precursor of
XX  the ganglioside GM2 activator, calgranulin B or saposin B protein
XX  families. The method is used for detecting, preventing or treating a
XX  degenerative, neurological and/or auto-immune disease. The
XX  polynucleotides and polypeptides are used for diagnosis, prognosis,
XX  prevention and treatment of multiple sclerosis (in its various forms and
XX  phases). They may also be useful in cases of e.g. Alzheimer's and
XX  Parkinson's diseases, amyotrophic lateral sclerosis, rheumatoid
XX  polyarthritis and lupus erythematosus, including use as vaccines and in
XX  gene therapy (expression of sense or antisense sequences). They can also
XX  be used to assess efficacy of potential therapeutic agents, particularly
XX  compounds that reduce or inhibit toxicity towards glial cells
XX
XX  SQ  Sequence 92 AA;

Alignment Scores:
Pred. No.: 4.06e-49 Length: 92
Score: 468.00 Matches: 92
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.11% Indels: 0

```

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DB:      4      Gaps:      0
US-09-910-208B-12 (1-276) x AAB31907 (1-92)
QY      1 ATGACAAAACCTGAAGAGCATCTGGAGGGAATTGTCAATATCTTCACCAATACTCAGTT 60
DB      1 MetThrLysLeuGluHisLeuGluGlyIleValAsnIlePheHisGlnTyrSerVal 20
QY      61 CGGAGGGGCGATTTTGACACCCCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTACAAAGGAG 120
DB      21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGlu 40
QY      121 CTTGCAACACCATCAAGATATCAAGATAAAGCTGTCTATTGATGAATATTTCCAAGGC 180
DB      41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60
QY      181 CTGGATGCTTAATCAAGATGAACAGGTCGACTTTCAAGAATTTCATATCCCTGGTAGCCATT 240
DB      61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80
QY      241 GCGCTGAAGGCTGCCATTACACACCCACCAAGAG 276
DB      81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92

RESULT 6
AAB31908
ID  AAB31908 standard; protein; 92 AA.
XX
XX  AAB31908;
XX
XX  15-MAY-2001 (first entry)
XX
XX  Amino acid sequence of a human protein.
XX
XX  Human; perlecan; retinol-binding plasma protein; calgranulin B; vaccine;
KW  ganglioside GM2 activator; saposin B; degenerative disease; glial cell;
KW  neurological disease; auto-immune disease; multiple sclerosis; toxicity;
KW  Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;
KW  rheumatoid polyarthritis; lupus erythematosus; gene therapy.
XX
XX  Homo sapiens.
XX
XX  WO200105422-A2.
XX
XX  25-JAN-2001.
XX
XX  17-JUL-2000; 2000WO-FR002057.
XX
XX  15-JUL-1999; 99FR-00009372.
XX
XX  (INNR ) BIOMERIEUX STELHYS.
XX
XX  Roecklin D, Kolbe H, Charles M, Malcus C, Santoro L, Perron H;
XX  WPI; 2001-159475/16.
XX
XX  Detecting, preventing and treating degenerative, neurological and
XX  autoimmune diseases, particularly multiple sclerosis, using specified
XX  polypeptides or related nucleic acid or ligand.
XX
XX  Claim 1; Page 167; 209pp; French.
XX
XX  The present sequence represents a human protein, which is used in the
XX  method of the invention. The specification describes a method which uses
XX  at least one polypeptide or polynucleotide sequence belonging to the
XX  perlecan, precursor of the retinol-binding plasma protein, precursor of
XX  the ganglioside GM2 activator, calgranulin B or saposin B protein
XX  families. The method is used for detecting, preventing or treating a
XX  degenerative, neurological and/or auto-immune disease. The
XX  polynucleotides and polypeptides are used for diagnosis, prognosis,
XX  prevention and treatment of multiple sclerosis (in its various forms and
XX  phases). They may also be useful in cases of e.g. Alzheimer's and
XX  Parkinson's diseases, amyotrophic lateral sclerosis, rheumatoid

```

CC polyarthritis and lupus erythematosus, including use as vaccines and in
CC gene therapy (expression of sense or antisense sequences). They can also
CC be used to assess efficacy of potential therapeutic agents, particularly
CC compounds that reduce or inhibit toxicity towards glial cells
XX
XX
SQ Sequence 92 AA;

Alignment Scores:
Pred. No.: 4,06e-49 Length: 92
Score: 468.00 Matches: 92
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.11% Indels: 0
DB: 4 Gaps: 0

US-09-910-208B-12 (1-276) x AAB31908 (1-92)

QY 1 ATGCAAACTTGAAGAGCATCTGGAGGAATTGTCAATATCTTCCACCAATCTCAGTT 60
Db 1 MetThrLysLeuGluGluHisLeuGluGlyIleValAsnIlePheHisGlnTyrSerVal 20
QY 61 CGGAAGGGGCATTTTGACACCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTACAAAGGAG 120
Db 21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGlu 40
QY 121 CTTGCAAAACCATCATCAAGAAATATCAAGATAAGCTGTTCATTGATCAATATTTCCAAGGC 180
Db 41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60
QY 181 CTGGATGCTTAATCAAGATCAACAGCTCGACTTTCAGAAATTCATATCCCTGTAGCCATT 240
Db 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80

QY 241 GCGCTGAAGGCTGCCATTACACACCCACAAAGAG 276
Db 81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92

RESULT 7
ADA93649
ID ADA93649 standard; protein; 92 AA.
XX
AC ADA93649;

XX 20-NOV-2003 (first entry)
XX Human calgranulin C protein SEQ ID NO:2.
XX inflammatory disease; calgranulin C; antiinflammatory; gene therapy;
KW vasculitis; Kawasaki disease; cystic fibrosis;
KW chronic inflammatory disease; ulcerative colitis; Crohn's disease;
KW chronic bronchitis; inflammatory arthritis; psoriatic arthritis;
KW rheumatoid arthritis; seronegative arthritis;
KW systemic onset juvenile rheumatoid arthritis; SORA; Still's disease;
KW acute inflammation; human.

XX Homo sapiens.
XX
XX WO2003069341-A2.
XX 21-AUG-2003.
XX 17-FEB-2003; 2003WO-EP001575.
XX 15-FEB-2002; 2002US-00077600.
XX (SWIT-) SWITCH BIOTECH AG.
PA (SORG/) SORG J.
PA (ROTH/) ROTH J.
XX Sorg C, Roth J;
XX WPI; 2003-671681/63.
DR N-PSDB; ADA93648.

XX Diagnosing, treating or preventing inflammatory diseases comprises
PT determining the amount and/or concentration of CALGRANULIN C polypeptide
PT and/or nucleic acids encoding the polypeptide present in a biological
PT sample.
XX
XX
PS Claim 7; Page 64; 64pp; English.

XX The present invention describes a method for diagnosing inflammatory
CC diseases, which comprises determining the amount and/or concentration of
CC calgranulin C polypeptide and/or nucleic acids encoding the polypeptide
CC present in the biological sample. Also described are methods for treating
CC or preventing an inflammatory disease in a mammal, and medical treatment
CC of the mammal, where the treatment is based on the stage of the disease
CC to be treated or prevented. Calgranulin C has antiinflammatory activity
CC and can be used in gene therapy. The method is useful for diagnosing,
CC treating or preventing inflammatory diseases, e.g. vasculitis
CC (particularly Kawasaki disease), cystic fibrosis, chronic inflammatory
CC diseases like ulcerative colitis or Crohn's disease, chronic bronchitis,
CC inflammatory arthritis (e.g. psoriatic arthritis, rheumatoid arthritis or
CC seronegative arthritis), systemic onset juvenile rheumatoid arthritis
CC (SORA or Still's disease), acute inflammation above the background of a
CC chronic inflammation, an acquired infection on the background of an
CC inflammatory disease, or an exacerbation of an already present disease.
CC The method is also useful for diagnosing specific stages of inflammatory
CC diseases, for determining the risk of relapse, and for discriminating
CC between diseases with similar symptoms. The present sequence represents
CC human calgranulin C, which is used in the exemplification of the present
CC invention.

XX Sequence 92 AA;

Alignment Scores:
Pred. No.: 4,06e-49 Length: 92
Score: 468.00 Matches: 92
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.11% Indels: 0
DB: 7 Gaps: 0

US-09-910-208B-12 (1-276) x ADA93649 (1-92)

QY 1 ATGCAAACTTGAAGAGCATCTGGAGGAATTGTCAATATCTTCCACCAATCTCAGTT 60
Db 1 MetThrLysLeuGluGluHisLeuGluGlyIleValAsnIlePheHisGlnTyrSerVal 20
QY 61 CGGAAGGGGCATTTTGACACCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTACAAAGGAG 120
Db 21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGlu 40
QY 121 CTTGCAAAACCATCATCAAGAAATATCAAGATAAGCTGTTCATTGATCAATATTTCCAAGGC 180
Db 41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60
QY 181 CTGGATGCTTAATCAAGATCAACAGCTCGACTTTCAGAAATTCATATCCCTGTAGCCATT 240
Db 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80
QY 241 GCGCTGAAGGCTGCCATTACACACCCACAAAGAG 276
Db 81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92

RESULT 8
ADN04192
ID ADN04192 standard; protein; 92 AA.
XX
AC ADN04192;
XX
DT 01-JUL-2004 (first entry)
XX
DE Antipsoriatic protein sequence #291.
XX
KW antipsoriatic; gene therapy; psoriasis; diagnosis.

XX Homo sapiens.
 XX WO2004028479-A2.
 XX 08-APR-2004.
 XX 25-SEP-2003; 2003WO-US030907.
 XX 25-SEP-2002; 2002US-0414006P.
 XX (GETH) GENENTECH INC.
 XX Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;
 XX Wu TD;
 XX WPI; 2004-305105/28.
 XX DR N-PSDB; ADN04191.
 XX New PRO nucleic acid or polypeptide, useful for preparing a
 PT pharmaceutical composition for diagnosing or treating psoriasis in a
 PT mammal.
 XX Claim 9; SEQ ID NO 586; 3069pp; English.
 XX The invention relates to novel polynucleotide and polypeptides for
 CC treating psoriasis or a sequence having at least 80% identity to the
 CC above sequences. The nucleic acid is useful for preparing a composition
 CC for diagnosing or treating psoriasis in a mammal. This sequence
 CC corresponds to one of the polypeptides of the invention.
 XX Sequence 92 AA;
 SQ
 Alignment Scores:
 Pred. No.: 4,06e-49 Length: 92
 Score: 468.00 Matches: 92
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 98.11% Indels: 0
 DB: 8 Gaps: 0
 US-09-910-208B-12 (1-276) x ADN04192 (1-92)
 QY 1 ATGCAAACTTGAAGAGCATCTGAGGGAATGTCAATATCTCCACCAATCTCAGTT 60
 Db 1 MetThrLysLeuGluGluHisLeuGluGlyIleValAsnIlePheHisGlnTyrSerVal 20
 QY 61 CGGAAGGGGCATTTTGACACCCCTCTTAAGGTGAGCTGAAGCAGCTCTTACAAAGAG 120
 Db 21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuThrLysGlu 40
 QY 121 CTTGCAACACCATCAAGAATATCAAGATAAGCTGTCATGTGAATATTCGAAGGC 180
 Db 41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60
 QY 181 CTGGATGCTAATCAAGATGAACAGCTCGACITTTCAAGATTTCATATCCCTGTAGCCATT 240
 Db 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80
 QY 241 GCGTGAAGGCTGCCCATTTACACACCCACCAAGAG 276
 Db 81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92
 RESULT 9
 ID ADO19540
 AC ADO19540 standard; protein; 92 AA.
 XX
 XX ADO19540;
 AC
 XX 12-AUG-2004 (first entry)
 DT
 XX Human PRO polypeptide #235.
 DE
 XX

KW Human; PRO; immune related disorder; systemic lupus erythematosus;
 KW rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis;
 KW systemic sclerosis; Sjogren's syndrome; vasculitis; sarcoidosis;
 KW autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis;
 KW diabetes mellitus; renal disease; demyelinating disease;
 KW central nervous system; peripheral nervous system;
 KW demyelinating polyneuropathy; Guillain-Barre syndrome;
 KW chronic inflammatory demyelinating polyneuropathy.
 XX Homo sapiens.
 XX WO2004043361-A2.
 XX 27-MAY-2004.
 XX 06-NOV-2003; 2003WO-US035268.
 XX 08-NOV-2002; 2002US-0425235P.
 XX (GETH) GENENTECH INC.
 XX Fong S, Dennis K, Clark H, Chiu H, Schoenfeld J, Williams PM;
 XX Wood WI, Wu TD;
 XX WPI; 2004-420067/39.
 XX DR N-PSDB; ADO19539.
 XX Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO86388 useful for
 PT treating an immune related disorder such as systemic lupus erythematosus,
 PT rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or
 PT spondyloarthritis.
 XX Claim 7; SEQ ID NO 470; 1731pp; English.
 XX The invention relates to human PRO polypeptides and the polynucleotides
 CC encoding them. The polypeptides and polynucleotides are useful for
 CC treating and diagnosing immune related disorders in mammals. The immune
 CC related disorders include systemic lupus erythematosus, rheumatoid
 CC arthritis, osteoarthritis, juvenile chronic arthritis, systemic
 CC sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune
 CC haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes
 CC mellitus, immune-mediated renal disease, demyelinating diseases of the
 CC central or peripheral nervous system, demyelinating polyneuropathy,
 CC Guillain-Barre syndrome and chronic inflammatory demyelinating
 CC polyneuropathy. This sequence represents a human PRO polypeptide of the
 CC invention.
 XX Sequence 92 AA;
 SQ
 Alignment Scores:
 Pred. No.: 4,06e-49 Length: 92
 Score: 468.00 Matches: 92
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 98.11% Indels: 0
 DB: 8 Gaps: 0
 US-09-910-208B-12 (1-276) x ADO19540 (1-92)
 QY 1 ATGCAAACTTGAAGAGCATCTGAGGGAATGTCAATATCTTCCACCAATCTCAGTT 60
 Db 1 MetThrLysLeuGluGluHisLeuGluGlyIleValAsnIlePheHisGlnTyrSerVal 20
 QY 61 CGGAAGGGGCATTTTGACACCCCTCTTAAGGTGAGCTGAAGCAGCTCTTACAAAGAG 120
 Db 21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuThrLysGlu 40
 QY 121 CTTGCAACACCATCAAGAATATCAAGATAAGCTGTCATGTGAATATTCGAAGGC 180
 Db 41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60
 QY 181 CTGGATGCTAATCAAGATGAACAGCTCGACITTTCAAGATTTCATATCCCTGTAGCCATT 240

Db 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80
 QY 241 GCGCTGAAGCGTCCCATTTACACACACCCACAAAGAG 276
 Db 81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92

RESULT 10
 ADP23921
 ID ADP23921 standard; protein; 92 AA.
 AC ADP23921;
 XX
 DT 21-OCT-2004 (first entry)
 DE Human NF-kappaB pathway-associated protein SeqID334.

KW NF-kappaB pathway; antiinflammatory; cytostatic; hepatotropic; virucide;
 KW antiarthritic; antirheumatic; gastrointestinal-Gen; antiasthmatic;
 KW antiarteriosclerotic; immunomodulator; cerebroprotective; vasotropic;
 KW immunosuppressive; vulnery; gene therapy; immune disorder;
 KW inflammatory disorder; NF-kappaB regulation; cancer; aberrant apoptosis;
 KW hepatic disorder; Hodgkin's lymphoma; haematopoietic tumour;
 KW hyper-IgM syndrome; hypohidrotic ectodermal dysplasia;
 KW X-linked anhidrotic ectodermal dysplasia; immunodeficiency;
 KW viral infection; HIV-1; HTLV-1; hepatitis B; hepatitis C; EBV; influenza;
 KW viral replication; host cell survival; evasion of immune response;
 KW rheumatoid arthritis; inflammatory bowel disease; colitis; asthma;
 KW atherosclerosis; cachexia; euthyroid sick syndrome; stroke; EAE;
 KW autoimmune disorder; hyper immune activity;
 KW aberrant acute phase response; hypercongenital condition; birth defect;
 KW necrotic lesion; wound; organ transplant rejection;
 KW aberrant signal transduction; proliferating disorder; cancer;
 KW HIV propagation; human.

OS Homo sapiens.
 XX
 PN WO2004065577-A2.
 XX
 XX 05-AUG-2004.
 XX
 XX 13-JAN-2004; 2004WO-US000798.
 XX
 XX 14-JAN-2003; 2003US-0440068P.
 PR 12-MAY-2003; 2003US-0469757P.
 XX
 XX (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX
 XX Nadler SG, Neubauer MG, Feder JN, Carman J;
 PI WPI; 2004-562168/54.
 DR N-PSDB; ADP23921.
 DR
 XX
 XX New isolated polynucleotides and polypeptides associated with NF-kappaB
 PT pathway, useful for diagnosing, treating, or preventing disorders or
 PT diseases associated with NF-kappaB pathway.
 XX
 XX Claim 6; SEQ ID NO 334; 237pp; English.
 XX
 XX This invention relates to the novel association of protein sequences (and
 CC the genes which encode them) to the NF-kappaB pathway. The invention may
 CC be useful for the production of compounds with an antiinflammatory,
 CC cytostatic, hepatotropic, virucide, antiarthritic, antirheumatic,
 CC gastrointestinal-Gen, antiasthmatic, antiarteriosclerotic,
 CC immunomodulator, cerebroprotective, vasotropic, immunosuppressive or
 CC vulnery activity or for gene therapy. The proteins and nucleotides are
 CC useful for diagnosing, preventing, treating, or ameliorating conditions
 CC or diseases associated with the NF-kappaB pathway. The condition is an
 CC immune disorder, an inflammatory disorder, an inflammatory disorder
 CC related to aberrant NF-kappaB regulation, cancer, aberrant apoptosis,
 CC hepatic disorders, Hodgkin's lymphoma, haematopoietic tumours, hyper-IgM
 CC syndromes, hypohidrotic ectodermal dysplasia, X-linked anhidrotic
 CC ectodermal dysplasia, immunodeficiency, viral infections, HIV-1, HTLV-1,
 CC hepatitis B, hepatitis C, EBV, influenza, viral replication, host cell

CC survival, evasion of immune responses, rheumatoid arthritis, inflammatory
 CC bowel disease, colitis, asthma, atherosclerosis, cachexia, euthyroid sick
 CC syndrome, stroke, EAE, autoimmune disorders, disorders related to hyper
 CC immune activity, disorders related to aberrant acute phase responses,
 CC hypercongenital conditions, birth defects, necrotic lesions, wounds,
 CC organ transplant rejection, conditions related to organ transplant
 CC rejection, disorders related to aberrant signal transduction,
 CC proliferating disorders, cancers and HIV propagation in cells infected
 CC with other viruses. The present sequence is that of a human protein which
 CC is subject to the novel association with the NF-kappaB pathway of the
 CC invention. Note: This sequence does not appear in the specification but
 CC was obtained by the indexer from Genbank.

XX
 SQ Sequence 92 AA;
 Alignment Scores:
 Pred. No.: 4,068-49 Length: 92
 Score: 468.00 Matches: 92
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 98.11% Indels: 0
 DB: 8 Gaps: 0

US-09-910-208B-12 (1-276) x ADP23921 (1-92)

QY 1 ATGCAAACTTGAAGAGCATCTGGAGGGAATTGTCAATATCTTCCACCAATCTCAGTT 60
 Db 1 MetThrLysLeuGluGluHisLeuGluGlyLeuValAsnIlePheHisGlnTyrSerVal 20
 QY 61 CGAAGGGGCGATTTTGACACCCCTCTTAAGGGTGAGTGAAGCAGCTGCTTACAAAGGAG 120
 Db 21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGlu 40
 QY 121 CTTCGCAACACCATCAAGATATCAAGATTAAGCTGTCTATTGATGAATATCCAGGC 180
 Db 41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheSerLeuValAlaIle 80
 QY 181 CTGGATGCTTAATCAAGATGAACAGCTCGACCTTTCAAGATTCATATCCCTGGTAGCCATT 240
 Db 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80
 QY 241 GCGCTGAAGCGTCCCATTTACACACACCCACAAAGAG 276
 Db 81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92

RESULT 11
 ADP23921
 ID ADP23921 standard; protein; 92 AA.
 AC ADP23921;
 XX
 DT 18-NOV-2004 (first entry)
 DE PRO polypeptide SEQ ID NO:1099.
 XX
 KW PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive;
 KW osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic;
 KW antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.
 XX
 OS Unidentified.
 XX
 PN WO2004041170-A2.
 XX
 PD 21-MAY-2004.
 XX
 XX 30-OCT-2003; 2003WO-US034312.
 PF
 PR 01-NOV-2002; 2002US-0423394P.
 XX
 XX (GETH) GENENTECH INC.
 PA
 XX Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI;
 PI Wu TD;

XX WPI; 2004-419628/39.
 DR N-PSDB; ADP23920.
 XX
 XX New PRO polypeptides and polynucleotides, useful for treating e.g.
 PT erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated
 PT renal disease, or demyelinating diseases of the central or peripheral
 PT nervous system.
 XX
 PS Claim 7; SEQ ID NO 1099; 2940pp; English.
 XX
 XX The invention relates to a novel isolated nucleic acid and the PRO
 CC polypeptide encoded by it. A protein of the invention has
 CC antiinflammatory, antiarthritic, antirheumatic, immunosuppressive,
 CC osteoprotective, antidiabetic, dermatological, antipsoriatic, antiallergic,
 CC antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide
 CC of the invention may have a use in gene therapy. The PRO polypeptide, its
 CC agonist, antagonist, or antibody that specifically binds to the
 CC polypeptide is useful for treating an immune related disorder such as
 CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
 CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
 CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
 CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
 CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
 CC disease, a demyelinating disease of the central or peripheral nervous
 CC system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,
 CC a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary
 CC disease, infectious or autoimmune chronic active hepatitis, primary
 CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
 CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
 CC disease, an autoimmune or immune-mediated skin disease, a bullous skin
 CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
 CC disease, asthma, allergic rhinitis, atopic dermatitis, food
 CC hypersensitivity, urticaria, an immunologic disease of the lung,
 CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
 CC pneumonitis, a transplantation associated disease, graft rejection or
 CC graft-versus-host disease. The present sequence represents a PRO protein
 CC of the invention.
 XX
 SQ Sequence 92 AA;
 Alignment Scores:
 Pred. No.: 4,06e-49 Length: 92
 Score: 468.00 Matches: 92
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 98.11% Indels: 0
 DB: 8 Gaps: 0
 US-09-910-208B-12 (1-276) x ADP23921 (1-92)
 QY 1 ATGACAAACTTGAAGACATCTGGAGGGAATTTGCAATATCTTCCACCAATACTCAGTT 60
 Db 1 MetThrLysLeuGluGluHisLeuGluGlyIleValAsnIlePheHisGlnTyrSerVal 20
 QY 61 CGAAGGGGCAATTTTCACACCTCTCTAAGGGTGAGCTCAAGCAGCTGCTTCAAGAGGAG 120
 Db 21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGlu 40
 QY 121 CTTGCAAAACACCATCAAGATATCAAGATAAAGCTGTTCATTGATGAATATTCACAGGC 180
 Db 41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60
 QY 181 CTGGATGCTATCAAGATGACAGCTCGACTTTCAGAAATTCATATCCCTGGTAGCCATT 240
 Db 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80
 QY 241 GCCTGAAGCTGCCATTACCAACACCAACAGAG 276
 Db 81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92

RESULT 12
 ADS74331

ID XX ADS74331 standard; protein; 92 AA.
 XX AC ADS74331;
 XX
 DT 16-DEC-2004 (first entry)
 DE PRO polypeptide PRO62943, role in immune-related disease.
 XX PRO62943; rheumatoid arthritis; psoriasis; antirheumatic; antiarthritic;
 KW antipsoriatic; gene therapy.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 4..47
 FT /note= "S-100/ICaBP type calcium binding domain"
 FT Region 60..65
 FT /note= "N-myristoylation site"
 XX
 XX WO2004081199-A2.
 XX
 XX 23-SEP-2004.
 XX
 XX 10-MAR-2004; 2004WO-US007862.
 XX
 XX 11-MAR-2003; 2003US-0454025P.
 XX
 XX (GSETH) GENENTECH INC.
 XX
 XX Baldwin D, Bodary S, Clark H, Fong S, Gurney AL, Williams PM;
 WPI; 2004-668955/65.
 DR N-PSDB; ADS74330.
 XX
 XX New nucleic acid encoding PRO polypeptide, useful for diagnosing and
 PT treating psoriasis, Crohn's disease, Ulcerative Colitis, or rheumatoid
 PT arthritis.
 XX
 XX Claim 9; SEQ ID NO 50; 166pp; English.
 XX
 CC The present sequence is the protein sequence of novel human PRO
 CC polypeptide PRO62943. The invention provides newly identified and
 CC isolated nucleotide sequences encoding polypeptides referred to as PRO
 CC polypeptides that are useful in the diagnosis and treatment of immune-
 CC related diseases. Microarray analysis showed that expression of PRO62943
 CC is up-regulated 4-fold in lesional skin as compared to non-lesional skin
 CC from psoriasis patients and up-regulated 2-fold in white blood cells from
 CC rheumatoid arthritis patients as compared to those from healthy donors.
 CC It is also down-regulated 2-fold upon activation of CD4 T cells with CD28
 CC or ICAM, down-regulated 6-fold upon differentiation of monocytes into
 CC macrophages after 7 days in differentiation media and up-regulated 4-fold
 CC upon activation of monocytes with LPS. PRO62943 can be used in a claimed
 CC method of identifying a compound that inhibits expression of the gene
 CC encoding it. The candidate compound is especially an antisense nucleic
 CC acid. The PRO polypeptide can be obtained by recombinant expression,
 CC especially in CHO, Escherichia coli or yeast host cells. The polypeptide,
 CC its antagonist or an antibody that binds the polypeptide are used in
 CC claimed methods for the alleviation or diagnosis of rheumatoid arthritis
 CC and psoriasis.
 XX
 SQ Sequence 92 AA;
 Alignment Scores:
 Pred. No.: 4,06e-49 Length: 92
 Score: 468.00 Matches: 92
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 98.11% Indels: 0
 DB: 8 Gaps: 0
 US-09-910-208B-12 (1-276) x ADS74331 (1-92)
 QY 1 ATGACAAACTTGAAGACATCTGGAGGGAATTTGCAATATCTTCCACCAATACTCAGTT 60

Db 1 MetThrLysLeuGluGluHisLeuGluGluGluValAsnIlePheHisGlnTyrSerVal 20
QY 61 CGGAAGGGGCATTTCACACCCCTCTTAAGGGTGAGCTGAAGCAGCTGCTTCAAGAGGAG 120
Db 21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGlu 40
QY 121 CTTGCAACACCATCAAGAAATATCAAGATAAAGCTGCTCATTCATGAATATTCACAGGC 180
Db 41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60
QY 181 CTGGATCTAATCAAGATCAAGAGCTGAGCTTTCAGAAATTCATATCCCTGCTAGCATT 240
Db 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80
QY 241 GCGCTGAAGGCTGCCCATTCACACACCCACAAAGAG 276
Db 81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92

RESULT 13

AAB31909
ID AAB31909 standard; protein; 91 AA.

XX AC AAB31909;

XX DT 15-MAY-2001 (first entry)

XX DE Amino acid sequence of a human protein.

XX KW Human; perlecan; retinol-binding plasma protein; calgranulin B; vaccine;
XX KW ganglioside GM2 activator; saposin B; degenerative disease; glial cell;
XX KW neurological disease; auto-immune disease; multiple sclerosis; toxicity;
XX KW Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;
XX KW rheumatoid polyarthritis; lupus erythematosus; gene therapy.

XX OS Homo sapiens.

XX PN WO200105422-A2.

XX PD 25-JAN-2001.

XX PF 17-JUL-2000; 2000WO-FR002057.

XX PR 15-JUL-1999; 99PR-00009372.

XX PA (INMR) BIOMERIEUX STELHYS.

XX PI Roeklin D, Kolbe H, Charles M, Malcus C, Santoro L, Perron H;

XX DR WPI; 2001-159475/16.

XX PT Detecting, preventing and treating degenerative, neurological and
XX PT autoimmune diseases, particularly multiple sclerosis, using specified
XX PT polypeptides or related nucleic acid or ligand.

XX PS Claim 1; Page 167; 209pp; French.

XX CC The present sequence represents a human protein, which is used in the
XX CC method of the invention. The specification describes a method which uses
XX CC at least one polypeptide or polynucleotide sequence belonging to the
XX CC perlecan, precursor of the retinol-binding plasma protein, precursor of
XX CC the ganglioside GM2 activator, calgranulin B or saposin B protein
XX CC families. The method is used for detecting, preventing or treating a
XX CC degenerative, neurological and/or auto-immune disease. The
XX CC polynucleotides and polypeptides are used for diagnosis, prognosis,
XX CC prevention and treatment of multiple sclerosis (in its various forms and
XX CC phases). They may also be useful in cases of e.g. Alzheimer's and
XX CC Parkinson's diseases, amyotrophic lateral sclerosis, rheumatoid
XX CC polyarthritis and lupus erythematosus, including use as vaccines and in
XX CC gene therapy (expression of sense or antisense sequences). They can also
XX CC be used to assess efficacy of potential therapeutic agents, particularly
XX CC compounds that reduce or inhibit toxicity towards glial cells

SQ Sequence 91 AA;

Alignment Scores:

Pred. No.: 1-7e-48 Length: 91
Score: 463.00 Matches: 91
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 97.06% Indels: 0
DB: 4 Gaps: 0

US-09-910-208B-12 (1-276) x AAB31909 (1-91)

QY 4 ACAAACTTGAAGACATCTGAGGGAATGTCAATATCTTCCACCAATACTCAGTTCG 63
Db 1 ThrLysLeuGluGluHisLeuGluGluGluValAsnIlePheHisGlnTyrSerVal 20
QY 64 AAGGGGCAATTTGACACCCCTCTTAAGGGTGAGCTGAAGCAGCTGCTTCAAGAGGCTT 123
Db 21 LysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGluLeu 40
QY 124 GCAAAACACCATCAAGAAATATCAAGATAAAGCTGTGCTATGATGAATATTTCCAAGCCCTG 183
Db 41 AlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGlyLeu 60
QY 184 GATGCTAATCAAGATGAACAGCTGCTTTCAGAAATTCATATCCCTGCTAGCATTGCG 243
Db 61 AspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIleAla 80
QY 244 CTGAAGGCTGCCCATTCACACACCCACAAAGAG 276

RESULT 14

ABG27582

ID ABG27582 standard; protein; 95 AA.

XX AC ABG27582;

XX DT 18-FEB-2002 (first entry)

XX DE Novel human diagnostic protein #27573.

XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX KW food supplement; medical imaging; diagnostic; genetic disorder.

XX OS Homo sapiens.

XX PN WO200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US008631.

XX PR 31-MAR-2000; 2000US-00540217.

XX PR 23-AUG-2000; 2000US-00649167.

XX PA (HYSE-) HYSEQ INC.

XX PI Drmanac RT, Liu C, Tang YT;

XX DR WPI; 2001-639362/73.

XX DR N-PSDB; AAS91769.

XX PT New isolated polynucleotide and encoded polypeptides, useful in
XX PT diagnostics, forensics, gene mapping, identification of mutations
XX PT responsible for genetic disorders or other traits and to assess
XX PT biodiversity.

XX PS Claim 20; SEQ ID NO 57941; 103pp; English.

XX CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
XX CC sequences. (I) is useful as hybridisation probes, polymerase chain
XX CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,

CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX

SQ Sequence 95 AA;

Alignment Scores: 7.07e-46 Length: 95
 Pred. No.: 442.00 Matches: 89
 Score: 96.74% Conservative: 0
 Percent Similarity: 96.74% Mismatches: 3
 Best Local Similarity: 92.66% Indels: 0
 Query Match: 4 Gaps: 0
 DB:

US-09-910-208B-12 (1-276) x ABG27582 (1-95)

QY 1 ATGACAAACTTGAAGGACATCTGAGGGAATGTCAATATCTCCACCAATCTCAGTT 60
 Db 4 MetThrLysLeuGluHisLeuGluGlyIleValAsnIleSerProGln***SerVal 23
 QY 61 CGGAAGGGGCAATTTGACACCCCTCTCTAAGGGTGAGCTGAACGACTGCTTACAAAGGAG 120
 Db 24 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuThrLysGlu 43
 QY 121 CTTCGAAACACCATCAAGATATCAAGATAAGCTGTCATTGATGAATATTTCCAAAGGC 180
 Db 44 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 63
 QY 181 CTGGATGCTAATCAAGATGAACAGTTCGACTTTTCAAGAAATTCATATCCCTGTAGCCATT 240
 Db 64 LeuaspAlaAsnGlnaspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 83
 QY 241 GCCTGAAGCTGCCATTACCAACACCCACCAAGAG 276
 Db 84 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 95

RESULT 15

AAW01826
 ID AAW01826 standard; protein; 91 AA.

AC AAW01826;

DT 16-OCT-1997 (first entry)

XX Component of bioactive metal RNA polypeptide.

XX Bioactive; metal; RNA polypeptide; RNP; modulation; analysis;
 KW angiogenesis; vascular state; mammalian tissue; transfer; cell;
 KW genetic information; selective; alteration; nucleic acid content;
 KW leukocyte; pig; monocyto-CURNP.

OS Sus scrofa.

XX DE19628895-A1.

XX 23-JAN-1997.

XX 17-JUL-1996; 96DE-01028895.

XX 17-JUL-1995; 95DE-01025992.
 PR 18-AUG-1995; 95DE-01030500.
 XX
 XX (FRAU) FRAUNHOFER GES FOERDERUNG ANGEWANDTEN.
 PA
 XX Wissler JH, Logemann E, Kieseewetter S, Heilmeyer IMG;
 PI WPI; 1997-088586/09.
 XX N-PSDB; AA762369.
 DR
 DR Bioactive metal RNA polypeptide - useful for modulating angiogenesis,
 PT etc.
 PT
 XX Claim 1; Page 15; 16pp; German.

XX A novel bioactive metal RNA polypeptide (RNP) has a RNA component
 CC including the sequence AAT62568 and a polypeptide component having the
 CC sequence AAW01826, which is encoded by AAT62569. The RNP, or anti-RNP
 CC immunoglobulins, can be used to modulate and/or analyse angiogenesis and
 CC the vascular state of mammalian tissue, transfer genetic information in
 CC cells and selectively alter the nucleic acid content of cells. Leukocytes
 CC from pig's blood were cultured in medium, and the supernatant treated
 CC with NH4 sulphate at 35, 45 and 90% saturation to precipitate protein
 CC fractions. The residual supernatant was diluted to 45% NH4 sulphate
 CC saturation and concentrated by ultrafiltration using a 0.5 kD membrane.
 CC The retentate was purified to give 8 mg of product described as monocyto-
 CC CURNP
 XX

SQ Sequence 91 AA;

Alignment Scores: 3.51e-32 Length: 91
 Pred. No.: 332.00 Matches: 64
 Score: 81.32% Conservative: 10
 Percent Similarity: 70.33% Mismatches: 17
 Best Local Similarity: 69.60% Indels: 0
 Query Match: 2 Gaps: 0
 DB:

US-09-910-208B-12 (1-276) x AAW01826 (1-91)

QY 4 ACAAACTTGAAGGACATCTGAGGGAATGTCAATATCTCCACCAATCTCAGTTCCG 63
 Db 1 ThrLysLeuGluAspHisLeuGluGlyIleIleAsnIlePheHisGlnTyrSerValArg 20
 QY 64 AAGGGGCAATTTGACACCCCTCTCTAAGGGTGAGCTGAACGACTGCTTACAAAGGAGCTT 123
 Db 21 LeuGlyHisTyrAspThrLeuIleLysArgGlnLeuLysGlnLeuIleThrLysGluLeu 40
 QY 124 GCAACACCATCAAGAATATCAAGATAAGCTGTCATTGATGAATATTTCCAAAGGCTG 183
 Db 41 ProAsnThrLeuLysAsnThrLysAspGlnGlyThrIleAspLysIlePheGlnAsnLeu 60
 QY 184 GATGCTAATCAAGATGAACAGGTCGACTTTCAAGAATTCATATCCCTGTAGCCATTGGC 243
 Db 61 AspAlaAsnGlnAspGluGlnValSerPheLysGluPheValLeuValLeuThrAspVal 80
 QY 244 CTGAAGGCTGCCATTATCCACACCCACAAAGAG 276
 Db 81 LeuIleThrAlaHisAspAsnIleHisLysGlu 91

Search completed: February 23, 2005, 12:08:59

Job time : 115 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model
Run on: February 23, 2005, 12:13:09 ; Search time 88.5 Seconds
(without alignments)
2041.097 Million cell updates/sec

Title: US-09-910-208B-12
Perfect score: 477
Sequence: 1 atgacaaaactgaagagca.....attaccacaccacaaagag 276

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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 1380268 seqs, 327241040 residues

Total number of hits satisfying chosen parameters: 2760536

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications AA:
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4: /cgn2_6/prodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/prodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/prodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/prodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep.*
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10: /cgn2_6/prodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/prodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/prodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/prodata/1/pubpaa/US10A_PUBCOMB.pep.*
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20: /cgn2_6/prodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	468	98.1	92	14	US-10-077-600-2
2	468	98.1	92	16	US-10-755-889-334
3	309	64.8	90	9	US-09-826-589-3
4	309	64.8	90	9	US-09-826-589-4
5	309	64.8	90	9	US-09-872-185B-11
6	309	64.8	90	9	US-09-872-185B-12
7	309	64.8	90	15	US-10-666-513-3
8	309	64.8	90	16	US-10-665-867-3
9	309	64.8	90	16	US-10-665-867-4
10	234	49.1	46	9	US-09-864-761-41579
11	214.5	45.0	114	9	US-09-214-272-4
12	214.5	45.0	114	14	US-10-134-841-4
13	214.5	45.0	114	14	US-10-308-279-32
14	214.5	45.0	114	15	US-10-116-275-225
15	214.5	45.0	114	15	US-10-131-410-146
16	214.5	45.0	114	15	US-10-424-599-159736
17	214.5	45.0	114	16	US-10-755-889-330
18	194	40.7	95	9	US-09-919-172-102
19	194	40.7	95	9	US-09-981-353-98
20	184	40.7	113	15	US-10-276-774-2377
21	189	39.6	50	9	US-09-826-589-2
22	189	39.6	50	9	US-09-872-185B-9
23	189	39.6	50	15	US-10-666-513-2
24	189	39.6	50	16	US-10-665-867-2
25	189	39.6	92	10	US-09-492-026-5
26	189	39.6	92	10	US-09-919-039-184
27	188	39.4	92	15	US-10-336-603A-102
28	187	39.2	97	16	US-10-363-829-412
29	180.5	37.8	112	14	US-10-205-219-161
30	180.5	37.8	113	10	US-09-492-026-7
31	179	37.5	91	14	US-10-106-698-6907
32	178.5	37.4	113	14	US-10-134-841-3
33	169.5	35.5	101	9	US-09-393-433-2
34	169.5	35.5	101	9	US-09-781-509-2
35	169.5	35.5	101	14	US-10-269-643-2
36	169.5	35.5	119	13	US-10-087-192-1155
37	168	35.2	477	15	US-10-161-927-62
38	161.5	33.9	94	14	US-10-097-340-270
39	158	33.1	93	9	US-09-214-272-2
40	158	33.1	93	14	US-10-134-841-2
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42	158	33.1	93	16	US-10-624-631-31
43	158	33.1	93	16	US-10-755-889-328
44	157.5	33.0	93	15	US-10-094-886-58
45	157.5	33.0	101	9	US-09-393-433-1

ALIGNMENTS

RESULT 1
US-10-077-600-2
; Sequence 2, Application US/10077600
; Publication NO. US2003017513A1
; GENERAL INFORMATION:
; APPLICANT: Switch Biotech AG
; TITLE OF INVENTION: Method for diagnosis of inflammatory diseases using Calgranulin
; FILE REFERENCE: S302740US
; CURRENT APPLICATION NUMBER: US/10/077,600
; CURRENT FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 92
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-077-600-2

Alignment Scores: 1.22e-48 Length: 92
Pred. No.: 468.00 Matches: 92
Score:

Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.11% Indels: 0
DB: 14 Gaps: 0

US-09-910-208B-12 (1-276) x US-10-077-600-2 (1-92)

QY 1 ATGCAAACTTGAGAGCATCTGAGGGAATTGTCAATATCTTCCACCAATCTCAGTT 60
DB 1 MetThrLysLeuGluGluHisLeuGluGlyIleValAsnIlePheHisGlnTyrSerVal 20
QY 61 CGGAAGGGCCATTTTGACACCCCTCTCTAAGGCTGAGCTGAAGCAGCTGCTTACAAAGGAG 120
DB 21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGlu 40
QY 121 CTGCAAAACACATCAAGATATCAAGATTAAGCTGTCATTGATGAATATTCAAAGGC 180
DB 41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60
QY 181 CTGGATGCTAATCAAGATGAACAGCTCGACTTCAAGATTCATATCCCTGTAGCCATT 240
DB 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80
QY 241 GCGCTGAAGGCTGCCATCTACACACCCACCAAAAGAG 276
DB 81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92

RESULT 2

US-10-755-889-334
; Sequence 334, Application US/10755889
; Publication No. US20040171823A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-kB
; FILE REFERENCE: D0284 NP
; CURRENT APPLICATION NUMBER: US/10/755,889
; CURRENT FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: U.S. 60/440,068
; PRIOR FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: U.S. 60/469,757
; PRIOR FILING DATE: 2003-05-12
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 334
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-755-889-334

Alignment Scores:
Pred. No.: 1,228-48 Length: 92
Score: 468.00 Matches: 92
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.11% Indels: 0
DB: 16 Gaps: 0

US-09-910-208B-12 (1-276) x US-10-755-889-334 (1-92)

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DB 1 MetThrLysLeuGluGluHisLeuGluGlyIleValAsnIlePheHisGlnTyrSerVal 20
QY 61 CGGAAGGGCCATTTTGACACCCCTCTCTAAGGCTGAGCTGAAGCAGCTGCTTACAAAGGAG 120
DB 21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGlu 40
QY 121 CTGCAAAACACATCAAGATATCAAGATTAAGCTGTCATTGATGAATATTCAAAGGC 180
DB 41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60
QY 181 CTGGATGCTAATCAAGATGAACAGCTCGACTTCAAGATTCATATCCCTGTAGCCATT 240

Db 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80
QY 241 GCGCTGAAGGCTGCCATCTACACACCCACCAAAAGAG 276
DB 81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92

RESULT 3

US-09-826-589-3
; Sequence 3, Application US/09826589
; Patent No. US20020106726A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Stern, David
; TITLE OF INVENTION: EXTRACELLULAR NOVEL RAGE BINDING PROTEIN (EN-RAGE) AND USES THERE
; FILE REFERENCE: 0575/55873-B-PCT-US
; CURRENT APPLICATION NUMBER: US/09/826,589
; CURRENT FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Bovine
US-09-826-589-3

Alignment Scores:
Pred. No.: 4,78e-29 Length: 90
Score: 309.00 Matches: 59
Percent Similarity: 80.00% Conservative: 13
Best Local Similarity: 64.56% Mismatches: 18
Query Match: 64.78% Indels: 0
DB: 9 Gaps: 0

US-09-910-208B-12 (1-276) x US-09-826-589-3 (1-90)

QY 4 ACAAACTTGAGAGCATCTGAGGGAATTGTCAATATCTTCCACCAATCTCAGTTGCG 63
DB 1 ThrLysLeuGluAspHisLeuGluGlyIleIleAsnIlePheHisGlnTyrSerValArg 20
QY 64 AAGGGCATTTTGACACCCCTCTCTAAGGCTGAGCTGAAGCAGCTGCTTACAAAGGAGCTT 123
DB 21 ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40
QY 124 GCAACACCATCAAGAATATCAAGATTAAGCTGCTCATTTGATGAATATTCCAAGGCTG 183
DB 41 ProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAspLeu 60
QY 184 GATGCTAATCAAGATGAACAGCTCGACTTTCAGAAATTCATATCCCTGTAGCCATTGCG 243
DB 61 AspAlaAspLysAspGlyAlaValSerPheGluGluPheValLeuValSerArgVal 80
QY 244 CTGAAGGCTGCCATCTACACACCCACCAAA 273
DB 81 LeuLysThrAlaHisIleAspIleHisLys 90

RESULT 4

US-09-826-589-4
; Sequence 4, Application US/09826589
; Patent No. US20020106726A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Stern, David
; TITLE OF INVENTION: EXTRACELLULAR NOVEL RAGE BINDING PROTEIN (EN-RAGE) AND USES THERE
; FILE REFERENCE: 0575/55873-B-PCT-US
; CURRENT APPLICATION NUMBER: US/09/826,589
; CURRENT FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Bovine

US-09-826-589-4 :

Alignment Scores:
Pred. No.: 4.78e-29 Length: 90
Score: 309.00 Matches: 59
Percent Similarity: 80.00% Conservative: 13
Best Local Similarity: 65.56% Mismatches: 18
Query Match: 64.78% Indels: 0
DB: 9 Gaps: 0

US-09-910-208b-12 (1-276) x US-09-826-589-4 (1-90)

QY 4 ACAAACCTTGAAGAGCATCTGGAGGAATTGTCAATATCTTCCACCAATCTCAGTTCGG 63
Db 1 ThrLysLeuGluAspHisLeuGluGlyIleAAsnIlePheHisGlnTyrSerValArg 20
QY 64 AAGGGGCATTTGACACCCCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTCAAAAGGAGCTT 123
Db 21 ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40
QY 124 GCAAAACACCATCAAGAAATATCAAGATGAAGCTGCTCATTGATGAATATTTCCAAAGCCCTG 183
Db 41 ProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAspLeu 60
QY 184 GATGCTAATCAAGATGAACAGCTCGACTTTCAAGAAATTCATATCCCTGCTAGCATTGCG 243
Db 61 AspAlaAspLysAspGlyAlaValSerPheGluGluPheValValLeuValSerArgVal 80
QY 244 CTGAAGGCTGCCATTACCACACCCCAAAA 273
Db 81 LeuLysThrAlaHisIleAspIleHisLys 90

RESULT 5

US-09-872-185B-11
; Sequence 11, Application US/09872185B
; Patent No. US20020122799A1
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Herold, Kevin
; APPLICANT: Yan, Shi Du
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Lamster, Ira
; FILE OF INVENTION: METHODS FOR TREATING INFLAMMATION
; CURRENT APPLICATION NUMBER: US/09/872,185B
; CURRENT FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 11
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Bovine

US-09-872-185B-11

Alignment Scores:
Pred. No.: 4.78e-29 Length: 90
Score: 309.00 Matches: 59
Percent Similarity: 80.00% Conservative: 13
Best Local Similarity: 65.56% Mismatches: 18
Query Match: 64.78% Indels: 0
DB: 9 Gaps: 0

US-09-910-208b-12 (1-276) x US-09-872-185B-11 (1-90)

QY 4 ACAAACCTTGAAGAGCATCTGGAGGAATTGTCAATATCTTCCACCAATCTCAGTTCGG 63
Db 1 ThrLysLeuGluAspHisLeuGluGlyIleAAsnIlePheHisGlnTyrSerValArg 20
QY 64 AAGGGGCATTTGACACCCCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTCAAAAGGAGCTT 123
Db 21 ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40
QY 124 GCAAAACACCATCAAGAAATATCAAGATGAAGCTGCTCATTGATGAATATTTCCAAAGCCCTG 183

Db 41 ProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAspLeu 60
QY 184 GATGCTAATCAAGATGAACAGCTCGACTTTCAAGAAATTCATATCCCTGCTAGCATTGCG 243
Db 61 AspAlaAspLysAspGlyAlaValSerPheGluGluPheValValLeuValSerArgVal 80
QY 244 CTGAAGGCTGCCATTACCACACCCCAAAA 273
Db 81 LeuLysThrAlaHisIleAspIleHisLys 90

RESULT 6

US-09-872-185B-12
; Sequence 12, Application US/09872185B
; Patent No. US20020122799A1
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Herold, Kevin
; APPLICANT: Yan, Shi Du
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Lamster, Ira
; FILE OF INVENTION: METHODS FOR TREATING INFLAMMATION
; CURRENT APPLICATION NUMBER: US/09/872,185B
; CURRENT FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 12
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Bovine

US-09-872-185B-12

Alignment Scores:
Pred. No.: 4.78e-29 Length: 90
Score: 309.00 Matches: 59
Percent Similarity: 80.00% Conservative: 13
Best Local Similarity: 65.56% Mismatches: 18
Query Match: 64.78% Indels: 0
DB: 9 Gaps: 0

US-09-910-208b-12 (1-276) x US-09-872-185B-12 (1-90)

QY 4 ACAAACCTTGAAGAGCATCTGGAGGAATTGTCAATATCTTCCACCAATCTCAGTTCGG 63
Db 1 ThrLysLeuGluAspHisLeuGluGlyIleAAsnIlePheHisGlnTyrSerValArg 20
QY 64 AAGGGGCATTTGACACCCCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTCAAAAGGAGCTT 123
Db 21 ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40
QY 124 GCAAAACACCATCAAGAAATATCAAGATGAAGCTGCTCATTGATGAATATTTCCAAAGCCCTG 183
Db 41 ProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAspLeu 60
QY 184 GATGCTAATCAAGATGAACAGCTCGACTTTCAAGAAATTCATATCCCTGCTAGCATTGCG 243
Db 61 AspAlaAspLysAspGlyAlaValSerPheGluGluPheValValLeuValSerArgVal 80
QY 244 CTGAAGGCTGCCATTACCACACCCCAAAA 273
Db 81 LeuLysThrAlaHisIleAspIleHisLys 90

RESULT 7

US-10-666-513-3
; Sequence 3, Application US/10666513
; Publication No. US20040043412A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Stern, David
; FILE OF INVENTION: Extracellular No. US20040043412A1el RAGE Binding Protein (EN-RAG)
; TITLE OF INVENTION: Uses Thereof
; FILE REFERENCE: 0575/55873

; CURRENT APPLICATION NUMBER: US/10/666,513
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/167,705B
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3

; LENGTH: 90
; TYPE: PRT
; ORGANISM: Human
US-10-666-513-3

Alignment Scores:
Pred. No.: 4.78e-29 Length: 90
Score: 309.00 Matches: 59
Percent Similarity: 80.00% Conservative: 13
Best Local Similarity: 65.56% Mismatches: 18
Query Match: 64.78% Indels: 0
DB: 15 Gaps: 0

US-09-910-208B-12 (1-276) x US-10-666-513-3 (1-90)

QY 4 ACAAACCTTGAGAGCATCTGGAGGAATTTGCAATATCTTCCACCAATATCTCAGTTGCG 63
Db 1 ThrLysLeuGluAspHisLeuGluGlylleleAsnIlePheHisGlnTySerValArg 20
QY 64 AAGGGGCAATTTTGACACCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTACAAAGGAGCTT 123
Db 21 ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40
QY 124 GCAACACCATCAAGAATATCAAGATAAAGCTGTCATTGATGAATATTTCCAAAGGCCTG 183
Db 41 ProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAspLeu 60
QY 184 GATGCTAATCAAGATGAACAGCTGACCTTTCAAGAATTCATATCCCTGGTAGCCATTGCG 243
Db 61 AspAlaAspLysAspGlyAlaValSerPheGluGluPheValValLeuValSerArgVal 80
QY 244 CTGAAGGCTGCCATTACCAACCCACAAA 273
Db 81 LeuLysThrAlaHisIleAspIleHisLys 90

RESULT 8

US-10-665-867-3
; Sequence 3, Application US/10665867
; Publication No. US20040121372A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Ann Marie
; TITLE OF INVENTION: EXTRACELLULAR NOVEL RAGE BINDING PROTEIN (EN-RAGE) AND USES THERE
; CURRENT APPLICATION NUMBER: US/10/665,867
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/826,589
; PRIOR FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Bovine
US-10-665-867-3

Alignment Scores:
Pred. No.: 4.78e-29 Length: 90
Score: 309.00 Matches: 59
Percent Similarity: 80.00% Conservative: 13
Best Local Similarity: 65.56% Mismatches: 18
Query Match: 64.78% Indels: 0
DB: 16 Gaps: 0

US-09-910-208B-12 (1-276) x US-10-665-867-3 (1-90)

QY 4 ACAAACCTTGAGAGCATCTGGAGGAATTTGCAATATCTTCCACCAATATCTCAGTTGCG 63
Db 1 ThrLysLeuGluAspHisLeuGluGlylleleAsnIlePheHisGlnTySerValArg 20
QY 64 AAGGGGCAATTTTGACACCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTACAAAGGAGCTT 123
Db 21 ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40
QY 124 GCAACACCATCAAGAATATCAAGATAAAGCTGTCATTGATGAATATTTCCAAAGGCCTG 183
Db 41 ProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAspLeu 60
QY 184 GATGCTAATCAAGATGAACAGCTGACCTTTCAAGAATTCATATCCCTGGTAGCCATTGCG 243
Db 61 AspAlaAspLysAspGlyAlaValSerPheGluGluPheValValLeuValSerArgVal 80
QY 244 CTGAAGGCTGCCATTACCAACCCACAAA 273
Db 81 LeuLysThrAlaHisIleAspIleHisLys 90

RESULT 9

US-10-665-867-4
; Sequence 4, Application US/10665867
; Publication No. US20040121372A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Ann Marie
; TITLE OF INVENTION: EXTRACELLULAR NOVEL RAGE BINDING PROTEIN (EN-RAGE) AND USES THERE
; FILE REFERENCE: 0575/55873-B-PCT-US
; CURRENT APPLICATION NUMBER: US/10/665,867
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/826,589
; PRIOR FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Bovine
US-10-665-867-4

Alignment Scores:
Pred. No.: 4.78e-29 Length: 90
Score: 309.00 Matches: 59
Percent Similarity: 80.00% Conservative: 13
Best Local Similarity: 65.56% Mismatches: 18
Query Match: 64.78% Indels: 0
DB: 16 Gaps: 0

US-09-910-208B-12 (1-276) x US-10-665-867-4 (1-90)

QY 4 ACAAACCTTGAGAGCATCTGGAGGAATTTGCAATATCTTCCACCAATATCTCAGTTGCG 63
Db 1 ThrLysLeuGluAspHisLeuGluGlylleleAsnIlePheHisGlnTySerValArg 20
QY 64 AAGGGGCAATTTTGACACCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTACAAAGGAGCTT 123
Db 21 ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40
QY 124 GCAACACCATCAAGAATATCAAGATAAAGCTGTCATTGATGAATATTTCCAAAGGCCTG 183
Db 41 ProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAspLeu 60
QY 184 GATGCTAATCAAGATGAACAGCTGACCTTTCAAGAATTCATATCCCTGGTAGCCATTGCG 243
Db 61 AspAlaAspLysAspGlyAlaValSerPheGluGluPheValValLeuValSerArgVal 80
QY 244 CTGAAGGCTGCCATTACCAACCCACAAA 273
Db 81 LeuLysThrAlaHisIleAspIleHisLys 90

RESULT 10

US-09-864-761-41579

Sequence 41579, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aeonica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 41579
LENGTH: 46
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC011666.18
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.7
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 7.1
OTHER INFORMATION: EST HUMAN HIT: AV715719.1, EVALUATE 1.00e-19
OTHER INFORMATION: SWISSPROT HIT: P80511, EVALUATE 1.00e-20
US-09-864-761-41579

DB: 9 Gaps: 0
US-09-910-208B-12 (1-276) x US-09-864-761-41579 (1-46)
QY 1 ATGACAAAACCTGAAGACATCTGAGGGAATTTGCAATATCTTCCACCAATCTCAGTT 60
Db 1 MetThrLysLeuGluGluHisLeuGluGlyLeuValAsnIlePheHisGlnTyrSerVal 20
QY 61 CGGAGGAGGGGCATTTTGACACCCCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTACAAAGGAG 120
Db 21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuThrLysGlu 40
QY 121 CTTGCAAAACACCATCAAG 138
Db 41 LeuAlaAsnThrIleLys 46
RESULT 11
US-09-214-272-4
Sequence 4, Application US/09214272
Publication No. US20010007674A1
GENERAL INFORMATION:
APPLICANT: Siegenthaler, Georges
TITLE OF INVENTION: Isolated Arachidonic Acid-Binding Heteromer and its Use in
FILE REFERENCE: 016800-254
CURRENT APPLICATION NUMBER: US/09/214,272
CURRENT FILING DATE: 1999-04-09
PRIOR APPLICATION NUMBER: PCT/FR97/01164
PRIOR FILING DATE: 1997-06-30
PRIOR APPLICATION NUMBER: FR 96/08219
PRIOR FILING DATE: 1996-07-02
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
LENGTH: 114
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Amino acid sequence of MRP-14.
US-09-214-272-4
Alignment Scores:
Pred. No.: 2.23e-17 Length: 114
Score: 214.50 Matches: 43
Percent Similarity: 70.65% Conservative: 22
Best Local Similarity: 46.74% Mismatches: 26
Query Match: 44.97% Indels: 1
Db: 9 Gaps: 1
US-09-910-208B-12 (1-276) x US-09-214-272-4 (1-114)
QY 1 ATGACAAAACCTGAAGACATCTGAGGGAATTTGCAATATCTTCCACCAATCTCAGTT 60
Db 5 MetSerGlnLeuGluArgAsnIleGluThrIleAsnThrPheHisGlnTyrSerVal 24
QY 61 CGGAGGAGGGGCATTTTGACACCCCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTACAAAGGAG 120
Db 25 LysLeuGlyHisPheProaspThrLeuAsnGlnGlyGluPheLysGluLeuValArgLysAsp 44
QY 121 CTTGCAAAACACCATC---AAGAATATCAAGATAAAGCTGTCATTGATGAATAATATCCAA 177
Db 45 LeuGlnAsnPheLeuLysGluAsnLysAsnGluLysValIleGluHisIleMetGlu 64
QY 178 GGCCTGGATGCTAATCAAGATGAACAGCTCGACTTTCAAGATTTCAAGATTTCAATCCCTGGTAGCC 237
Db 65 AspLeuAspThrAsnAlaAspLysGlnLeuSerPheGluGluPheIleMetLeuMetAla 84
QY 238 ATTCGGCTGAAGGCTGCCCATTTACCACACCCACAA 273
Db 85 ArgLeuThrTrpAlaSerHisGluLysMethISGlu 96
RESULT 12
US-10-134-841-4

```

; Sequence 4, Application US/10134841
; Publication No. US20030003482A1
; GENERAL INFORMATION:
; APPLICANT: HALLE, JORN-PETER
; APPLICANT: GORPELT, ANDREAS
; TITLE OF INVENTION: MRP8/MRP14 heterodimer, or its
; TITLE OF INVENTION: individual components in combination, for treating and/or
; TITLE OF INVENTION: preventing skin diseases, wounds and/or wound-healing
; TITLE OF INVENTION: disturbances, having a reduced quantity of MRP8/MRP14
; TITLE OF INVENTION: heterodimers
; FILE REFERENCE: 50125/031002
; CURRENT APPLICATION NUMBER: US/10/134,841
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: US 60/322,925
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: DE 10121254.2
; PRIOR FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-134-841-4

Alignment Scores:
Pred. No.: 2,23e-17 Length: 114
Score: 214.50 Matches: 43
Percent Similarity: 70.65% Conservative: 22
Best Local Similarity: 46.74% Mismatches: 26
Query Match: 44.97% Indels: 1
DB: 14 Gaps: 1

US-09-910-208B-12 (1-276) x US-10-134-841-4 (1-114)
; Sequence 32, Application US/10308279
; Publication No. US20030170742A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE DEVELOPMENT
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS
; FILE REFERENCE: D0190 NP
; CURRENT APPLICATION NUMBER: US/10/308,279
; CURRENT FILING DATE: 2002-12-03
; PRIOR APPLICATION NUMBER: 60/337,429
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 114
; TYPE: PRT
US-10-308-279-32

; Sequence 4, Application US/10134841
; Publication No. US20030003482A1
; GENERAL INFORMATION:
; APPLICANT: HALLE, JORN-PETER
; APPLICANT: GORPELT, ANDREAS
; TITLE OF INVENTION: MRP8/MRP14 heterodimer, or its
; TITLE OF INVENTION: individual components in combination, for treating and/or
; TITLE OF INVENTION: preventing skin diseases, wounds and/or wound-healing
; TITLE OF INVENTION: disturbances, having a reduced quantity of MRP8/MRP14
; TITLE OF INVENTION: heterodimers
; FILE REFERENCE: 50125/031002
; CURRENT APPLICATION NUMBER: US/10/134,841
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: US 60/322,925
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: DE 10121254.2
; PRIOR FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-134-841-4

Alignment Scores:
Pred. No.: 2,23e-17 Length: 114
Score: 214.50 Matches: 43
Percent Similarity: 70.65% Conservative: 22
Best Local Similarity: 46.74% Mismatches: 26
Query Match: 44.97% Indels: 1
DB: 14 Gaps: 1

US-09-910-208B-12 (1-276) x US-10-134-841-4 (1-114)
; Sequence 32, Application US/10308279
; Publication No. US20030170742A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE DEVELOPMENT
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS
; FILE REFERENCE: D0190 NP
; CURRENT APPLICATION NUMBER: US/10/308,279
; CURRENT FILING DATE: 2002-12-03
; PRIOR APPLICATION NUMBER: 60/337,429
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 114
; TYPE: PRT
US-10-308-279-32

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; ORGANISM: homo sapiens
US-10-308-279-32

Alignment Scores:
Pred. No.: 2,23e-17 Length: 114
Score: 214.50 Matches: 43
Percent Similarity: 70.65% Conservative: 22
Best Local Similarity: 46.74% Mismatches: 26
Query Match: 44.97% Indels: 1
DB: 14 Gaps: 1

US-09-910-208B-12 (1-276) x US-10-308-279-32 (1-114)
QY 1 ATGACAAAACCTTGAAGAGCATCTGGAGGAATGTCAATATCTTCCACCAATCTCAGTT 60
DB 5 MetSerGlnLeuGluArgAsnIleGluThrIleAsnThrPheHisGlnTySerVal 24
QY 61 CGGAAGGGGCATTTTGACACCCCTCTCTAAGGTGAGCTGAAGCAGCTGCTTACAAAGGAG 120
DB 25 LysLeuGlyHisProAspThrLeuAsnGlnGlyGluPheLysGluLeuValArgLysAsp 44
QY 121 CTTCGAAAACACCATC---AAGAATATCAAGATAAAGCTGTCTATTGATGAATATCCAA 177
DB 45 LeuGlnAsnPheLeuLysLysGluAsnLysAsnGluLysValIleGluHisIleMetGlu 64
QY 178 GGCTGGATGCTAATCAAGATGAACAGGTGCGACTTTCAAGAAATTCATATCCCTGGTAGCC 237
DB 65 AspLeuAspThrAsnAlaAspLysGlnLeuSerPheGluGluPheIleMetLeuMetAla 84
QY 238 ATTGCGCTGAAGCTGCCATTCACACCCACAAA 273
DB 85 ArgLeuThrTrpAlaSerHisGluLysMetHisGlu 96

RESULT 14
US-10-116-275-225
; Sequence 225, Application US/10116275
; Publication No. US20030211476A1
; GENERAL INFORMATION:
; APPLICANT: Elan Pharmaceutical Technology
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Brayden, David
; APPLICANT: Byrne, Daragh
; APPLICANT: Lambkin, Imelda
; APPLICANT: Higgins, Lisa
; TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and
; TITLE OF INVENTION: Compositions Targeting Peyer's Patches and M Cell Receptors
; FILE REFERENCE: E1067/20087
; CURRENT APPLICATION NUMBER: US/10/116,275
; CURRENT FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 225
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-116-275-225

Alignment Scores:
Pred. No.: 2,23e-17 Length: 114
Score: 214.50 Matches: 43
Percent Similarity: 70.65% Conservative: 22
Best Local Similarity: 46.74% Mismatches: 26
Query Match: 44.97% Indels: 1
DB: 15 Gaps: 1

US-09-910-208B-12 (1-276) x US-10-116-275-225 (1-114)
QY 1 ATGACAAAACCTTGAAGAGCATCTGGAGGAATGTCAATATCTTCCACCAATCTCAGTT 60
DB 5 MetSerGlnLeuGluArgAsnIleGluThrIleAsnThrPheHisGlnTySerVal 24
QY 61 CGGAAGGGGCATTTTGACACCCCTCTCTAAGGTGAGCTGAAGCAGCTGCTTACAAAGGAG 120
DB 25 LysLeuGlyHisProAspThrLeuAsnGlnGlyGluPheLysGluLeuValArgLysAsp 44
QY 121 CTTCGAAAACACCATC---AAGAATATCAAGATAAAGCTGTCTATTGATGAATATCCAA 177
DB 45 LeuGlnAsnPheLeuLysLysGluAsnLysAsnGluLysValIleGluHisIleMetGlu 64
QY 178 GGCTGGATGCTAATCAAGATGAACAGGTGCGACTTTCAAGAAATTCATATCCCTGGTAGCC 237
DB 65 AspLeuAspThrAsnAlaAspLysGlnLeuSerPheGluGluPheIleMetLeuMetAla 84
QY 238 ATTGCGCTGAAGCTGCCATTCACACCCACAAA 273
DB 85 ArgLeuThrTrpAlaSerHisGluLysMetHisGlu 96

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Search completed: February 23, 2005, 12:30:09
Job time : 89.5 secs

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QY      121 CTTGCAAAACACCATC---AAGAAATATCAAGATAAAGCTGTCATTGATGAAATATTCCAA 177
Db      45 LeuGlnAsnPheLeuLysLysGluAsnLysAsnGluLysValIleGluHisIleMetGlu 64
QY      178 GGCCTGGATGCTAATCAAGATGAACAGGTCGACTTTCAAGAATTCAATATCCCTGGTAGCC 237
Db      65 AspLeuAspThrAsnAlaAspLysGlnLeuSerPheGluGluPheIleMetLeuMetAla 84
QY      238 ATTGGCTGAAGGCTGCCCATTTACCACACCCACAAA 273
Db      85 ArgLeuThrTrpAlaSerHisGluLysMetHisGlu 96

RESULT 15
US-10-131-410-146
; Sequence 146, Application US/10131410
; Publication No. US20030235915A1
; GENERAL INFORMATION:
; APPLICANT: SPÉCHT, THOMAS
; APPLICANT: HINZMANN, BERND
; APPLICANT: SCHMITT, ARMIN
; APPLICANT: PILARSKY, CHRISTIAN
; APPLICANT: DAHL, EDGAR
; APPLICANT: ROSENTHAL, ANDRE
; TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM TISSUE OF BREAST
; FILE REFERENCE: SCH-1763
; CURRENT APPLICATION NUMBER: US/10/131,410
; PRIOR FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: 09/646,673
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: PCT/DE99/00908
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 202
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 146
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-131-410-146

Alignment Scores:
Pred. No.:      2,23e-17      Length:      114
Score:          214.50      Matches:      43
Percent Similarity: 70.65%      Conservative: 22
Best Local Similarity: 46.74%      Mismatches: 26
Query Match:    44.97%      Indels:      1
DB:            15          Gaps:        1

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QY      61 CGGAAGGGGCATTTTGACACCCCTCTCTAAGGCTGAGCTGAAGCAGCTGCTTACAAAGGAG 120
Db      25 LysLeuGlyHisProAspThrLeuAsnGlnGlyGluPheLysGluLeuValArgLysAsp 44
QY      121 CTTGCAAAACACCATC---AAGAAATATCAAGATGAAGCTGTCATTGATGAAATATTCCAA 177
Db      45 LeuGlnAsnPheLeuLysLysGluAsnLysAsnGluLysValIleGluHisIleMetGlu 64
QY      178 GGCCTGGATGCTAATCAAGATGAACAGGTCGACTTTCAAGAATTCAATATCCCTGGTAGCC 237
Db      65 AspLeuAspThrAsnAlaAspLysGlnLeuSerPheGluGluPheIleMetLeuMetAla 84
QY      238 ATTGGCTGAAGGCTGCCCATTTACCACACCCACAAA 273
Db      85 ArgLeuThrTrpAlaSerHisGluLysMetHisGlu 96
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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: February 23, 2005, 12:02:13 ; Search time 29.5 Seconds
(without alignments)
1396.823 Million cell updates/sec

Title: US-09-910-208B-12

Perfect score: 477

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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0
Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 1027090

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THRSADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents AA:
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	468	98.1	92	3	US-09-270-455-20
3	332	69.6	91	3	US-08-794-000-2
4	332	69.6	91	4	US-09-646-651C-1
5	319	66.9	92	2	US-08-568-310D-19
6	319	66.9	92	3	US-09-270-455-19
7	309	64.8	90	4	US-09-263-312-3
8	309	64.8	90	4	US-09-826-589-3
9	309	64.8	90	4	US-09-826-589-4
10	214.5	45.0	114	1	US-08-385-241-3
11	214.5	45.0	114	4	US-09-214-272-4
12	214.5	45.0	114	4	US-09-806-382A-4

13	209.5	43.9	109	1	US-07-987-272A-8	Sequence 8, Appli
14	205	43.0	51	2	US-08-568-310D-2	Sequence 2, Appli
15	205	43.0	51	3	US-09-270-455-2	Sequence 2, Appli
16	194	40.7	95	4	US-09-919-172-102	Sequence 102, App
17	194	40.7	95	4	US-09-976-594-467	Sequence 467, App
18	194	40.7	102	4	US-09-949-016-10557	Sequence 10557, A
19	189	39.6	50	4	US-09-263-312-2	Sequence 2, Appli
20	189	39.6	50	4	US-09-826-589-2	Sequence 2, Appli
21	189	39.6	92	2	US-08-918-727-5	Sequence 5, Appli
22	189	39.6	92	3	US-09-205-680A-5	Sequence 5, Appli
23	189	39.6	92	4	US-09-919-039-184	Sequence 184, App
24	187	39.2	92	2	US-09-051-589-1	Sequence 1, Appli
25	184	38.6	91	1	US-07-987-272A-11	Sequence 11, Appli
26	180.5	37.8	113	2	US-08-918-727-7	Sequence 7, Appli
27	180.5	37.8	113	3	US-09-205-680A-7	Sequence 7, Appli
28	170	35.6	74	4	US-09-513-999C-5490	Sequence 5490, Ap
29	161.5	33.9	131	4	US-09-949-016-11241	Sequence 11241, A
30	158	33.1	93	1	US-07-987-272A-7	Sequence 7, Appli
31	158	33.1	93	1	US-07-987-272A-16	Sequence 16, Appli
32	158	33.1	93	1	US-08-385-241-1	Sequence 1, Appli
33	158	33.1	93	4	US-09-214-272-2	Sequence 2, Appli
34	158	33.1	93	4	US-09-806-382A-3	Sequence 3, Appli
35	157.5	33.0	101	1	US-08-190-560-2	Sequence 2, Appli
36	157.5	33.0	101	1	US-08-468-946-2	Sequence 2, Appli
37	157.5	33.0	101	2	US-08-468-946-2	Sequence 2, Appli
38	157.5	33.0	101	2	US-08-468-942-2	Sequence 2, Appli
39	157.5	33.0	101	4	US-09-298-625-2	Sequence 2, Appli
40	157	32.9	105	2	US-08-918-727-6	Sequence 6, Appli
41	157	32.9	105	3	US-09-205-680A-6	Sequence 6, Appli
42	154	32.3	88	1	US-07-987-272A-1	Sequence 1, Appli
43	154	32.3	89	1	US-07-987-272A-14	Sequence 14, Appli
44	153.5	32.2	97	1	US-07-662-198B-2	Sequence 2, Appli
45	153.5	32.2	110	4	US-09-949-016-11242	Sequence 11242, A

ALIGNMENTS

RESULT 1
US-08-568-310D-20
; Sequence 20, Application US/08568310D
; Patent No. 5976832
; GENERAL INFORMATION:
; APPLICANT: HITOMI, JIRO
; APPLICANT: YAMAGUCHI, KEN
; APPLICANT: YAMAMURA, TOKUJIRO
; APPLICANT: KIMURA, TATSUJI
; TITLE OF INVENTION: NOVEL CALCIUM-BINDING PROTEINS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WYATT GERBER, MELLER & O'ROURKE
; STREET: 99 PARK AVENUE
; STREET: 6th FLOOR
; CITY: NEW YORK CITY
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH, 720 Kb
; MEDIUM TYPE: STORAGE
; COMPUTER: IBM-PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS 6.2
; SOFTWARE: WORDPERFECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/568,310D
; FILING DATE: DECEMBER 6, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 7-70468 and 7-45564 (both Japan)
; FILING DATE: 3/6/95 and 3/6/95, respectively
; ATTORNEY/AGENT INFORMATION:
; NAME: KLEIN, MILTON
; REGISTRATION NUMBER: 27101
; REFERENCE/DOCKET NUMBER: 3316

Wed Feb 23 12:56:15 2005

```
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)953-3350
; TELEFAX: (212)953-3352
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 92
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; PUBLICATION INFORMATION:
; RELEVANT RESIDUES IN SEQ ID NO: 20:
; RELEVANT RESIDUES IN SEQ ID NO: FROM 1 TO 92
US-08-568-310D-20

Alignment Scores:
Pred. No.: 6.6e-54 Length: 92
Score: 468.00 Matches: 92
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.11% Indels: 0
DB: 2 Gaps: 0

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QY 61 CGGAAGGGCGCATTTTGACACCCCTCTAAGGTGAGCTGAAGCAGCTCTTACAAAGGAG 120
Db 21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGlu 40
QY 121 CTTCGAAACACCATCAAGAATATCAAGATTAAGCTGTCATTGATGAATATTTCCAAAGC 180
Db 41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60
QY 181 CTGGATGCTAATCAAGATGAACAGCTCGACTTTCAAGATTCATATCCCTGTAGCCATT 240
Db 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80
QY 241 GCGCTGAAGCTGCCATTATCCACACCCCAAGAG 276
Db 81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92

RESULT 2
US-09-270-455-20
; Sequence 20, Application US/09270455
; Patent No. 6313267
; GENERAL INFORMATION:
; APPLICANT: HITOMI, JIRO
; APPLICANT: YAMAGUCHI, KEN
; APPLICANT: YAMAMURA, TOKUJIRO
; APPLICANT: KIMURA, TATSUJI
; TITLE OF INVENTION: NOVEL CALCIUM-BINDING PROTEINS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WYATT, GERBER, MELLER & O'ROURKE
; STREET: 99 PARK AVENUE
; STREET: 6th FLOOR
; CITY: NEW YORK CITY
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH, 720 KB
; MEDIUM TYPE: STORAGE
; COMPUTER: IBM-PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS 6.2
; SOFTWARE: WORDPERFECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/270,455
; FILING DATE:

; TELECOMMUNICATION INFORMATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/568,310
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: KLEIN, MILTON
; REGISTRATION NUMBER: 27101
; REFERENCE/DOCKET NUMBER: 3316
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)953-3350
; TELEFAX: (212)953-3352
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 92
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; PUBLICATION INFORMATION:
; RELEVANT RESIDUES IN SEQ ID NO: 20: FROM 1 TO 92
US-09-270-455-20

Alignment Scores:
Pred. No.: 6.6e-54 Length: 92
Score: 468.00 Matches: 92
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.11% Indels: 0
DB: 3 Gaps: 0

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Db 1 MetThrLysLeuGluHisLeuGluGlyIleValAsnIlePheHisGlnTyrSerVal 20
QY 61 CGGAAGGGCGCATTTTGACACCCCTCTAAGGTGAGCTGAAGCAGCTCTTACAAAGGAG 120
Db 21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGlu 40
QY 121 CTTCGAAACACCATCAAGAATATCAAGATTAAGCTGTCATTGATGAATATTTCCAAAGC 180
Db 41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60
QY 181 CTGGATGCTAATCAAGATGAACAGCTCGACTTTCAAGATTCATATCCCTGTAGCCATT 240
Db 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80
QY 241 GCGCTGAAGCTGCCATTATCCACACCCCAAGAG 276
Db 81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92

RESULT 3
US-08-794-000-2
; Sequence 2, Application US/08794000
; Patent No. 6087123
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Metal-Containing Ribonucleotide Polypeptides
; NUMBER OF SEQUENCES: 4
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/794,000
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/DE96/01337
; FILING DATE: 17-JUL-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 195 25 992.0
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; FILING DATE: 17-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 195 30 500.0
; FILING DATE: 18-AUG-1995
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 91 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-08-794-000-2
Alignment Scores:
Pred. No.: 9.86e-36 Length: 91
Score: 332.00 Matches: 64
Percent Similarity: 81.32% Conservative: 10
Best Local Similarity: 70.33% Mismatches: 17
Query Match: 69.60% Indels: 0
DB: 3 Gaps: 0

US-09-910-208B-12 (1-276) x US-08-794-000-2 (1-91)
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QY 64 AAGGGGCATTGTCACACCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTACAAAGGAGCTT 123
Db 21 LeuGlyHisTyrAspThrLeuIleLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40
QY 124 GCARACACCATCAAGAAATATCAAGATAAAGCTGTCAATGATGAATAATTTCAAGCCCTG 183
Db 41 ProAsnThrLeuLysAsnThrLysAspGlnGlyThrIleAspLysIlePheGlnAsnLeu 60
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Db 61 AspAlaAsnGlnAspGluGlnValSerPheLysGluPheValIleValThrAspVal 80
QY 244 CTGAAGGCTGCCATTACCACCCACCAAGAG 276
Db 81 LeuIleThrAlaHisAspAsnIleHisLysGlu 91

RESULT 5
US-08-568-310D-19
; Sequence 19, Application US/08568310D
; Patent No. 5976832
; GENERAL INFORMATION:
; APPLICANT: HITOMI, JIRO
; APPLICANT: YAMAGUCHI, KEN
; APPLICANT: YAMAMURA, TOKUJIRO
; APPLICANT: KIMURA, TATSUJI
; TITLE OF INVENTION: NOVEL CALCIUM-BINDING PROTEINS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WYATT GERBER, MELLER & O'ROURKE
; STREET: 99 PARK AVENUE
; CITY: NEW YORK CITY
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH, 720 KB
; MEDIUM TYPE: STORAGE
; COMPUTER: IBM-PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS 6.2
; SOFTWARE: WORDPERFECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/568,310D
; FILING DATE: DECEMBER 6, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 7-70468 and 7-45564 (both Japan)
; FILING DATE: 3/6/95 and 3/6/95, respectively
; ATTORNEY/AGENT INFORMATION:
; NAME: KLEIN, MILTON
; REGISTRATION NUMBER: 27101
; REFERENCE/DOCKET NUMBER: 3316
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)953-3350
; TELEFAX: (212)953-3352
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 92
; TYPE: amino acid
; STRANDEDNESS:
;
US-09-910-208B-12 (1-276) x US-08-794-000-2 (1-91)
QY 4 ACARAACTTGAAGAGCATCTGAGGGAATGTCAATATCTTCACCAATACTCAGTTGG 63
Db 1 ThrLysLeuGluAspHisLeuGluGlyIleAenIlePheHisGlnTyrSerValArg 20
QY 64 AAGGGGCATTGTCACACCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTACAAAGGAGCTT 123
Db 21 LeuGlyHisTyrAspThrLeuIleLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40
QY 124 GCARACACCATCAAGAAATATCAAGATAAAGCTGTCAATGATGAATAATTTCAAGCCCTG 183
Db 41 ProAsnThrLeuLysAsnThrLysAspGlnGlyThrIleAspLysIlePheGlnAsnLeu 60
QY 184 GATGCTAATCAAGATGAACAGCTGCACCTTCAAGAAATTCATATCCTGTCAGCCATTGG 243
Db 61 AspAlaAsnGlnAspGluGlnValSerPheLysGluPheValIleValThrAspVal 80
QY 244 CTGAAGGCTGCCATTACCACCCACCAAGAG 276
Db 81 LeuIleThrAlaHisAspAsnIleHisLysGlu 91

RESULT 4
US-09-646-651C-1
; Sequence 1, Application US/09646651C
; Patent No. 6770455
; GENERAL INFORMATION:
; APPLICANT: Kiesewetter, Stefan
; APPLICANT: Kuhn, Eckehard
; APPLICANT: Koch-Pelster, Brigitte
; APPLICANT: Brunner, Herwig
; TITLE OF INVENTION: METAL-CONTAINING RIBONUCLEOTIDE POLYPEPTIDES
; FILE REFERENCE: 206579
; CURRENT APPLICATION NUMBER: US/09/646,651C
; CURRENT FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: PCT/EP98/07722
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: DE 198 11 047.2
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1..7)
; OTHER INFORMATION: Angiotropin-related protein
;
US-09-646-651C-1
Alignment Scores:
Pred. No.: 9.86e-36 Length: 91
Score: 332.00 Matches: 64
Percent Similarity: 81.32% Conservative: 10
Best Local Similarity: 70.33% Mismatches: 17
Query Match: 69.60% Indels: 0
DB: 3 Gaps: 0
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TOPOLOGY: linear
MOLECULE TYPE: cDNA
PUBLICATION INFORMATION:
RELEVANT RESIDUES IN SEQ ID NO: 19:
RELEVANT RESIDUES IN SEQ ID NO: FROM 1 TO 92
US-08-568-310D-19

Alignment Scores:
Pred. No.: 5.4e-34 Length: 92
Score: 319.00 Matches: 61
Percent Similarity: 80.43% Conservative: 13
Best Local Similarity: 66.30% Mismatches: 18
Query Match: 66.88% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-12 (1-276) x US-08-568-310D-19 (1-92)

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DB 1 MetThrLysLeuGluAspHisLeuGluGlyIleIleAsnIlePheHisGlnTySerVal 20

QY 61 CGGAAGGGGCAATTTGACACCCCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTACAAAGGAG 120
DB 21 ArgValGlyHisPheAspThrLeuAsnLysArgGlnLeuLysGlnLeuIleThrLysGlu 40

QY 121 CTGCAAAACACCATCAAGATATCAAGATTAAGCTGTCATTGATGAATATTCACAAAGGC 180
DB 41 LeuProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAsp 60

QY 181 CTGGATGCTAATCAAGATCAACAGCTCGACATTTCAAGAAATTCATATCCCTGCTAGCCATT 240
DB 61 LeuAspAlaAspLysAspGlyAlaValSerPheGluGluPheValValLeuValSerArg 80

QY 241 GCGCTGAAGGTCGCCATTACACACCCACAAAGAG 276
DB 81 ValLeuLysThrAlaHisIleAspIleHisLysGlu 92

RESULT 6
US-09-270-455-19
Sequence 19, Application US/09270455
Patent No. 6313267
GENERAL INFORMATION:
APPLICANT: HITOMI, JIRO
APPLICANT: YAMAGUCHI, KEN
APPLICANT: YAMAMURA, TOKUJIRO
APPLICANT: KIMURA, TATSUJI
TITLE OF INVENTION: NOVEL CALCIUM-BINDING PROTEINS
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: WYATT, GERBER, MELLER & O'ROURKE
STREET: 99 PARK AVENUE
STREET: 6th FLOOR
CITY: NEW YORK CITY
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH, 720 KB
MEDIUM TYPE: STORAGE
COMPUTER: IBM-PC COMPATIBLE
OPERATING SYSTEM: PC-DOS 6.2
SOFTWARE: WORDPERFECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/270,455
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/568,310
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: KLEIN, MILTON
REGISTRATION NUMBER: 27101
REFERENCE/DOCKET NUMBER: 3316

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)953-3350
TELEFAX: (212)953-3352
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 92
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: cDNA
PUBLICATION INFORMATION:
RELEVANT RESIDUES IN SEQ ID NO: 19: FROM 1 TO 92
US-09-270-455-19

Alignment Scores:
Pred. No.: 5.4e-34 Length: 92
Score: 319.00 Matches: 61
Percent Similarity: 80.43% Conservative: 13
Best Local Similarity: 66.30% Mismatches: 18
Query Match: 66.88% Indels: 0
DB: 3 Gaps: 0

US-09-910-208B-12 (1-276) x US-09-270-455-19 (1-92)

QY 1 ATGACAAAACCTTGAGAGCATCTGGAGGAATTGTCAATATCTTCCACCAATCTCAGTT 60
DB 1 MetThrLysLeuGluAspHisLeuGluGlyIleIleAsnIlePheHisGlnTySerVal 20

QY 61 CGGAAGGGGCAATTTGACACCCCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTACAAAGGAG 120
DB 21 ArgValGlyHisPheAspThrLeuAsnLysArgGlnLeuLysGlnLeuIleThrLysGlu 40

QY 121 CTGCAAAACACCATCAAGATATCAAGATTAAGCTGTCATTGATGAATATTCACAAAGGC 180
DB 41 LeuProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAsp 60

QY 181 CTGGATGCTAATCAAGATCAACAGCTCGACATTTCAAGAAATTCATATCCCTGCTAGCCATT 240
DB 61 LeuAspAlaAspLysAspGlyAlaValSerPheGluGluPheValValLeuValSerArg 80

QY 241 GCGCTGAAGGTCGCCATTACACACCCACAAAGAG 276
DB 81 ValLeuLysThrAlaHisIleAspIleHisLysGlu 92

RESULT 7
US-09-263-312-3
Sequence 3, Application US/09263312
Patent No. 655340
GENERAL INFORMATION:
APPLICANT: Schmidt, Ann Marie
APPLICANT: Stern, David
TITLE OF INVENTION: Extracellular No. 655340el RAGE Binding Protein (EN-RAGE) and
TITLE OF INVENTION: Uses Thereof
FILE REFERENCE: 0575/55873-A
CURRENT APPLICATION NUMBER: US/09/263,312
CURRENT FILING DATE: 1999-03-05
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 90
TYPE: PRT
ORGANISM: Human
US-09-263-312-3

Alignment Scores:
Pred. No.: 1.16e-32 Length: 90
Score: 309.00 Matches: 59
Percent Similarity: 80.00% Conservative: 13
Best Local Similarity: 65.56% Mismatches: 18
Query Match: 64.78% Indels: 0
DB: 4 Gaps: 0

US-09-910-208B-12 (1-276) x US-09-263-312-3 (1-90)


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QY 4 ACAAACTTGAAGAGCATCTGGAGGAATTGTCAATATCTTCCACCAATCTCAGTTCCG 63
Db 1 ThrLysLeuGluAspHisLeuGluGlylleAenllePheHisGlnTyrSerValArg 20
QY 64 AAGGGCATTTCACACCCCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTACAAAGGAGCTT 123
Db 21 ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40
QY 124 GCAACACCATCAAGAAATCAAGATAAAGCTGTCATTGATGAATATTCACAGCCCTG 183
Db 41 ProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAspLeu 60
QY 184 GATGCTAATCAAGATGAACAGCTCGACTTTCAAGAAATTCATATCCTCGTAGCCATTGCG 243
Db 61 AspAlaAspLysAspGlyAlaValSerPheGluGluPheValValLeuValSerArgVal 80
QY 244 CTGAAGGCTGCCATTACACACCCACAAA 273
Db 81 LeuLysThrAlaHisIleAspIleHisLys 90
RESULT 8
US-09-826-589-3
; Sequence 3, Application US/09826589
; Patent No. 6670136
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Ann Marie
; TITLE OF INVENTION: EXTRACELLULAR NOVEL RAGE BINDING PROTEIN (EN-RAGE) AND USES THERE
; FILE REFERENCE: 0575/58873-B-PCT-US
; CURRENT APPLICATION NUMBER: US/09/826,589
; CURRENT FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Bovine
US-09-826-589-3
Alignment Scores:
Pred. No.: 1.16e-32 Length: 90
Score: 309.00 Matches: 59
Percent Similarity: 80.00% Conservativity: 13
Best Local Similarity: 65.56% Mismatches: 18
Query Match: 64.78% Indels: 0
DB: Gaps: 0
US-09-910-208B-12 (1-276) x US-09-826-589-3 (1-90)
QY 4 ACAAACTTGAAGAGCATCTGGAGGAATTGTCAATATCTTCCACCAATCTCAGTTCCG 63
Db 1 ThrLysLeuGluAspHisLeuGluGlylleAenllePheHisGlnTyrSerValArg 20
QY 64 AAGGGCATTTCACACCCCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTACAAAGGAGCTT 123
Db 21 ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40
QY 124 GCAACACCATCAAGAAATCAAGATAAAGCTGTCATTGATGAATATTCACAGCCCTG 183
Db 41 ProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAspLeu 60
QY 184 GATGCTAATCAAGATGAACAGCTCGACTTTCAAGAAATTCATATCCTCGTAGCCATTGCG 243
Db 61 AspAlaAspLysAspGlyAlaValSerPheGluGluPheValValLeuValSerArgVal 80
QY 244 CTGAAGGCTGCCATTACACACCCACAAA 273
Db 81 LeuLysThrAlaHisIleAspIleHisLys 90
RESULT 9
US-09-826-589-4
; Sequence 4, Application US/09826589
; Patent No. 6670136
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Ann Marie
; TITLE OF INVENTION: EXTRACELLULAR NOVEL RAGE BINDING PROTEIN (EN-RAGE) AND USES THERE
; FILE REFERENCE: 0575/58873-B-PCT-US
; CURRENT APPLICATION NUMBER: US/09/826,589
; CURRENT FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Bovine
US-09-826-589-4
Alignment Scores:
Pred. No.: 1.16e-32 Length: 90
Score: 309.00 Matches: 59
Percent Similarity: 80.00% Conservativity: 13
Best Local Similarity: 65.56% Mismatches: 18
Query Match: 64.78% Indels: 0
DB: Gaps: 0
US-09-910-208B-12 (1-276) x US-09-826-589-3 (1-90)
QY 4 ACAAACTTGAAGAGCATCTGGAGGAATTGTCAATATCTTCCACCAATCTCAGTTCCG 63
Db 1 ThrLysLeuGluAspHisLeuGluGlylleAenllePheHisGlnTyrSerValArg 20
QY 64 AAGGGCATTTCACACCCCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTACAAAGGAGCTT 123
Db 21 ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40
QY 124 GCAACACCATCAAGAAATCAAGATAAAGCTGTCATTGATGAATATTCACAGCCCTG 183
Db 41 ProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAspLeu 60
QY 184 GATGCTAATCAAGATGAACAGCTCGACTTTCAAGAAATTCATATCCTCGTAGCCATTGCG 243
Db 61 AspAlaAspLysAspGlyAlaValSerPheGluGluPheValValLeuValSerArgVal 80
QY 244 CTGAAGGCTGCCATTACACACCCACAAA 273
Db 81 LeuLysThrAlaHisIleAspIleHisLys 90
RESULT 9
US-09-826-589-4
; Sequence 4, Application US/09826589
; Patent No. 6670136
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Ann Marie
; TITLE OF INVENTION: EXTRACELLULAR NOVEL RAGE BINDING PROTEIN (EN-RAGE) AND USES THERE
; FILE REFERENCE: 0575/58873-B-PCT-US
; CURRENT APPLICATION NUMBER: US/09/826,589
; CURRENT FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Bovine
US-09-826-589-4
Alignment Scores:
Pred. No.: 1.16e-32 Length: 90
Score: 309.00 Matches: 59
Percent Similarity: 80.00% Conservativity: 13
Best Local Similarity: 65.56% Mismatches: 18
Query Match: 64.78% Indels: 0
DB: Gaps: 0
US-09-910-208B-12 (1-276) x US-09-826-589-4 (1-90)
QY 4 ACAAACTTGAAGAGCATCTGGAGGAATTGTCAATATCTTCCACCAATCTCAGTTCCG 63
Db 1 ThrLysLeuGluAspHisLeuGluGlylleAenllePheHisGlnTyrSerValArg 20
QY 64 AAGGGCATTTCACACCCCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTACAAAGGAGCTT 123
Db 21 ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu 40
QY 124 GCAACACCATCAAGAAATCAAGATAAAGCTGTCATTGATGAATATTCACAGCCCTG 183
Db 41 ProLysThrLeuGlnAsnThrLysAspGlnProThrIleAspLysIlePheGlnAspLeu 60
QY 184 GATGCTAATCAAGATGAACAGCTCGACTTTCAAGAAATTCATATCCTCGTAGCCATTGCG 243
Db 61 AspAlaAspLysAspGlyAlaValSerPheGluGluPheValValLeuValSerArgVal 80
QY 244 CTGAAGGCTGCCATTACACACCCACAAA 273
Db 81 LeuLysThrAlaHisIleAspIleHisLys 90
RESULT 10
US-08-385-241-3
; Sequence 3, Application US/08385241
; Patent No. 5776348
; GENERAL INFORMATION:
; APPLICANT: Selengut Ph.D., Jeremy D.
; APPLICANT: Orme-Johnson Ph.D., William H.
; APPLICANT: Dretler M.D., Stephen P.
; APPLICANT: Asakura M.D., Hirotsuka
; TITLE OF INVENTION: SYSTEM AND METHOD FOR INHIBITING
; TITLE OF INVENTION: FORMATION OF CRYSTALLINE STRUCTURES THAT INCLUDE STRUVITE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Choate, Hall & Stewart
; STREET: 53 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2891
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/385,241
; FILING DATE:
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; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Herschbach Ph.D., Brenda M.
; REGISTRATION NUMBER: P-39,223
; REFERENCE/DOCKET NUMBER: 492611-000 (MIT6915)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-5175
; TELEFAX: (617) 248-4000
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; CLONE: hMRP-14 protein
US-08-385-241-3

Alignment Scores:
Pred. No.: 5.35e-20 Length: 114
Score: 214.50 Matches: 43
Percent Similarity: 70.65% Conservative: 22
Best Local Similarity: 46.74% Mismatches: 26
Query Match: 44.97% Indels: 1
DB: 1

US-09-910-208B-12 (1-276) x US-08-385-241-3 (1-114)

QY 1 ATGACAAACTTGAGAGCATCTGGAGGAAATTCCTCAATATCTTCCACCAATCTCAGTT 60
Db 5 MetSerGlnLeuGluArgAsnIleGluThrIleAsnThrPheHisGlnTySerVal 24
QY 61 CGGAAGGGGCATTTTGACACCCCTCTCTAAGGGTGAGCTGAAGCAGCTCTTACAAAGGAG 120
Db 25 LysLeuGlyHisProAspThrLeuAsnGlnGlyGluPheLysGluLeuValArgLysAsp 44
QY 121 CTTGCAAAACACCATC---AGAATATCAAGATAAAGCTGTCATTCATGATGAATAATTCCAA 177
Db 45 LeuGlnAsnPheLeuLysLysGluAsnLysAsnGluLysValIleGluHisIleMetGlu 64
QY 178 GGCCTGGATGCTAATCAAGATGAACAGCTCGACTTTCAAGAAATTCATATCCTCGTAGCC 237
Db 65 AspLeuAspThrAsnAlaAspLysGlnLeuSerPheGluGluPheIleMetLeuMetAla 84
QY 238 ATTGCGCTGAAGGCTGCCCATTTACCACACCCACAAA 273
Db 85 ArgLeuThrTrpAlaSerHisGluLysMethHisGlu 96

RESULT 11
US-09-214-272-4
; Sequence 4, Application US/09214272
; Patent No. 6620790
; GENERAL INFORMATION:
; APPLICANT: Siegenthaler, Georges
; TITLE OF INVENTION: Isolated Arachidonic Acid-Binding Heteromer and its Use in
; FILE REFERENCE: Cosmetics and Pharmaceuticals
; CURRENT APPLICATION NUMBER: US/09/214,272
; CURRENT FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: PCT/FR97/01164
; PRIOR FILING DATE: 1997-06-30
; PRIOR APPLICATION NUMBER: FR 96/08219
; PRIOR FILING DATE: 1996-07-02
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
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; OTHER INFORMATION: Amino acid sequence of MRP-14.
US-09-214-272-4
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Alignment Scores:
Pred. No.: 5.35e-20 Length: 114
Score: 214.50 Matches: 43
Percent Similarity: 70.65% Conservative: 22
Best Local Similarity: 46.74% Mismatches: 26
Query Match: 44.97% Indels: 1
DB: 1
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US-09-910-208B-12 (1-276) x US-09-214-272-4 (1-114)

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QY 1 ATGACAAACTTGAGAGCATCTGGAGGAAATTCCTCAATATCTTCCACCAATCTCAGTT 60
Db 5 MetSerGlnLeuGluArgAsnIleGluThrIleAsnThrPheHisGlnTySerVal 24
QY 61 CGGAAGGGGCATTTTGACACCCCTCTCTAAGGGTGAGCTGAAGCAGCTCTTACAAAGGAG 120
Db 25 LysLeuGlyHisProAspThrLeuAsnGlnGlyGluPheLysGluLeuValArgLysAsp 44
QY 121 CTTGCAAAACACCATC---AGAATATCAAGATAAAGCTGTCATTCATGATGAATAATTCCAA 177
Db 45 LeuGlnAsnPheLeuLysLysGluAsnLysAsnGluLysValIleGluHisIleMetGlu 64
QY 178 GGCCTGGATGCTAATCAAGATGAACAGCTCGACTTTCAAGAAATTCATATCCTCGTAGCC 237
Db 65 AspLeuAspThrAsnAlaAspLysGlnLeuSerPheGluGluPheIleMetLeuMetAla 84
QY 238 ATTGCGCTGAAGGCTGCCCATTTACCACACCCACAAA 273
Db 85 ArgLeuThrTrpAlaSerHisGluLysMethHisGlu 96
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RESULT 12
US-09-806-382A-4
; Sequence 4, Application US/09806382A
; Patent No. 6706683
; GENERAL INFORMATION:
; APPLICANT: SETO, MINORU
; APPLICANT: FUKUDA, KOUICHIROU
; TITLE OF INVENTION: METHOD OF CONTROLLING SECRETION OF GRANULES
; FILE REFERENCE: ASahi-3-PC-1
; CURRENT APPLICATION NUMBER: US/09/806,382A
; CURRENT FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: PCT/JP99/05302
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: JP 10/274574
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-806-382A-4
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Alignment Scores:
Pred. No.: 5.35e-20 Length: 114
Score: 214.50 Matches: 43
Percent Similarity: 70.65% Conservative: 22
Best Local Similarity: 46.74% Mismatches: 26
Query Match: 44.97% Indels: 1
DB: 1
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US-09-910-208B-12 (1-276) x US-09-806-382A-4 (1-114)

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QY 1 ATGACAAACTTGAGAGCATCTGGAGGAAATTCCTCAATATCTTCCACCAATCTCAGTT 60
Db 5 MetSerGlnLeuGluArgAsnIleGluThrIleAsnThrPheHisGlnTySerVal 24
QY 61 CGGAAGGGGCATTTTGACACCCCTCTCTAAGGGTGAGCTGAAGCAGCTCTTACAAAGGAG 120
Db 25 LysLeuGlyHisProAspThrLeuAsnGlnGlyGluPheLysGluLeuValArgLysAsp 44
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US-09-910-208B-12 (1-276) x US-09-270-455-2 (1-51)

QY	4	ACAAACTTGAAGAGCATCTGAGGGAATTCATATCTCCACCAATCTCAGTTTCGG	63
Db	1	ThrLysLeuGluAspHisLeuGluGlyIleIleAsnIlePheHisGlnTyrSerValarg	20
QY	64	AAGGGGCATTTTGACACCCCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTACAAAGAGCTT	123
Db	21	ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu	40
QY	124	GCAACACCATCAAGAAATATCAAGATAAA	153
Db	41	ProLysThrLeuGlnAsnThrLysAspGln	50

Search completed: February 23, 2005, 12:15:03
Job time : 30.5 secs

US-09-910-208B-12 (1-276) x US-08-568-310D-2 (1-51)

QY	4	ACAAACTTGAAGAGCATCTGAGGGAATTCATATCTCCACCAATCTCAGTTTCGG	63
Db	1	ThrLysLeuGluAspHisLeuGluGlyIleIleAsnIlePheHisGlnTyrSerValarg	20
QY	64	AAGGGGCATTTTGACACCCCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTACAAAGAGCTT	123
Db	21	ValGlyHisPheAspThrLeuAsnLysArgGluLeuLysGlnLeuIleThrLysGluLeu	40
QY	124	GCAACACCATCAAGAAATATCAAGATAAA	153
Db	41	ProLysThrLeuGlnAsnThrLysAspGln	50

RESULT 15
US-09-270-455-2
; Sequence 2, Application US/09270455
; Patent No. 6313267
; GENERAL INFORMATION:
; APPLICANT: HITOMI, JIRO
; APPLICANT: YAMAGUCHI, KEN
; APPLICANT: YAMAMURA, TOKUJIRO
; APPLICANT: KIMURA, TATSUJI
; TITLE OF INVENTION: NOVEL CALCIUM-BINDING PROTEINS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSER: WYATT, GERBER, MELLER & O'ROURKE
; STREET: 99 PARK AVENUE
; CITY: NEW YORK CITY
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH, 720 KB
; MEDIUM TYPE: STORAGE
; COMPUTER: IBM-PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS 6.2
; SOFTWARE: WORDPERFECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/270,455
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/568,310
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: KLEIN, MILTON
; REGISTRATION NUMBER: 27101
; REFERENCE/DOCKET NUMBER: 3316
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)953-3350
; TELEFAX: (212)953-3352
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 51
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; PUBLICATION INFORMATION:
; RELEVANT RESIDUES IN SEQ ID NO: 2: FROM 1 TO 51

US-09-270-455-2

Alignment Scores:	7.68e-19	Length:	51
Pred. No.:	205.00	Matches:	38
Score:	90.00%	Conservative:	7
Best Local Similarity:	76.00%	Mismatches:	5
Query Match:	42.98%	Indels:	0
DB:	3	Gaps:	0

GenCore version 5.1.1.6
: Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: February 23, 2005, 12:26:35 ; Search time 27 Seconds
(without alignments)
1967.098 Million cell updates/sec

Title: US-09-910-208B-12
Perfect score: 92
Sequence: 1 atgacaaaactgaagagca.....attaccacaccacaagag 276

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Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues

Word size: 1

Total number of hits satisfying chosen parameters: 565918

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 500 summaries

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-Q/cgn2_1/USPTO_spool_p/HADDAD-09-910208B/runat_23022005_102316_15808/app_query.fasta_1
-DB=PIR_79 -Qfmt=ifastan -SUFFIX=oligo.rpr -MINMATCH=0.1 -LOOPCU=0 -LOOPEXT=0
-UNITS=Bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi -LIST=500
-DOALIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc
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-TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DSELEX=7

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1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	9	9.8	91	2 A55406	calgranulin c - pi
3	9	9.8	122	1 A42628	calgranulin B - bo
4	8	8.8	254	2 S25281	glTF protein precu
5	8	8.7	404	2 D82150	conserved hypotet
6	8	8.8	525	2 G95374	probable ABC trans
7	8	8.8	900	2 T39800	probable DNA-bind
8	8	8.7	962	2 S03818	carboxymethylcellu
9	7	7.7	34	2 F71350	hypothetical prote
10	7	7.6	50	4 B34912	hypothetical prote
11	7	7.7	111	2 S69743	probable membrane
12	7	7.6	132	1 A48418	interleukin-5 prec
13	7	7.6	133	1 ICWS5	interleukin-5 prec
14	7	7.7	147	2 S72253	hemoglobin, extrac

hypothetical prote
hypothetical prote
NADH dehydrogenase
probable calcineur
phosphoprotein pho
phosphoribosylamin
virion protein j13
probable membrane
membrane protein a
arom protein limpo
protein of aro ope
pancoate-beta-alan
hypothetical prote
hypothetical prote
conserved hypotet
xyloglucan endo-tr
methylenetetrahydr
hypothetical prote
hypothetical prote
conserved hypotet
phosphate ABC tran
binding protein co
DNA-directed DNA p
NADH2 dehydrogenas
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
urea/short chain-a
hypothetical prote
probable oxidoredu
8-amino-7-oxononan
hypothetical prote
transcription regu
conserved hypotet
hypothetical prote
manganese transpor
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
gastrin/cholecysto
gastrin/cholecysto
gastrin receptor -
probable C4-dicarb
hypothetical prote
UDEG glucosyltrans
protein farnesyltr
farnesyltranstrans
conserved hypotet
surface glycoprote
surface glycoprote
surface glycoprote
hypothetical prote
probable disease r
importin 2 - Afric
probable membrane
probable substrate
probable Na+/H+ ex
hypothetical prote
hypothetical prote
DNA helicase limpo
ABC-type transport
2',3'-cyclic-nucle
ATP-dependent heli
translation elonga
probable disease r
gp150 protein - fr
ubiquitin-specific
leucine-tRNA ligas
DNA exonuclease ho
protein phosphatas
chromosome segrega
isoleucine-tRNA li

88	7	7.6	1335	2	T18289	161	6	6.5	129	2	I37779	Ig variable region
89	7	7.6	1450	2	T45888	162	6	6.5	129	2	S75257	hypothetical prote
90	7	7.6	1504	2	T17426	163	6	6.5	132	2	T44301	hypothetical prote
91	7	7.6	1647	2	T11267	164	6	6.5	133	2	A99981	hypothetical prote
92	7	7.6	1674	2	G96736	165	6	6.5	135	2	H97156	transcription term
93	7	7.6	2254	2	D86215	166	6	6.5	135	2	I64147	lactylglutathione
94	7	7.6	35	2	E70243	167	6	6.5	136	2	E83766	hypothetical prote
95	6	6.5	40	2	I39944	168	6	6.5	137	2	G75471	hypothetical prote
96	6	6.5	45	2	E30956	169	6	6.5	138	2	S05258	Ig heavy chain v r
97	6	6.5	45	2	D82798	170	6	6.5	138	2	SI7941	export protein xps
98	6	6.5	46	2	A26929	171	6	6.5	138	2	AD0281	conserved hypothet
99	6	6.5	47	2	A22162	172	6	6.5	139	2	S69458	hypothetical prote
100	6	6.5	53	2	PH0107	173	6	6.5	140	2	T01170	ferredoxin [2Fe-2S
101	6	6.5	58	2	S78111	174	6	6.5	141	2	E55855	lyeA protein - pha
102	6	6.5	59	2	C72663	175	6	6.5	141	2	E75336	aminoglycoside ace
103	6	6.5	61	2	AC2666	176	6	6.5	141	2	F83675	hypothetical prote
104	6	6.5	61	2	AC0576	177	6	6.5	142	2	T27038	hypothetical prote
105	6	6.5	69	2	H81436	178	6	6.5	142	2	H71022	hypothetical prote
106	6	6.5	72	2	AE2771	179	6	6.5	143	2	S03747	small membrane pro
107	6	6.5	73	1	W5WL18	180	6	6.5	143	1	B64330	hypothetical prote
108	6	6.5	75	2	E90974	181	6	6.5	145	2	T22373	hypothetical prote
109	6	6.5	78	1	A40850	182	6	6.5	145	2	T50276	hypothetical prote
110	6	6.5	79	2	G85722	183	6	6.5	147	2	T28131	probable membrane
111	6	6.5	79	2	S75193	184	6	6.5	148	2	AF0712	hypothetical prote
112	6	6.5	83	2	F71485	185	6	6.5	148	2	F85789	hypothetical prote
113	6	6.5	85	2	I40691	186	6	6.5	148	2	B90941	hypothetical prote
114	6	6.5	87	2	D61547	187	6	6.5	148	2	E64939	transcription regu
115	6	6.5	87	2	T17874	188	6	6.5	149	2	D83758	hypothetical prote
116	6	6.5	90	2	T17643	189	6	6.5	149	2	B71067	hypothetical prote
117	6	6.5	93	2	AG1442	190	6	6.5	150	2	S29890	Ribosomal protein
118	6	6.5	95	1	S35985	191	6	6.5	150	2	JC4243	transcription CCAA
119	6	6.5	95	2	A02777	192	6	6.5	152	2	B26471	Ig heavy chain pre
120	6	6.5	96	2	H86681	193	6	6.5	152	2	AH3245	conserved hypothet
121	6	6.5	97	2	A30129	194	6	6.5	153	2	B84043	hypothetical prote
122	6	6.5	98	2	I40616	195	6	6.5	154	2	D89406	protein F16H6.10 [
123	6	6.5	100	2	A41988	196	6	6.5	155	2	B70370	hypothetical prote
124	6	6.5	100	2	A84949	197	6	6.5	155	2	AC1665	shikimate kinase h
125	6	6.5	100	2	T48706	198	6	6.5	157	2	H72650	hypothetical prote
126	6	6.5	101	2	T49857	199	6	6.5	158	2	G87623	chemotaxis protein
127	6	6.5	101	2	G72759	200	6	6.5	158	2	C81662	cytosolic acyl-CoA
128	6	6.5	103	2	T10397	201	6	6.5	159	2	A72709	hypothetical prote
129	6	6.5	103	2	B30857	202	6	6.5	160	2	C69352	conserved hypothet
130	6	6.5	105	2	D82962	203	6	6.5	160	2	B64225	dihydrofolate redu
131	6	6.5	105	2	A83175	204	6	6.5	160	2	B82565	hypothetical prote
132	6	6.5	106	2	S40282	205	6	6.5	161	2	A83066	hypothetical prote
133	6	6.5	106	2	T10224	206	6	6.5	162	2	I39170	benzoate 1,2-dioxy
134	6	6.5	106	2	S76805	207	6	6.5	163	2	B41659	cyclin A/CDK2-asso
135	6	6.5	106	2	B64001	208	6	6.5	163	2	A57630	transcription-asso
136	6	6.5	108	2	JV0105	209	6	6.5	163	2	AN0248	platelet-derived g
137	6	6.5	108	2	S75384	210	6	6.5	166	2	JN0248	hypothetical prote
138	6	6.5	108	2	F69369	211	6	6.5	167	2	H96739	hypothetical prote
139	6	6.5	111	2	F70338	212	6	6.5	168	2	T07640	pEARLI 1 protein -
140	6	6.5	112	2	B96951	213	6	6.5	168	2	AC0824	CS3 fimbrial prote
141	6	6.5	112	1	B31848	214	6	6.5	168	2	A34952	type 4 fimbrial bi
142	6	6.5	115	2	T17090	215	6	6.5	168	2	H83075	hypothetical prote
143	6	6.5	115	2	S04754	216	6	6.5	169	2	T50166	B-G antigen - chic
144	6	6.5	115	2	D71194	217	6	6.5	169	2	T33727	conserved hypothet
145	6	6.5	117	1	HVM539	218	6	6.5	170	2	A57277	beta-3 endonexin,
146	6	6.5	117	1	HVM557	219	6	6.5	171	2	AC0824	chaperone protein
147	6	6.5	117	1	HVM584	220	6	6.5	171	2	JQ1995	envelope protein v
148	6	6.5	117	2	S66720	221	6	6.5	171	2	B87018	probable membrane
149	6	6.5	118	2	E71158	222	6	6.5	171	2	T18167	hypothetical prote
150	6	6.5	118	2	G02438	223	6	6.5	172	2	A71263	hypothetical prote
151	6	6.5	118	2	JE0162	224	6	6.5	172	2	AB2848	hypothetical prote
152	6	6.5	120	2	A61301	225	6	6.5	172	2	AB3214	hypothetical prote
153	6	6.5	121	2	F84133	226	6	6.5	173	2	T11336	ABC transporter, s
154	6	6.5	122	2	A27097	227	6	6.5	174	2	D47245	NADH2 dehydrogenas
155	6	6.5	122	2	B27097	228	6	6.5	174	2	T47245	calcineurin regula
156	6	6.5	122	2	AB1416	229	6	6.5	176	2	D84676	hypothetical prote
157	6	6.5	122	2	A11791	230	6	6.5	176	2	E72565	hypothetical prote
158	6	6.5	124	2	D71183	231	6	6.5	176	2	T21573	hypothetical prote
159	6	6.5	125	2	S49604	232	6	6.5	176	2	D71146	hypothetical prote
160	6	6.5	126	2	S52255	233	6	6.5	177	2	T07642	pEARLI 1 protein h

c 234	6	6.6	177	2	S25845	dimerase - Strepto	307	6	6.5	215	2	S08220	platelet-derived g
235	6	6.5	178	2	S74636	hypothetical prote	c 308	6	6.6	215	2	T36153	probable permease
236	6	6.5	179	2	S44624	C50C3.5 protein -	c 309	6	6.6	215	2	G81993	hypothetical prote
237	6	6.5	180	2	C83425	hypothetical prote	c 310	6	6.6	215	2	G81223	conserved hypotet
c 238	6	6.6	180	2	T50530	hypothetical prote	311	6	6.5	216	2	AG2591	peptide methionine
239	6	6.6	182	2	T36540	probable orotate p	312	6	6.5	218	2	T01076	transcription fact
240	6	6.5	183	2	T51495	hypothetical prote	313	6	6.5	218	2	A36673	immunoglobulin enh
c 241	6	6.6	183	2	JH0803	tyrosine kinase re	c 314	6	6.6	219	2	S27332	probable endopep
242	6	6.5	183	2	C75082	hypothetical prote	315	6	6.5	220	2	G85872	probable lipoprote
243	6	6.5	184	2	H83631	conserved hypotet	316	6	6.5	220	2	T08628	hypothetical prote
244	6	6.5	184	2	E90035	hypothetical prote	317	6	6.5	220	2	T26434	hypothetical prote
c 245	6	6.6	185	2	E69884	hypothetical prote	c 318	6	6.6	221	2	B64188	arginine transport
246	6	6.5	185	2	T34286	hypothetical prote	319	6	6.5	221	2	T15848	hypothetical prote
247	6	6.5	186	2	G86154	hypothetical prote	320	6	6.5	221	2	H83608	probable transcrip
248	6	6.5	186	2	B75421	probable pilin, ty	321	6	6.5	223	2	C82555	heme ABC transport
249	6	6.5	187	2	H97478	cycl protein [impo	c 322	6	6.6	223	2	H95106	conserved hypotet
250	6	6.5	188	2	A70256	hypothetical prote	c 323	6	6.6	223	2	F83703	hypothetical prote
c 251	6	6.6	189	2	A69272	tungsten formylmet	c 324	6	6.6	223	2	B97975	hypothetical prote
c 252	6	6.6	189	2	D75213	hypothetical prote	c 325	6	6.6	224	2	B87197	hypothetical prote
c 253	6	6.6	190	2	H75162	anthranilate synth	c 326	6	6.6	224	2	E70790	probable transcrip
254	6	6.5	190	2	T43172	probable protein-t	327	6	6.5	224	2	C97587	succinoglycan bios
c 255	6	6.6	192	2	F71169	hypothetical prote	c 328	6	6.6	226	1	J01570	major surface anti
c 256	6	6.6	193	2	JQ2185	coat protein - app	c 329	6	6.6	226	1	J01573	major surface anti
257	6	6.5	193	2	S01975	gene D5 protein -	c 330	6	6.6	226	1	J01578	major surface anti
c 258	6	6.6	194	2	S59793	SKP1 protein - yea	c 331	6	6.6	226	1	J01579	major surface anti
259	6	6.5	194	2	A64331	hypothetical prote	c 332	6	6.6	226	1	J01580	major surface anti
260	6	6.5	195	2	E86469	protein F12K31.10	c 333	6	6.6	226	1	J01581	major surface anti
261	6	6.5	195	2	A95731	unknown protein F5	c 334	6	6.5	226	2	B86830	3-dehydroquinat d
262	6	6.5	195	2	A35074	transcription regu	335	6	6.5	226	2	I51550	platelet-derived g
263	6	6.5	196	2	A37359	platelet-derived g	c 336	6	6.6	226	2	JQ2058	surface antigen -
264	6	6.5	196	2	A48851	platelet-derived g	c 337	6	6.6	226	2	JQ2087	surface antigen -
265	6	6.5	196	2	B28964	platelet-derived g	c 338	6	6.6	226	2	JQ2089	surface antigen -
266	6	6.5	196	2	T50018	MADS box protein F	c 339	6	6.6	226	2	JQ2085	surface antigen -
267	6	6.5	197	2	S25096	platelet-derived g	c 340	6	6.6	226	2	JQ2119	surface antigen -
268	6	6.5	197	2	F82921	conserved hypotet	c 341	6	6.6	226	2	JQ2092	surface antigen -
269	6	6.5	197	2	S73688	hypothetical prote	c 342	6	6.6	226	2	JQ2061	surface antigen -
270	6	6.5	197	2	AE2808	succinoglycan bios	c 343	6	6.6	226	2	JQ2116	surface antigen -
c 271	6	6.6	197	2	D86316	probable membrane	c 344	6	6.6	226	2	JQ2225	small surface prot
c 272	6	6.6	197	2	S48377	protein T10022.9 [c 345	6	6.6	226	2	JQ2060	surface antigen -
273	6	6.5	197	2	H83038	hypothetical prote	c 346	6	6.6	226	2	JQ2090	surface antigen -
274	6	6.5	198	2	AJ2696	cycl protein limpo	c 347	6	6.6	226	2	JQ2091	surface antigen -
275	6	6.5	198	2	SJ0735	platelet-derived g	c 348	6	6.6	226	2	JQ2121	surface antigen -
276	6	6.5	198	2	I39670	rold protein - Agr	c 349	6	6.6	226	2	JQ2057	surface antigen -
c 277	6	6.6	199	2	A97310	probable cAMP-bind	c 350	6	6.6	226	2	JQ2088	surface antigen -
278	6	6.5	199	2	D98212	probable tetx-fam1	c 351	6	6.6	226	2	JQ2110	surface antigen -
279	6	6.5	200	2	I51551	platelet-derived g	c 352	6	6.6	226	2	JQ2062	surface antigen -
280	6	6.5	202	2	T31452	probable 4-vinyl r	c 353	6	6.6	226	2	JQ2059	surface antigen -
281	6	6.5	202	2	T50396	conserved hypotet	c 354	6	6.6	226	2	G96789	protein T23E18.14
282	6	6.5	202	2	A90139	hypothetical prote	355	6	6.5	227	2	G69762	two-component resp
283	6	6.5	204	2	I50163	B-G antigen - chic	356	6	6.5	227	2	D84943	hypothetical prote1
284	6	6.5	207	2	AF0080	probable exported	357	6	6.5	228	2	S60639	cytochrome-c oxida
c 285	6	6.6	207	2	JQ0397	nods protein - Azo	358	6	6.5	228	2	H97373	hypothetical prote
286	6	6.5	207	2	F90093	U3 snRNP protein	359	6	6.5	228	2	S45677	proteinase inhibit
c 287	6	6.6	208	2	D71529	probable antranil	c 360	6	6.6	229	2	G82420	arginine ABC trans
c 288	6	6.5	209	2	A55632	proteasome LMP2.s	361	6	6.5	229	2	S41086	translation elonga
c 289	6	6.6	209	2	S04827	gene 40A protein -	c 362	6	6.6	229	2	F64398	hypothetical prote
290	6	6.5	209	2	I50223	enhancer binding p	363	6	6.5	230	2	H97838	DNA-directed DNA p
c 291	6	6.6	211	1	S40836	formate dehydrogen	c 364	6	6.6	230	2	T03752	hypothetical prote
292	6	6.5	211	1	PFHUG1	platelet-derived g	365	6	6.5	231	2	AD0773	hypothetical prote
293	6	6.5	211	1	XMECDD	dedb protein - Esc	c 366	6	6.6	231	2	E86338	protein F5M15.16 l
c 294	6	6.6	211	2	AD0946	formate dehydrogen	367	6	6.5	232	2	S43188	orotidine-5'-phosp
c 295	6	6.6	211	2	B91231	formate dehydrogen	368	6	6.5	232	2	B83285	orotidine 5'-phosp
c 296	6	6.6	211	2	A86078	formate dehydrogen	369	6	6.5	232	2	AH0026	30S ribosomal prot
297	6	6.5	211	2	F91028	probable lipoprote	370	6	6.5	232	2	D72037	macromolecule tran
c 298	6	6.6	211	2	D69397	GTP-binding protei	371	6	6.5	232	2	G86588	sapb protein limpo
c 299	6	6.6	212	2	F84481	Mutator-like trans	c 372	6	6.6	232	2	G69703	hypothetical prote
c 300	6	6.6	212	2	E83936	hypothetical prote	373	6	6.5	232	2	AE2456	ribosomal protein
301	6	6.5	213	2	S76070	hypothetical prote	374	6	6.5	233	1	R3EC3	30S ribosomal subu
302	6	6.5	213	2	AB2213	hypothetical prote	375	6	6.5	233	2	G85996	30S ribosomal chai
303	6	6.5	213	2	A83614	hypothetical prote	376	6	6.5	233	2	AG1006	30S ribosomal subu
c 304	6	6.6	213	2	T44588	probable transcrip	377	6	6.5	233	2	C91151	30S ribosomal subu
c 305	6	6.6	214	2	T51061	hypothetical prote	378	6	6.5	234	2	S76625	hypothetical prote
c 306	6	6.6	215	2	A29318	ubiquinol-cytochro	379	6	6.5	235	2	S26300	transcription fact

transcription fact
protein Y106G6H.14
phosphoribosylamin
hypothetical prote
hypothetical prote
probable lipase -
hypothetical prote
amino acid ABC-tra
hypothetical prote
lipolytic enzyme h
glycerophosphoryl
ABC transporter, A
probable ABC trans
acetoacetyl-CoA re
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
lumQ protein - Syn
spherulin 1b precu
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
probable outer mem
probable exported
hypothetical prote
probable membrane
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
carboxylesterase (
granzyme C (EC 3.4
spherulin 1a precu
granzyme M (EC 3.4
transcription regu
hypothetical prote
conserved hypotet
hypothetical prote
major prion PrP-Sc
glycerol uptake fa
hypothetical zinc
conserved hypotet
conserved hypotet
BR1 protein tona
short chain dehydr
reductase (AL13282
major prion PrP27-
hypothetical prote
CT262 hypothetical
conserved hypotet
gene 2 protein - M
hypothetical prote
short chain dehydr
hypothetical prote
SN-glycerol-3-phos
cytochrome-c oxida
probable carboxype
probable carboxype
alkylphosphonate A
dihydrodipicolinat
dihydrodipicolinat
conserved hypotet
conserved hypotet

380 2 T48518
381 2 H87976
382 2 AB0372
383 2 H71974
384 2 A64532
385 2 G75316
386 2 C83880
387 2 AD1368
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389 2 A12126
390 2 A1381
391 2 AC2745
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451 2 H70434
452 2 AF2928

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6 6.5 292 2 AF0834

ALIGNMENTS

RESULT 1

JC4712
S-100 calcium-binding protein A12 - human
N:Alternate names: calcium-binding amniotic fluid protein 1 (CAAF1); calgranulin C; calg
utrophil protein
C:Species: Homo sapiens (man)
C:Date: 10-May-1996 #sequence
C:Accession: JC4712; JC4717; JC4891; S56113; S56114
R:Yamamura, T.; Hitomi, J.; Nagasaki, K.; Suzuki, M.; Takahashi, E.; Saito, S.; Tsukada,
Biochem. Biophys. Res. Commun. 221, 356-360, 1996
A:Title: Human CAAF1 gene - molecular cloning, gene structure, and chromosome mapping.
A:Reference number: JC4712; MUID:96192053; PMID:8619860
A:Accession: JC4712
A:Molecule type: mRNA
A:Residues: 1-92 <YAM>
A:Cross-references: UNIPROT:P80511; DDBJ:D83657; NID:gi502284; PIDN:BAA12030.1; PID:gi150
R:Marti, T.; Ertmann, K.D.; Gallin, M.Y.
Biochem. Biophys. Res. Commun. 221, 454-458, 1996
A:Title: Host-parasite interaction in human onchocerciasis: Identification and sequence
A:Reference number: JC4717; MUID:96192069; PMID:8619876
A:Accession: JC4717

A:Molecule type: protein
A:Residues: 2-92 <MAR>
A:Experimental source: Onchocerca volvulus infecting human tissue
R:Ilq, E.C.; Troxler, H.; Buergliesser, D.M.; Kuster, T.; Markert, M.; Guignard, F.; Hunzel
Biochem. Biophys. Res. Commun. 225, 146-150, 1996
A:Title: Amino acid sequence determination of human S100 A12 (P6, Calgranulin C, CGRP, C
A:Reference number: JC4891; MUID:96332419; PMID:8769108
A:Accession: JC4891
A:Molecule type: protein
A:Residues: 2-92 <ILG>
R:Guignard, F.; Maue, J.; Markert, M.
Biochem. J. 309, 395-401, 1995
A:Title: Identification and characterization of a novel human neutrophil protein related
A:Reference number: S56113; MUID:95351965; PMID:7626002
A:Accession: S56113
A>Status: preliminary
A:Molecule type: protein
A:Residues: 'XX', 4-14, X', 16-17, 'XXXX' <GUI1>
A:Experimental source: isoform 6a
A:Accession: S56114
A>Status: preliminary
A:Molecule type: protein
A:Residues: 2-21 <GUI2>
A:Experimental source: isoform 6b
A:Comment: This protein is released by activated neutrophils in the course of inflammato
C:Genetics:
A:Gene: GDB:S100A12; P6; MRP6; CGRP; CAAFI
A:Cross-references: GDB:S218374
A:Map position: 1q21-1q21
C:Complex: monomer
C:Superfamily: S-100 protein; calmodulin repeat homology
C:Keywords: calcium binding; EF hand; monomer; neutrophil; zinc
F:2-92/Product: S-100 calcium-binding protein A12 #status experimental <MAT>
F:6-39/Domain: calmodulin repeat homology <EPI>
F:49-81/Domain: calmodulin repeat homology <EPI>
F:86-90/Region: zinc binding #status predicted

Alignment Scores:
Pred. No.: 2,36e-91 Length: 92
Score: 92.00 Matches: 92
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-12 (1-276) x JC4712 (1-92)

QY 1 ATGCAAACTTGAAGAGCATCTGGAGGAATTGTCAATATCTTCCACCAATCTCAGTT 60
- Db 1 MetThrLysLeuGluGluHisLeuGluGlyIleValAsnIlePheHisGlnTyrSerVal 20

QY 61 CGGAAGGGGCATTGTCACACCTCTCTAAGGCTGAGCTGAAGCAGCTGCTTACAAGGAG 120
Db 21 ArGlyysGlyHisPheAspThrLeuSerLysGlyGlyLeuLeuLeuThrLysGlu 40

QY 121 CTTGCAACACCATCAAGAAATATCAAGATAAAGCTGTCTATTCATGCAATATTCACAGGC 180
Db 41 LeuAlaenThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60

QY 181 CTGGATGCTAATCAAGTGAACAGCTGCTTCAAGATTTCATATCCCTGGTAGCCATT 240
Db 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80

QY 241 GCGCTGAAGCTGCCCATTTACCAACCCCAAGAG 276
Db 81 AlaLeuLysAlaAlaHisThrHisThrHisLysGlu 92

RESULT 2
A55406
calgranulin c - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 09-Jul-2004
C:Accession: A55406

R:Dell'Angelica, E.C.; Schleicher, C.H.; Santome, J.A.
J. Biol. Chem. 269, 28929-28936, 1994
A:Title: Primary structure and binding properties of calgranulin C, a novel S100-like c
A:Reference number: A55406; MUID:95050708; PMID:7961855
A:Accession: A55406
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-91
A:Cross-references: UNIPROT:P80310
C:Superfamily: S-100 protein; calmodulin repeat homology
C:Keywords: calcium binding; EF hand
F:48-80/Domain: calmodulin repeat homology <EP2>

Alignment Scores:
Pred. No.: 0.456 Length: 91
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 9.78% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-12 (1-276) x A55406 (1-91)

QY 37 AATATCTTCCACCAATACTCTCAGTTCCG 63
Db 12 AsnIlePheHisGlnTyrSerValArg 20

RESULT 3
A42628
calgranulin B - bovine (fragment)
N:Alternate names: calcium-binding protein MRP-14; macrophage migration inhibitory fact
in 2
C:Species: Bos primigenius taurus (cattle)
C:Date: 30-Sep-1993 #sequence_revision 23-May-1997 #text_change 23-May-1997
C:Accession: B22309; A42628
R:Tang, T.K.; Hong, T.M.; Lin, C.Y.; Lai, M.L.; Liu, C.H.L.; Lo, H.J.; Wang, M.E.; Chen,
submitted to the Protein Sequence Database, July 1992
A:Reference number: A22309
A:Accession: B22309
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-122 <TRAN>
R:Dianoux, A.C.; Stasia, M.J.; Garin, J.; Gagnon, J.; Vignais, P.V.
Biochemistry 31, 5898-5905, 1992
A:Title: The 23-kilodalton protein, a substrate of protein kinase C, in bovine neutroph
A:Reference number: A42628; MUID:92304974; PMID:1610833
A:Accession: A42628
A:Molecule type: protein
A:Residues: 4-32, F', 34-56 <DIA>
C:Complex: heterodimer and higher complexes with calgranulin A
C:Superfamily: S-100 protein; calmodulin repeat homology
C:Keywords: blocked amino end; calcium binding; EF hand; heterodimer; inflammation; pho
F:50-82/Domain: calmodulin repeat homology <EP1>

Alignment Scores:
Pred. No.: 0.448 Length: 122
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 9.78% Indels: 0
DB: 1 Gaps: 0

US-09-910-208B-12 (1-276) x A42628 (1-122)

QY 37 AATATCTTCCACCAATACTCTCAGTTCCG 63
Db 13 AsnIlePheHisGlnTyrSerValArg 21

RESULT 4
S25281
glTF protein precursor - Escherichia coli (strain K-12)
C:Species: Escherichia coli

C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C;Accession: S25281; H65112
R;Castano, I.; Flores, N.; Valle, F.; Covarrubias, A.A.; Bolivar, F.
Mol. Microbiol. 6, 2733-2741, 1992
A;Title: gltF, a member of the gltBDF operon of Escherichia coli, is involved in nitroge
A;Reference number: S25281; MUID:93078627; PMID:1447980
A;Accession: S25281
A;Molecule type: DNA
A;Residues: 1-254 <AS>
A;Cross-references: UNIPROT:P28721; EMBL:M74162; NID:gl46213; PIDN:AAA23909.1; PID:gl1462
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.I.; Burland, V.; Riley, M.; Co
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: H65112
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-254 <BLAT>
A;Cross-references: GB:AE000401; GB:U00096; NID:gl1789607; PIDN:AAC76246.1; PID:gl1789608;
A;Experimental source: strain K-12, substrain MG1655
C;Genetics:
A;Gene: gltF
C;Keywords: transmembrane protein
F;1-25/Domain: signal sequence #status predicted <SIG>
F;27-254/Product: gltF protein #status predicted <MAT>
F;213-229/Domain: transmembrane #status predicted <TMM>

Alignment Scores:
Pred. No.: 5.24 Length: 254
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 8.79% Indels: 0
Gaps: 0
DB:

US-09-910-208B-12 (1-276) x S25281 (1-254)

Qy 254 GCAGCCTTCAGCGCAATGCTACC 231
Db 19 AlaAlaPheSerAlaMetAlaThr 26

RESULT 5
D82150
conserved hypothetical protein VC1851 [imported] - Vibrio cholerae (strain N16961 serog
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: D82150
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, H
l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: D82150
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-404 <HEI>
A;Cross-references: UNIPROT:Q9KQZ6; GB:AE004260; GB:AE003852; NID:99656368; PIDN:AAF9499
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
A;Gene: VC1851
A;Map position: 1
C;Superfamily: comB protein

Alignment Scores:
Pred. No.: 5.09 Length: 404
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 8.70% Indels: 0
Gaps: 0
DB:

US-09-910-208B-12 (1-276) x D82150 (1-404)

Qy 220 TTCATATCCCTGGTAGCCATTGCG 243
Db 268 PheleSerLeuValaIleAala 275

RESULT 6
G95374
probable ABC transporter, periplasmic solute-binding protein Sma1651 [imported] - Sinorh
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C;Accession: G95374
R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows
; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilot
A;Reference number: A95262; MUID:21396509; PMID:11481432
A;Accession: G95374
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-525 <KUR>
A;Cross-references: UNIPROT:Q92YH7; GB:AE006469; PIDN:AAK65561.1; PID:gl4524039; GSPDB:G
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
heault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
A;Contents: annotation
C;Genetics:
A;Gene: Sma1651
A;Genome: plasmid

Alignment Scores:
Pred. No.: 5.01 Length: 525
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 8.79% Indels: 0
Gaps: 0
DB:

US-09-910-208B-12 (1-276) x G95374 (1-525)

Qy 96 CTCACCCCTAGAGAGGCGTCAAA 73
Db 96 LeuThrIeuArgGluGlyVallys 103

RESULT 7
T39800
probable DNA-binding protein - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T39800
R;McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.; Skelton, J.; Churcher, C.M.
submitted to the EMBL Data Library, July 1999
A;Reference number: Z21880
A;Accession: T39800
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-900 <MCD>
A;Cross-references: UNIPROT:Q9UUD1; EMBL:AL109731; PIDN:CAB52036.1; GSPDB:GN00067; SPDB
A;Experimental source: strain 972h-; cosmid cl9C2
C;Genetics:
A;Gene: SPDB:SPBC19C2.09
A;Map position: 2

Alignment Scores:
Pred. No.: 4.84 Length: 900
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
DB:

Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 8.79% Indels: 0
 DB: 2 Gaps: 0

US-09-910-208B-12 (1-276) x T39800 (1-900)

QY 137 TTGATGGTGTTCGACGCTCTTT 114

DB 577 LeuMetValPheAlaSerSerPhe 584

RESULT 8

S03818 carboxymethylcellulase (EC 3.2.1.-) precursor - Pseudomonas fluorescens subsp. cellulosa

C:Species: Pseudomonas fluorescens subsp. cellulosa

C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 04-Apr-2004

C:Accession: S03818

R:Hall, J.; Gilbert, H.J.

Mol. Gen. Genet. 213, 112-117, 1988

A:Title: The nucleotide sequence of a carboxymethylcellulase gene from Pseudomonas fluorescens subsp. cellulosa

A:Reference number: S03818; MUID:89127129; PMID:2851699

A:Accession: S03818

A:Molecule type: DNA

A:Residues: 1-962 <HAL>

A:Cross-references: EMBL:X12570; NID:g45503; PIDN:CAA31082.1; PID:g45504

A:Note: The authors translated the codon CAG for residue 18 as Gly, ATC for residue 503

C:Keywords: glycosidase; hydrolase

F:670-707/Domain: glycosidase GWSW

F:865-962/Domain: bacterial cellulose-binding domain homology <GWS>

F:866-961/Disulfide bonds: #status predicted

Alignment Scores:

Pred. No.: 4.82 Length: 962
 Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 8.70% Indels: 0
 DB: 2 Gaps: 0

US-09-910-208B-12 (1-276) x S03818 (1-962)

QY 18 GCATCTGGGGAATTGTCATAT 41

DB 861 AlaSerGlyGlyAsnCysGlnTyr 868

RESULT 9

F71350 hypothetical protein TP0224 - syphilis spirochete

C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)

C:Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004

C:Accession: F71350

R:Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin

son, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McD

they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.

Science 281, 375-388, 1998

A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.

A:Reference number: A71250; MUID:98332770; PMID:9665876

A:Accession: F71350

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-34 <COL>

A:Cross-references: UNIPROT:083253; GB:AE000520; NID:g3322492; PIDN:AAC6521

A:Experimental source: strain Nichols

C:Genetics:

A:Gene: TP0224

Alignment Scores:

Pred. No.: 72.6 Length: 34
 Score: 7.00 Matches: 7
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 7.69% Indels: 0
 DB: 2 Gaps: 0

US-09-910-208B-12 (1-276) x F71350 (1-34)

QY 219 TTCTTGAAGTCGACCTGTTC 199

DB 10 PheLeuLysValAspLeuPhe 16

RESULT 10

B34912

hypothetical protein ftr 5'-region - Methanobacterium thermoautotrophicum (strain Delta

C:Species: Methanobacterium thermoautotrophicum

C:Date: 16-Apr-1999 #sequence_revision 16-Apr-1999 #text_change 09-Jul-2004

C:Accession: B34912

R:DiMarco, A.A.; Sment, K.A.; Konisky, J.; Wolfe, R.S.

J. Biol. Chem. 265, 472-476, 1990

A:Title: The formylmethanofuran:tetrahydromethanopterin formyltransferase from Methanob.

A:Reference number: A34912; MUID:90094441; PMID:2403564

A:Accession: B34912

A:Molecule type: DNA

A:Residues: 1-50 <DIM>

A:Cross-references: UNIPROT:Q9P994; GB:J05173; NID:g1196490; PIDN:AAA8221.1; PID:g1196

A:Experimental source: strain Delta H

C:Comment: This is the hypothetical translation of a sequence that was not reported as

Alignment Scores:

Pred. No.: 70.9 Length: 50
 Score: 7.00 Matches: 7
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 7.61% Indels: 0
 DB: 4 Gaps: 0

US-09-910-208B-12 (1-276) x B34912 (1-50)

QY 25 GAGGGAATTGTCATATCTTC 45

DB 10 GluGlyIleValAsnIlePhe 16

RESULT 11

S69743

probable membrane protein YPR170c - yeast (Saccharomyces cerevisiae)

C:Species: Saccharomyces cerevisiae

C:Date: 22-Nov-1996 #sequence_revision 22-Nov-1996 #text_change 26-Aug-1999

C:Accession: S69743; S69742

R:Pauley, A.

A:Description: The sequence of S. cerevisiae cosmid 9705.

A:Reference number: S59829

A:Accession: S69743

A:Molecule type: DNA

A:Residues: 1-81 <PAU>

A:Cross-references: EMBL:U25842; MIPS:YPR170C

R:Hallsworth, K.

submitted to the EMBL Data Library, April 1995

A:Description: The sequence of S. cerevisiae cosmid 9325.

A:Reference number: S59821

A:Accession: S69742

A:Molecule type: DNA

A:Residues: 82-111 <HAL>

A:Cross-references: EMBL:U25840; MIPS:YPR170C

C:Genetics:

A:Map position: 16R

C:Superfamily: Saccharomyces probable membrane protein YPR170C

C:Keywords: transmembrane protein

F:23-39/Domain: transmembrane #status predicted <TMM>

Alignment Scores:

Pred. No.: 67.5 Length: 111
 Score: 7.00 Matches: 7
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 7.69% Indels: 0
 DB: 2 Gaps: 0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 7.69% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-12 (1-276) x S72253 (1-147)

QY 113 GTAAGCAGCTGCTTCAAGCTCA 93
DB 123 ValSerSerCysPheSerSer 129

RESULT 15

A64476
hypothetical protein MJ1410 - Methanococcus jannaschii
C:Species: Methanococcus jannaschii
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: A64476
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
reson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C
A:Title: Completed genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A:Reference number: A64300; MUID:96337999; PMID:8688087
A:Accession: A64476
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-159 <BUL>
A:Cross-references: UNIPROT:Q58805; GB:U67581; GB:L77117; NID:g2826404; PIDN:AAB99417.1;
C:Genetics:
A:Map position: REV1371312-1370833

Alignment Scores:

Pred. No.: 66 Length: 159
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 7.61% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-12 (1-276) x A64476 (1-159)

QY 133 ATCAGATATCAAGATATAA 153
DB 145 IleLysAsnIleLysAspLys 151

Search completed: February 23, 2005, 12:39:07
Job time : 36 secs

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GenCore version 5.1.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: February 23, 2005, 12:15:09 ; Search time 115 Seconds

(without alignments)
2457.980 Million cell updates/sec

Title: US-09-910-208B-12

Perfect score: 92

Sequence: 1 atgacaaaacttgagagca.....attaccacacccacaaagag 276

Scoring table: OLIGO

Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1612378 seqs, 512079187 residues

Word size: 1

Total number of hits satisfying chosen parameters: 3224408

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO spool_p/HADAD-09-910208B/runat_23022005.102315.15797/app_query.fasta.1
-DB=UniProt_03 -QFMT=fastan -SUFFIX=oligo.rup -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=500 -DOALIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=HADAD-09-910208B @CGN 1.1.244 @runat_23022005.102315.15797 -NCPU=6
-ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THRAADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	91	98.9	91	1 S112 HUMAN	P80511 homo sapien
2	9	9.8	70	2 Q9TR16	Q9tr16 bos taurus
3	9	9.8	81	1 S112 RABIT	P77791 oryctolagus
4	9	9.8	91	1 S112 BOVIN	P79105 bos taurus
5	9	9.8	91	1 S112 PIG	P80310 sus scrofa
6	9	9.8	118	1 S109 RABIT	P50117 oryctolagus
7	9	9.8	122	1 S109 BOVIN	P28783 bos taurus
8	9	9.8	402	2 Q6XE66	Q6xe66 uncultured
9	8	8.7	92	1 S106 HORSE	Q77691 equus caball
10	8	8.7	95	2 Q6XG62	Q6xg62 brachydanio
11	8	8.7	175	1 CALB ASHGO	Q757b7 ashbya goss
12	8	8.7	213	2 Q9H4U1	Q9h4u1 homo sapien
13	8	8.8	248	2 Q87I93	Q87i93 vibrio para
14	8	8.8	254	1 GLTF_ECOLI	P28721 escherichia
15	8	8.8	264	2 Q72V46	Q72v46 leptospira
16	8	8.8	264	2 Q8EZR3	Q8ezr3 leptospira

Q6mc24	parachlamyd	311	2	Q6MC24	8.8	8	17	c
Q87tx0	pseudomonas	355	2	Q87TX0	8.7	8	18	c
Q689y0	turnip mosa	362	2	Q689Y0	8.8	8	19	c
Q87ok2	vibrio para	404	2	Q87OK2	8.7	8	20	c
Q9kz6	vibrio chol	404	2	Q9KZ6	8.7	8	21	c
Q8eun4	streptococc	516	2	Q8EUN4	8.8	8	22	c
Q8eas	streptococc	516	2	Q8EAS	8.8	8	23	c
Q92yh7	rhizobium m	525	2	Q92YH7	8.8	8	24	c
Q8iln4	plasmodium	660	2	Q8ILN4	8.7	8	25	c
Q8rvq5	arabidopsis	829	1	SC10 ARATH	8.7	8	26	c
Q7rsl0	plasmodium	869	2	Q7RSL0	8.8	8	27	c
Q8t9f2	drosophila	874	2	Q8T9F2	8.7	8	28	c
Q9fj11	arabidopsis	888	2	Q9FJ11	8.8	8	29	c
Q9uud1	schizosacch	900	2	Q9UUD1	8.8	8	30	c
P10476	pseudomonas	962	1	GUNA PSEFL	8.7	8	31	c
Q9vuc2	drosophila	1780	2	Q9VUC2	8.7	8	32	c
Q7rix5	plasmodium	1976	2	Q7RIX5	8.7	8	33	c
Q7xpb4	oryza sativ	3331	2	Q7XPB4	8.8	8	34	c
Q83253	treponema p	34	1	Y224 TREPA	7.7	7	35	c
Q7mey1	vibrio vuln	45	2	Q7MEY1	7.7	7	36	c
Q9p994	methanobact	50	2	Q9P994	7.6	7	37	c
Q9gpt5	dictyosteli	64	2	Q9GPT5	7.6	7	38	c
Q63e24	bacillus ce	64	2	Q63E24	7.6	7	39	c
Q73bf2	bacillus ce	64	2	Q73BF2	7.6	7	40	c
Q81g60	bacillus ce	64	2	Q81G60	7.6	7	41	c
Q81tb9	bacillus th	64	2	Q81TB9	7.6	7	42	c
Q6hlj9	bacillus th	64	2	Q6HLJ9	7.6	7	43	c
Q6v5x6	human immun	66	2	Q6V5X6	7.6	7	44	c
Q6mpb8	bdellovibri	89	2	Q6MPB8	7.6	7	45	c
Q98953	gallus gall	92	1	S106 CHICK	7.6	7	46	c
Q8wxg8	homo sapien	98	1	S10Z HUMAN	7.6	7	47	c
Q7y3w6	bacterioph	99	2	Q7Y3W6	7.7	7	48	c
Q8maq3	parachlamyd	102	2	Q8MAQ3	7.6	7	49	c
Q8ka6	pseudomonas	104	2	Q8KA6	7.6	7	50	c
Q7w021	bordetella	108	2	Q7W021	7.6	7	51	c
Q7wce1	bordetella	108	2	Q7WCE1	7.6	7	52	c
Q7wge1	bordetella	108	2	Q7WGE1	7.6	7	53	c
Q987b3	urtica dioi	112	2	Q9S7B3	7.6	7	54	c
Q98yrs	urtica dioi	112	2	Q9SYRS	7.6	7	55	c
Q82zp0	pyrobaculum	119	2	Q8ZP0	7.6	7	56	c
Q6f89	acinetobact	120	2	Q6F89	7.7	7	57	c
Q9ddw9	xenopus lae	121	2	Q9DDW9	7.7	7	58	c
Q9x4m4	lactobacill	131	2	Q9X4M4	7.6	7	59	c
Q62575	meriones un	132	1	IL5 MERUN	7.6	7	60	c
Q08125	rattus norv	132	1	IL5 RAT	7.6	7	61	c
Q62tm0	bacillus li	132	2	Q62TM0	7.7	7	62	c
Q9r2c9	rattus norv	132	2	Q9R2C9	7.6	7	63	c
P04401	mus musculu	133	1	IL5 MOUSE	7.6	7	64	c
Q82263	enterococcu	139	2	Q82Z63	7.7	7	65	c
Q6zu59	homo sapien	143	2	Q6ZU59	7.6	7	66	c
Q9gy87	rattus norv	144	2	Q9GY87	7.7	7	67	c
Q7m418	oligobrachi	147	1	GLBC OLIMA	7.7	7	68	c
Q8bj13	mus musculu	148	2	Q8BJ13	7.6	7	69	c
Q7pm6	fusobacteri	150	2	Q7P4M6	7.6	7	70	c
Q9ft5	arabidopsis	154	2	Q9FPT5	7.6	7	71	c
Q7psx7	anopheles g	157	2	Q7PSX7	7.7	7	72	c
Q6z2k1	oryza sativ	157	2	Q6Z2K1	7.6	7	73	c
Q58805	methanococc	159	2	Q58805	7.6	7	74	c
Q97vy3	sulfolobus	165	1	LEUD_SULSO	7.6	7	75	c
Q88r01	pseudomonas	166	2	Q88R01	7.6	7	76	c
Q88ae1	pseudomonas	167	2	Q88AE1	7.6	7	77	c
Q974g9	sulfolobus	168	2	LEUD_SULTO	7.6	7	78	c
Q8g3l2	bifidobacte	168	2	Q8G3L2	7.7	7	79	c
Q8y1w2	ralstonia s	169	2	Q8Y1W2	7.7	7	80	c
Q6n6t6	rhodopseudo	170	2	Q6N6T6	7.6	7	81	c
Q6cge6	yarrowia li	173	1	CALB_YARLI	7.6	7	82	c
Q957y8	casuaricus c	173	2	Q95Y8	7.7	7	83	c
Q9uu93	schizosacch	174	1	CALB_SCHPO	7.6	7	84	c
P25296	saccharomyc	175	1	CALB_YEAST	7.6	7	85	c
Q6fli4	candida gla	175	1	CALB_CANGA	7.6	7	86	c
Q874t7	kluveromyc	175	1	CALB_KUULA	7.6	7	87	c
Q7mh50	vibrio vuln	175	2	Q7MH50	7.7	7	88	c
Q9ryc7	deinococcus	177	2	Q9RYC7	7.7	7	89	c

90	7	7.6	182	2	Q62N06	Q62n06 bacillus li	c 163	7	7.7	319	2	Q7NYF2	Q7nyf2 chromobacte
c 91	7	7.7	183	2	Q65194	Q65194 african swi	c 164	7	7.6	325	2	Q6HGP3	Q6hgp3 bacillus th
c 92	7	7.7	184	2	Q65272	Q65272 african swi	c 165	7	7.7	326	2	Q7VUJ0	Q7vuj0 helicobacte
c 93	7	7.7	185	2	Q7QM90	Q7qm90 anopheles g	c 166	7	7.7	326	2	Q8DXV8	Q8dxv8 streptococc
c 94	7	7.7	185	2	Q8EJ16	Q8ej16 shewanella	c 167	7	7.7	326	2	Q8E3H6	Q8e3h6 streptococc
c 95	7	7.6	187	2	Q8URJ7	Q8urj7 brachyspira	c 168	7	7.6	327	2	Q735E8	Q735e8 bacillus ce
c 96	7	7.7	188	2	Q756U6	Q756u6 ashbya goss	c 169	7	7.6	328	1	PE59_ARATH	Q39034 arabidopsis
c 97	7	7.7	188	2	Q9FJH3	Q9fjh3 arabidopsis	c 170	7	7.6	334	1	DPOB_HUMAN	Q8k409 mus musculu
c 98	7	7.6	189	2	Q65D80	Q65d80 bacillus li	c 171	7	7.6	334	1	DPOB_MOUSE	Q8k409 mus musculu
c 99	7	7.6	192	2	Q6EBC0	Q6ebc0 trichoplusi	c 172	7	7.6	334	1	DPOB_MOUSE	Q8k409 mus musculu
100	7	7.6	196	2	Q8TNB7	Q8tnb7 methanosarc	c 173	7	7.6	334	2	Q639D4	Q639d4 bacillus ce
c 101	7	7.7	197	1	YZZ7_YEAST	YZZ7 yeast	c 174	7	7.7	334	2	Q745H5	Q745h5 pseudomonas
c 102	7	7.6	208	2	Q9EMH3	Q9emh3 ansata moe	c 175	7	7.6	334	2	Q9HYL8	Q9hyl8 pseudomonas
c 103	7	7.7	217	2	Q7F7B3	Q7f7b3 fusobacteri	c 176	7	7.6	335	2	Q8XJW3	Q8xjw3 clostridium
c 104	7	7.6	218	2	Q7MWA1	Q7mwa1 porphyromon	c 177	7	7.6	336	2	Q8BGM5	Q8bgm5 paramedum
c 105	7	7.7	219	2	Q6QVY6	Q6qvye pedicularis	c 178	7	7.6	336	2	Q8B2K9	Q8b2k9 pseudomonas
c 106	7	7.6	223	2	Q72XQ2	Q72xq2 bacillus ce	c 179	7	7.6	336	2	Q8BXX5	Q8bxx5 mus musculu
c 107	7	7.6	225	1	NR0M_ECOLI	NR0403 escherichia	c 180	7	7.6	339	2	O20385	Q20385 rubus hawai
c 108	7	7.7	225	2	Q8QPY1	Q8qpy1 mimulus kel	c 181	7	7.7	339	2	Q9C6V3	Q9c6v3 arabidopsis
c 109	7	7.7	225	2	Q8FKD8	Q8fkds escherichia	c 182	7	7.7	343	2	Q7YFU6	Q7yfu6 manica rubi
c 110	7	7.7	225	2	Q8XEA6	Q8xea6 escherichia	c 183	7	7.7	344	2	Q8VE58	Q8ve58 mus musculu
c 111	7	7.6	226	2	Q8PN66	Q8pn66 xanthomonas	c 184	7	7.6	345	2	Q9BT58	Q9bt58 mus musculu
c 112	7	7.6	226	2	Q6MRV7	Q6mr7 mycoplasma	c 185	7	7.6	347	2	Q810Y7	Q810y7 caenorhabdi
c 113	7	7.7	227	2	Q6QPY2	Q6qpy2 leucocarpus	c 186	7	7.6	350	2	Q22946	Q22946 caenorhabdi
c 114	7	7.7	229	2	Q6UWS1	Q6uws1 homo sapien	c 187	7	7.6	350	2	Q8TIE2	Q8tie2 dictyosteli
c 115	7	7.7	229	2	Q9H5X9	Q9h5x9 homo sapien	c 188	7	7.6	352	2	Q8CNQ8	Q8cnq8 staphylococ
c 116	7	7.7	233	1	NT7_BRARE	NT73797 brachydanio	c 189	7	7.6	353	2	Q8NVU8	Q8nvu8 staphylococ
c 117	7	7.7	235	2	Q74Z63	Q74z63 ashbya goss	c 190	7	7.6	353	2	Q99T19	Q99t19 staphylococ
c 118	7	7.6	241	2	Q8PBL1	Q8pb11 xanthomonas	c 191	7	7.6	353	2	Q7A4U0	Q7a4u0 staphylococ
c 119	7	7.7	243	2	Q6ZV13	Q6zv13 homo sapien	c 192	7	7.6	353	2	Q6G874	Q6g874 staphylococ
c 120	7	7.7	247	2	Q8KC40	Q8kc40 chlorobium	c 193	7	7.6	353	2	Q6GFJ7	Q6gfj7 staphylococ
c 121	7	7.6	247	2	Q9D015	Q9d015 mus musculu	c 194	7	7.7	354	2	Q7XXQ4	Q7xxq4 oryza sativ
c 122	7	7.6	259	2	Q9XBG2	Q9xbg2 burkholderi	c 195	7	7.7	355	2	Q65NU4	Q65nu4 bacillus li
c 123	7	7.7	261	2	Q8AA73	Q8aa73 bacteroides	c 196	7	7.7	355	2	Q8UQ42	Q8uq42 agrobacteri
c 124	7	7.6	262	2	Q8GBS6	Q8gbs6 treponema m	c 197	7	7.6	362	2	Q689X3	Q689x3 streptomyce
c 125	7	7.6	266	2	Q98Y57	Q98y57 reptilian p	c 198	7	7.6	362	2	Q82E53	Q82e53 homo sapien
c 126	7	7.6	266	2	Q98Y58	Q98y58 reptilian p	c 199	7	7.6	365	1	SMS2_HUMAN	SMS2 human
c 127	7	7.6	266	2	Q98Y60	Q98y60 reptilian p	c 200	7	7.6	365	1	Q8UJ06	Q8uj06 streptomyce
c 128	7	7.6	266	2	Q98Y61	Q98y61 reptilian p	c 201	7	7.6	367	2	Q9X888	Q9x888 streptomyce
c 129	7	7.6	267	2	Q8A631	Q8a631 bacteroides	c 202	7	7.7	370	2	Q73PD0	Q73pd0 treponema d
c 130	7	7.6	268	1	LGT_SYNEL	LGT synechococc	c 203	7	7.6	370	2	Q81149	Q81149 caenorhabdi
c 131	7	7.6	273	2	Q64FU7	Q64fu7 bacteroides	c 204	7	7.6	373	2	Q8TVP9	Q8tvp9 methanopyru
c 132	7	7.7	274	2	Q73JEA	Q73je4 treponema d	c 205	7	7.6	373	2	O21149	O21149 caenorhabdi
c 133	7	7.7	274	2	Q8R136	Q8r136 fusobacteri	c 206	7	7.6	380	2	Q74DF3	Q74df3 geobacter s
c 134	7	7.6	276	1	PANC_HELPU	PANC heliocobacte	c 207	7	7.6	382	2	Q7D348	Q7d348 agrobacteri
c 135	7	7.7	278	2	Q8GS03	Q8gs03 oryza sativ	c 208	7	7.7	383	2	Q97P35	Q97p35 streptococc
c 136	7	7.7	278	2	Q8FQZ7	Q8fqz7 corynebacte	c 209	7	7.7	383	2	Q8DNN0	Q8dnn0 streptococc
c 137	7	7.7	278	2	Q8FQZ7	Q8fqz7 corynebacte	c 210	7	7.6	386	2	Q8C3H3	Q8c3h3 mus musculu
c 138	7	7.6	279	2	Q6JE40	Q6je40 humulus jap	c 211	7	7.7	391	2	Q974X7	Q974x7 sulfolobus
c 139	7	7.6	279	2	Q7PTS8	Q7pts8 anopheles g	c 212	7	7.7	395	2	Q891R0	Q891r0 clostridium
c 140	7	7.7	282	2	Q9M0T7	Q9m0t7 arabidopsis	c 213	7	7.7	395	2	Q891R0	Q891r0 clostridium
c 141	7	7.7	283	2	Q9ALN3	Q9aln3 saccharopol	c 214	7	7.6	396	2	Q75824	Q75824 homo sapien
c 142	7	7.6	288	2	Q7RV11	Q7rv11 neurospora	c 215	7	7.6	401	2	Q8DLV1	Q8dlv1 synechococc
c 143	7	7.7	288	2	Q7VHG2	Q7vng2 helicobacte	c 216	7	7.6	401	2	Q8BUT5	Q8bul5 debaryomyce
c 144	7	7.7	292	2	Q61EX5	Q61ex5 homo sapien	c 217	7	7.6	402	2	Q9NT09	Q9nt09 homo sapien
c 145	7	7.7	293	1	XT31_ARATH	XT31 arabidopsis	c 218	7	7.6	402	2	Q86VW6	Q86vw6 homo sapien
c 146	7	7.7	293	2	Q8LVV8	Q8lvv8 polytomella	c 219	7	7.6	409	1	MNTH_YERPE	MNTH yerpe
c 147	7	7.6	293	2	Q9D140	Q9d140 mus musculu	c 220	7	7.6	409	1	Q668N2	Q668n2 yersinia ps
c 148	7	7.7	294	2	Q6N476	Q6n476 rhodospseud	c 221	7	7.6	411	2	Q82VF8	Q82vf8 nitrosomona
c 149	7	7.6	299	2	Q8Z086	Q8z086 anabaena sp	c 222	7	7.6	413	2	Q8EFO2	Q8efg2 shewanella
c 150	7	7.6	300	2	Q755Z4	Q755z4 ashbya goss	c 223	7	7.6	415	2	Q8P5L8	Q8p5l8 brachydanio
c 151	7	7.7	303	1	PCPR_SPHCR	P55524 sphingobium	c 224	7	7.6	417	2	Q66KC4	Q66kc4 xenopus tro
c 152	7	7.7	305	2	Q8N308	Q8n308 homo sapien	c 225	7	7.6	417	2	Q66KC4	Q66kc4 xenopus tro
c 153	7	7.7	307	2	Q94333	Q94333 bradyrhizob	c 226	7	7.6	418	2	Q66KC4	Q66kc4 xenopus tro
c 154	7	7.6	308	2	Q8RGK4	Q8rgk4 fusobacteri	c 227	7	7.7	419	2	Q7PTX3	Q7ptx3 anopheles g
c 155	7	7.6	310	1	PANE_AQUAE	P56719 aquifex aeo	c 228	7	7.6	421	2	Q895H9	Q895h9 clostridium
c 156	7	7.7	315	1	YAI4_HAEIN	P44094 haemophilus	c 229	7	7.6	421	2	Q895H9	Q895h9 clostridium
c 157	7	7.7	315	2	Q9CL82	Q9cl82 pasteurella	c 230	7	7.7	430	2	Q895H9	Q895h9 clostridium
c 158	7	7.7	316	2	Q8CGR1	Q8cgr1 mus musculu	c 231	7	7.7	431	2	Q84G45	Q84g45 rhizobium l
c 159	7	7.7	316	2	Q8D3V4	Q8d3v4 mus musculu	c 232	7	7.7	431	2	Q84G45	Q84g45 rhizobium l
c 160	7	7.7	318	1	O4HC_HUMAN	Q8ng74 homo sapien	c 233	7	7.6	434	2	Q8BMC7	Q8bmc7 mus musculu
c 161	7	7.6	318	2	Q9KM43	Q9km43 vibrio chol	c 234	7	7.6	434	2	Q8BMC7	Q8bmc7 mus musculu
c 162	7	7.7	319	2	Q9HS11	Q9hs11 halobacteri	c 235	7	7.6	438	2	Q735V8	Q735v8 bacillus ce

236	7	7.6	442	2	Q20755	Q20755 caenorhabdi	309	7	7.6	631	2	QMSS3	Q6mss3 mycoplasma
237	7	7.7	443	2	Q7MA91	Q8uac12 wolinnella s	c 310	7	7.7	638	2	Q7SGM0	Q7sgm0 oryza sativ
238	7	7.7	443	2	Q8UC12	Q8uc12 agrobacteri	311	7	7.6	639	2	Q7SON7	Q7son7 neurospora
239	7	7.6	447	1	GASR_HUMAN	P32239 homo sapien	312	7	7.6	641	2	Q9H6W3	Q9h6w3 homo sapien
240	7	7.6	447	2	Q16144	Q16144 homo sapien	313	7	7.6	641	2	Q7QU29	Q7qu29 giardia lam
241	7	7.6	447	2	Q92492	Q92492 homo sapien	314	7	7.6	643	2	Q7PPE7	Q7ppe7 anopheles g
242	7	7.6	452	1	GASR_RABIT	P46627 oryctolagus	315	7	7.6	643	2	Q926G3	Q926g3 vibrio para
243	7	7.6	453	1	GASR_CANFA	P30552 canis famil	316	7	7.6	643	2	Q87MJ8	Q87mj8 vibrio para
244	7	7.6	454	1	GASR_BOVIN	P79266 bos taurus	c 317	7	7.6	650	2	Q8EP63	Q8ep63 oceanobacil
245	7	7.7	458	2	G60957	G60957 leishmania	c 318	7	7.7	651	2	Q9DDN7	Q9ddn7 apteronotus
246	7	7.7	458	2	Q9PNA3	Q9pna3 campylobact	319	7	7.6	656	2	Q73RI8	Q73ri8 treponema d
247	7	7.7	459	2	Q80WT9	Q80wt9 mus musculu	320	7	7.6	660	2	Q8PRE6	Q8pre6 helicobacte
248	7	7.7	460	2	Q6FIJ3	Q6fi1j3 mesoplasma	c 321	7	7.6	662	2	Q74CW0	Q74cw0 geobacter s
249	7	7.6	465	2	Q91ZD8	Q91zld8 arabidopsis	c 322	7	7.7	662	2	Q6DJL3	Q6djl3 xenopus lae
250	7	7.7	469	2	Q96HN8	Q96hn8 homo sapien	c 323	7	7.7	667	2	Q8ELZ9	Q8elz9 oceanobacil
251	7	7.7	469	2	Q9NVE1	Q9nvel1 homo sapien	c 324	7	7.7	676	2	Q89HT3	Q89ht3 bradyrhizob
252	7	7.7	469	2	Q624S6	G6z4s6 oryza sativ	c 325	7	7.7	678	2	Q9RTM4	Q9rtm4 deinococcus
253	7	7.6	470	2	Q04679	Q04679 lycopersico	326	7	7.6	682	2	Q9GPR8	Q9gpr8 dictyosteli
254	7	7.6	470	2	P93228	P93228 lycopersico	327	7	7.6	683	2	Q8CKE4	Q8cke4 oceanobacil
255	7	7.6	476	2	Q7SKD7	Q7skd7 brachydanio	c 328	7	7.7	701	2	Q8TFH1	Q8tfh1 caedibacter
256	7	7.6	478	2	Q83920	Q83920 treponema p	c 329	7	7.6	704	2	Q8P7W7	Q8p7w7 xanthomonas
257	7	7.6	481	2	Q9BZC0	Q9bzc0 homo sapien	c 330	7	7.7	711	2	Q6FQB4	Q6fqb4 candida gla
258	7	7.6	481	2	Q7KFF8	Q7kff8 drosophila	c 331	7	7.7	712	2	Q67KG5	Q67kg5 symbiobacte
259	7	7.6	482	1	VGLY_TACV7	P31842 tacaribe vi	332	7	7.7	712	2	Q8EF46	Q8ef46 shewanella
260	7	7.6	483	1	VGLY_TACV5	P31841 tacaribe vi	333	7	7.6	718	1	HOK3_HUMAN	Q86vs8 homo sapien
261	7	7.6	483	1	VGLY_TACVT	P31840 tacaribe vi	334	7	7.6	718	1	HOK3_MOUSE	Q8buk6 mus musculu
262	7	7.6	483	2	Q8Y7T3	Q8y7t3 listeria mo	c 335	7	7.6	719	2	Q6GQ73	Q6gq73 xenopus lae
263	7	7.7	484	2	Q9NVU9	Q9nvu9 homo sapien	336	7	7.6	721	2	Q6NRB0	Q6nrbo xenopus lae
264	7	7.7	484	2	Q6VMT3	Q6vmt3 myxococcus	337	7	7.6	722	2	Q7X5J8	Q7x5j8 leuconostoc
265	7	7.6	485	2	Q8N6W0	Q8n6w0 homo sapien	c 338	7	7.7	723	2	Q7Z402	Q7z402 homo sapien
266	7	7.6	485	2	Q8SZ35	Q8sz35 drosophila	c 339	7	7.7	723	2	Q7Z5M4	Q7z5m4 homo sapien
267	7	7.6	485	2	Q9VNM1	Q9vnm1 drosophila	c 340	7	7.7	723	2	Q86WX0	Q86wx0 homo sapien
268	7	7.7	487	2	Q969J4	Q969j4 homo sapien	c 341	7	7.7	731	1	CND2_MOUSE	Q8cl156 mus musculu
269	7	7.7	489	2	Q96BY8	Q96by8 homo sapien	342	7	7.6	733	2	Q9DYB8	Q9dyb8 tt virus. h
270	7	7.7	489	2	Q6UX01	Q6ux01 homo sapien	343	7	7.6	739	2	Q8TW7	Q8tw7 methanopyru
271	7	7.6	492	2	Q9EX69	Q9ex69 alcaligenes	c 344	7	7.7	747	2	Q9S9Y3	Q9sy93 arabidopsis
272	7	7.6	495	1	VGLY_TACV	P18141 tacaribe vi	345	7	7.7	758	2	Q7U1V4	Q7u1v4 rhodopirell
273	7	7.6	496	2	Q99LV2	Q99lv2 mus musculu	c 346	7	7.7	768	2	Q8EUF9	Q8euf9 mycoplasma
274	7	7.7	506	2	Q630V8	Q630v8 bacillus ce	347	7	7.6	770	2	Q6O999	Q6o999 dictyosteli
275	7	7.7	506	2	Q72XG3	Q72xg3 bacillus ce	348	7	7.6	784	2	Q7N0L5	Q7n0l5 photorhabdu
276	7	7.7	506	2	Q81K10	Q81k10 bacillus an	349	7	7.6	793	2	Q8KAF7	Q8kaf7 chlorobium
277	7	7.7	506	2	Q6HAZ5	Q6haz5 bacillus th	350	7	7.6	821	2	Q8IC16	Q8ic16 plasmodium
278	7	7.6	508	2	Q6DFS1	Q6dfs1 xenopus tro	c 351	7	7.7	822	2	Q7P9M6	Q7p9m6 rickettsia
279	7	7.7	509	2	Q9SVM2	Q9svm2 arabidopsis	c 352	7	7.7	822	2	Q92GK9	Q92gk9 rickettsia
280	7	7.6	516	2	Q96LC6	Q96lc6 homo sapien	353	7	7.6	827	2	Q6H8R9	Q6h8r9 ustilago ma
281	7	7.6	516	2	Q9NVK7	Q9nvk7 homo sapien	354	7	7.6	839	2	Q74B54	Q74b54 geobacter s
282	7	7.7	517	2	Q672X2	Q672x2 corymborkis	c 355	7	7.7	842	1	EF2_PICPA	Q874b9 pichia past
283	7	7.6	522	1	IMA2_XENLA	P52171 xenopus lae	c 356	7	7.7	842	1	EF2_SCHPO	Q14460 schizosacch
284	7	7.7	523	2	Q07904	Q07904 saccharomyc	c 357	7	7.7	842	2	Q6CI99	Q6ci99 yarrowia li
285	7	7.6	523	2	Q8EYV4	Q8eyv4 mycoplasma	c 358	7	7.7	844	1	EF2_NEUCR	Q96x45 neurospora
286	7	7.7	529	2	Q65CB5	Q65cb5 streptomyce	c 359	7	7.7	845	2	Q6AVG4	Q6avg4 oryza sativ
287	7	7.7	530	2	Q751C5	Q751c5 ashbya goss	360	7	7.6	845	2	Q7VSO4	Q7vsg4 bordetella
288	7	7.6	530	2	Q6KBZ2	Q6kbz2 alicyclobac	c 361	7	7.6	849	2	Q23253	Q23253 arabidopsis
289	7	7.6	530	2	Q8KD27	Q8kd27 chlorobium	362	7	7.6	870	2	Q7W363	Q7w363 bordetella
290	7	7.7	542	2	Q7ZEB2	Q7zb2 streptomyce	363	7	7.6	880	2	Q7WE10	Q7we10 bordetella
291	7	7.7	549	1	YJCE_ECOLI	P32703 escherichia	c 364	7	7.7	881	2	Q88FU9	Q88fu9 pseudomonas
292	7	7.7	549	2	Q7A924	Q7a924 escherichia	365	7	7.6	882	2	Q8BUI9	Q8bui9 mus musculu
293	7	7.7	549	2	Q8X5U0	Q8x5u0 escherichia	366	7	7.6	889	2	Q8BL87	Q8bl87 mus musculu
294	7	7.7	549	2	Q8FAZ5	Q8faz5 escherichia	c 367	7	7.7	891	2	Q83YT3	Q83yt3 arabidopsis
295	7	7.7	549	2	Q83IR1	Q83ir1 shigella fl	c 368	7	7.7	931	2	Q882J5	Q882j5 pseudomonas
296	7	7.7	550	2	Q980I2	Q980i2 sulfolobus	c 369	7	7.7	942	2	Q6CVL6	Q6cvl6 kluyveromyc
297	7	7.7	556	2	Q7R198	Q7r198 plasmodium	370	7	7.6	959	2	Q6NBB4	Q6nbb4 rhodopseuo
298	7	7.7	571	2	P78802	P78802 schizosacch	371	7	7.6	981	2	Q75H66	Q75h66 oryza sativ
299	7	7.6	578	2	Q822I0	Q822i0 chlamydophi	372	7	7.6	1010	2	Q76BE3	Q76be3 amia calva
300	7	7.7	581	2	Q98HN2	Q98hn2 rhizobium l	373	7	7.6	1030	2	Q875U4	Q875u4 saccharomyc
301	7	7.6	585	2	Q9BNK6	Q9bnk6 spraguea lo	374	7	7.6	1051	2	Q24007	Q24007 drosophila
302	7	7.6	588	2	Q6Y7R8	Q6y7r8 staphylococ	375	7	7.6	1051	2	Q95PA9	Q95pa9 drosophila
303	7	7.6	588	2	Q7NCV8	Q7ncv8 gloebacter	c 376	7	7.7	1055	2	Q6P0M4	Q6pom4 homo sapien
304	7	7.7	593	2	Q92P44	Q92p44 rhizobium m	377	7	7.6	1059	2	Q7YN57	Q7yn57 eimeria ten
305	7	7.6	594	2	Q8SY19	Q8sy19 arabidopsis	378	7	7.6	1076	2	Q8MLT4	Q8mlt4 drosophila
306	7	7.6	601	2	P73278	P73278 synechocyst	379	7	7.6	1076	2	Q6AWQ3	Q6awq3 drosophila
307	7	7.7	605	2	Q75J23	Q75j23 oryza sativ	380	7	7.6	1083	2	Q48839	Q48839 arabidopsis
308	7	7.6	614	2	Q7P5F5	Q7p5f5 fusobacteri	381	7	7.6	1088	2	Q6ZUM6	Q6zum6 homo sapien

382	7	7.6	1123	1	SYLC NEUCR	Pl0857 neurospora	C 455	6	6.6	60	2	Q7Y3P4	Q7Y3P4 enterobacte
383	7	7.6	1130	1	SBCC BAGSU	Q06714 bacillus su	456	6	6.5	60	2	Q55092	Q55092 synecocyst
384	7	7.6	1135	2	Q84W49	Q84W49 arabidopsis	C 457	6	6.5	61	2	Q8UHF3	Q8UHF3 agrobacteri
385	7	7.6	1152	2	Q72355	Q72355 homo sapien	458	6	6.5	61	2	Q81Z37	Q81Z37 bacillus an
386	7	7.6	1154	2	Q6K685	Q6K685 oryza sativ	459	6	6.5	62	2	Q72MN5	Q72MN5 leptospira
387	7	7.6	1157	2	Q6K685	Q6K685 schizosacch	460	6	6.5	62	2	Q8CLA8	Q8CLA8 yersinia pe
388	7	7.6	1188	2	Q9KA07	Q9KA07 bacillus ha	461	6	6.5	65	2	Q8XEW5	Q8XEW5 salmonella
389	7	7.6	1192	2	Q9A525	Q9A525 dictyosteli	462	6	6.5	65	2	Q7COZ8	Q7COZ8 salmonella
390	7	7.6	1231	2	Q97140	Q97140 dictyosteli	C 463	6	6.6	67	2	Q61293	Q61293 antocidaxi
391	7	7.6	1239	1	Y478 HUMAN	Q9nuas8 homo sapien	464	6	6.5	67	2	Q6MDM7	Q6MDM7 parochlamyd
392	7	7.6	1242	2	Q723J5	Q723J5 homo sapien	C 465	6	6.6	68	2	Q649K8	Q649K8 uncultured
393	7	7.6	1262	1	SVI_MOUSE	Q8bu30 mus musculu	C 466	6	6.6	68	2	Q931L0	Q931L0 hepatitis b
394	7	7.6	1262	2	Q6NXX4	Q6NXX4 homo sapien	C 467	6	6.6	69	2	Q9NP09	Q9NP09 forelius ch
395	7	7.6	1262	2	Q6NXX4	Q6NXX4 mus musculu	C 468	6	6.6	69	2	Q64JX4	Q64JX4 plagiolepis
396	7	7.6	1266	1	SVI_HUMAN	P41252 homo sapien	C 469	6	6.6	69	2	Q64JY2	Q64JY2 myrmecocyst
397	7	7.6	1271	2	Q6PGU7	Q6PGU7 brachydanio	C 470	6	6.6	69	2	Q64JY4	Q64JY4 lasius psam
398	7	7.6	1307	2	Q62A85	Q62A85 burkholderi	C 471	6	6.6	69	2	Q64JY6	Q64JY6 lasius psam
399	7	7.6	1319	2	Q63NS2	Q63NS2 burkholderi	C 472	6	6.6	69	2	Q64JY8	Q64JY8 lasius nige
400	7	7.6	1335	2	Q60886	Q60886 dictyosteli	C 473	6	6.6	69	2	Q64JZ0	Q64JZ0 lasius emar
401	7	7.6	1366	1	RPC2 PROMP	Q7v008 prochloroco	C 474	6	6.6	69	2	Q64JZ2	Q64JZ2 lasius brun
402	7	7.6	1419	2	Q813G5	Q813G5 plasmodium	C 475	6	6.6	69	2	Q64JZ4	Q64JZ4 lasius alie
403	7	7.6	1450	2	Q9LFG0	Q9LFG0 arabidopsis	C 476	6	6.6	69	2	Q64K06	Q64K06 lasius flav
404	7	7.6	1504	2	Q9ZGA6	Q9ZGA6 streptomyce	C 477	6	6.6	69	2	Q74ES1	Q74ES1 geobacter s
405	7	7.6	1539	2	Q7R2Y4	Q7R2Y4 giardia lam	C 478	6	6.5	69	2	Q9PIU4	Q9PIU4 campylobact
406	7	7.6	1580	2	Q754A4	Q754A4 ashbya goss	C 479	6	6.6	70	2	Q64JZ6	Q64JZ6 lasius umbr
407	7	7.6	1647	2	Q7R8847	P78847 schizosacch	C 480	6	6.6	70	2	Q64JZ8	Q64JZ8 lasius jens
408	7	7.6	1674	2	Q9FVU8	Q9FVU8 arabidopsis	C 481	6	6.6	70	2	Q64K00	Q64K00 lasius meri
409	7	7.6	1693	2	Q7S1Z7	Q7S1Z7 neurospora	C 482	6	6.6	70	2	Q64K02	Q64K02 lasius fuli
410	7	7.6	1906	1	DICE_MOUSE	Q8r418 mus musculu	C 483	6	6.6	70	2	Q64K04	Q64K04 acanthomyop
411	7	7.6	1944	2	Q8RUAS	Q8RUAS oryza sativ	C 484	6	6.6	70	2	Q64K08	Q64K08 pseudomonas
412	7	7.6	2001	2	Q9M658	Q9M658 arabidopsis	C 485	6	6.5	71	2	Q6PVH5	Q6PVH5 pantoea cit
413	7	7.6	2001	2	Q9M659	Q9M659 arabidopsis	C 486	6	6.6	71	2	Q9X5W8	Q9X5W8 human immu
414	7	7.6	2218	2	Q93705	Q93705 lassa virus	C 487	6	6.6	71	2	Q9YRP7	Q9YRP7 agrobacteri
415	7	7.6	2219	2	Q6GWR8	Q6GWR8 lassa virus	C 488	6	6.6	72	2	Q8UFI7	Q8UFI7 human papil
416	7	7.6	2219	2	Q6GWS2	Q6GWS2 lassa virus	C 489	6	6.6	73	1	VE5 HPV18	VE5 HPV18 bacillus su
417	7	7.6	2220	2	Q6GWS2	Q6GWS2 lassa virus	C 490	6	6.5	74	2	Q94E55	Q94E55 bacillus su
418	7	7.6	2220	2	Q6V630	Q6V630 lassa virus	C 491	6	6.6	74	2	Q8EPJ2	Q8EPJ2 oceanobacil
419	7	7.6	2254	2	Q9LN02	Q9LN02 arabidopsis	C 492	6	6.6	75	2	Q6LIQ3	Q6LIQ3 picorophilus
420	7	7.6	2254	2	Q7RJV1	Q7RJV1 plasmodium	C 493	6	6.6	75	2	Q8X293	Q8X293 escherichia
421	7	7.6	2254	2	Q8IM60	Q8IM60 plasmodium	C 494	6	6.6	75	2	Q73P77	Q73P77 bacillus ce
422	7	7.6	3364	2	Q8IEH5	Q8IEH5 plasmodium	C 495	6	6.6	76	2	Q9DEX4	Q9DEX4 gallus gall
423	7	7.6	3377	2	Q7RIW0	Q7RIW0 plasmodium	C 496	6	6.6	76	2	Q7VIX6	Q7VIX6 prochloroco
424	7	7.6	3985	2	Q9J179	Q9J179 rattus norv	C 497	6	6.5	77	2	Q8VBD6	Q8VBD6 white spot
425	7	7.6	4306	2	Q6VJK2	Q6VJK2 strongyloce	C 498	6	6.6	77	2	Q8VBD6	Q8VBD6 white spot
426	7	7.6	4394	2	Q6VJK2	Q6VJK2 strongyloce	C 499	6	6.6	78	1	XPI_XENUA	XPI_XENUA xenopus lae
427	7	7.6	4696	2	Q6VJK2	Q6VJK2 strongyloce	C 500	6	6.6	78	2	Q94G67	Q94G67 amarantus
428	6	6.5	28	2	Q9BM69	Q9BM69 aphid sp. i		6	6.5	78	2	P70713	P70713 rattus norv
429	6	6.5	28	2	Q86528	Q86528 grapevine f							
430	6	6.5	30	2	Q9MJF6	Q9MJF6 candida alb							
431	6	6.6	33	2	Q8EBD6	Q8EBD6 shewanella							
432	6	6.6	35	2	Q50884	Q50884 borrelia bu							
433	6	6.5	40	2	Q95Z13	Q95Z13 ceratitiss r							
434	6	6.6	41	2	Q91F85	Q91F85 chilo iride							
435	6	6.6	42	2	Q6TA42	Q6TA42 schistosoma							
436	6	6.6	42	2	Q8X215	Q8X215 escherichia							
437	6	6.6	45	2	Q9PFS9	Q9PFS9 xylella fas							
438	6	6.6	45	2	Q9PFS9	P12051 bacillus li							
439	6	6.5	46	1	DEGO_BACLI	Q6i6d1 escherichia							
440	6	6.6	46	2	Q616D1	Q65fh3 bacillus li							
441	6	6.5	46	2	Q65FH3	Q7qqu1 giardia lam							
442	6	6.6	47	2	Q7QQU1	Q71zde oncorhynch							
443	6	6.6	47	2	Q7LZD6	Q742a9 mycobacteri							
444	6	6.6	50	2	Q742A9	Q64rs8 bacteroides							
445	6	6.5	52	2	Q64RS8	Q98809 yam mosaic							
446	6	6.5	52	2	Q98809	Q7rbd8 plasmodium							
447	6	6.6	53	2	Q7RBD8	Q94sj0 antgonia c							
448	6	6.6	55	2	Q94SU0	Q64220 rattus sp.							
449	6	6.6	57	2	Q64220	Q7r0d1 giardia lam							
450	6	6.6	58	2	Q7R0D1	Q6zh10 oryza sativ							
451	6	6.5	58	2	Q6ZHL0	Q7p6y5 fusobacteri							
452	6	6.5	58	2	Q7P6Y5	Q8zsl3 pyrobaculum							
453	6	6.5	59	1	Y586 PYRAE	Q9ye39 aeropyrum p							
454	6	6.6	59	2	Q6UUL6	Q6uul6 oryza sativ							

ALIGNMENTS

RESULT 1	S112 HUMAN	S112 HUMAN	STANDARD;	PRT;	91 AA.
ID	S112 HUMAN	S112 HUMAN	STANDARD;	PRT;	91 AA.
AC	P80511; P83219;	AC	P80511; P83219;		
DT	01-OCT-1996 (Rel. 34, Created)	DT	01-OCT-1996 (Rel. 34, Created)		
DT	01-OCT-1996 (Rel. 34, Last sequence update)	DT	01-OCT-1996 (Rel. 34, Last sequence update)		
DT	25-OCT-2004 (Rel. 45, Last annotation update)	DT	25-OCT-2004 (Rel. 45, Last annotation update)		
DE	Calgranulin C (CAGC) (CGRP) (Neutrophil S100 protein) (Calcium-binding protein in amniotic fluid 1) (CAAF1) (p6) [Contains: Calcitermin].	DE	Calgranulin C (CAGC) (CGRP) (Neutrophil S100 protein) (Calcium-binding protein in amniotic fluid 1) (CAAF1) (p6) [Contains: Calcitermin].		
GN	Name=S100A12;	GN	Name=S100A12;		
OS	Homo sapiens (Human).	OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;	OX	NCBI_TaxID=9606;		
RX	SEQUENCE FROM N.A.	RX	SEQUENCE FROM N.A.		
RA	MEDLINE=97138564; PubMed=8985590; DOI=10.1016/S0143-4160(96)90087-1;	RA	MEDLINE=97138564; PubMed=8985590; DOI=10.1016/S0143-4160(96)90087-1;		
RT	Wiki B., Marenholz I., Mischke D., Schaefer B.W., Heizmann C.W.;	RT	Wiki B., Marenholz I., Mischke D., Schaefer B.W., Heizmann C.W.;		
RT	"Characterization of the human S100A12 (calgranulin C, p6, CAAF1, CGRP) gene, a new member of the S100 gene cluster on chromosome 1q21.1";	RT	"Characterization of the human S100A12 (calgranulin C, p6, CAAF1, CGRP) gene, a new member of the S100 gene cluster on chromosome 1q21.1";		
RL	Cell Calcium 20:459-464 (1996).	RL	Cell Calcium 20:459-464 (1996).		
RN	[1]	RN	[1]		
RN	[2]	RN	[2]		

RP SEQUENCE FROM N.A.
 RX MEDLINE=96192053; PubMed=8619860; DOI=10.1006/bbrc.1996.0600;
 RA Yamamura T.; Hitomi J.; Nagasaki K.; Suzuki M.; Takahashi E.,
 SA Saito S.; Takada T.; Yamaguchi K.;
 RT "Human CAAFI gene -- molecular cloning, gene structure, and chromosome
 mapping."; Biochem. Biophys. Res. Commun. 221:356-360(1996).
 RL Biochem. Biophys. Res. Commun. 221:356-360(1996).
 RN [3]
 RP SEQUENCE.
 RX MEDLINE=96192069; PubMed=8619876; DOI=10.1006/bbrc.1996.0616;
 RA Marti T.; Ertmann K.D.; Gallin M.Y.;
 RT "Host-parasite interaction in human onchocerciasis: identification and
 sequence analysis of a novel human calgranulin."; Biochem. Biophys. Res. Commun. 221:454-458(1996).
 RL Biochem. Biophys. Res. Commun. 221:454-458(1996).
 RN [4]
 RP SEQUENCE.
 RC TISSUE=Neutrophils;
 RX MEDLINE=96332419; PubMed=8769108; DOI=10.1006/bbrc.1996.1144;
 RA Ilg E.C.; Troxler H.; Buergisser D.M.; Kuster T.; Markert M.,
 RT "Amino acid sequence determination of human S100A12 (P6, calgranulin
 C, CGRP, CAAFI) by tandem mass spectrometry."; Biochem. Biophys. Res. Commun. 225:146-150(1996).
 RL Biochem. Biophys. Res. Commun. 225:146-150(1996).
 RN [5]
 RP SEQUENCE OF 1-20.
 RX MEDLINE=95351965; PubMed=7626002;
 RA Guignard F.; Maue J.; Markert M.;
 RT "Identification and characterization of a novel human neutrophil
 protein related to the S100 family."; Biochem. J. 309:395-401(1995).
 RL Biochem. J. 309:395-401(1995).
 RN [6]
 RP SEQUENCE OF 77-91, ANTIMICROBIAL ACTIVITY, AND MASS SPECTROMETRY.
 RC TISSUE=Nasal mucus;
 RX MEDLINE=21413725; PubMed=11522286; DOI=10.1016/S0014-5793(01)02731-4;
 RA Cole A.M.; Kim Y.-H.; Tahk S.; Hong T.; Weis P.; Waring A.J.; Ganz T.;
 RT "Calcitermin, a novel antimicrobial peptide isolated from human airway
 secretions."; FEBS Lett. 504:5-10(2001).
 RL FEBS Lett. 504:5-10(2001).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (1.95 ANGSTROMS).
 RX MEDLINE=21065388; PubMed=11134923; DOI=10.1107/S090744490001458X;
 RA Moroz O.V.; Atson A.A.; Murshudov G.N.; Maitland N.J.; Dodson G.G.,
 RA Wilson K.S.; Skibshoj I.; Lukanidin E.M.; Bronstein I.B.;
 RT "The three-dimensional structure of human S100A12."; Acta Crystallogr. D 57:20-29(2001).
 RL Acta Crystallogr. D 57:20-29(2001).
 CC -!- FUNCTION: Calcitermin possesses antifungal activity against
 CC C. albicans and is also active against E.coli and P.aeruginosa but
 CC not L.monocytogenes and S.aureus.
 CC -!- SUBUNIT: Homodimer.
 CC -!- TISSUE SPECIFICITY: Monocytes and lymphocytes.
 CC -!- MASS SPECTROMETRY: MW=10444; METHOD=Electrospray; RANGE=1-91;
 CC NOTE=Ref.6.
 CC -!- MASS SPECTROMETRY: MW=1688.9; METHOD=MALDI; RANGE=77-91;
 CC NOTE=Ref.6.
 CC -!- SIMILARITY: Belongs to the S-100 family.
 CC -!- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
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 CC
 DR EMBL; X97859; CAA66453.1; -;
 DR EMBL; X98288; CAA66934.1; -;
 DR EMBL; X98289; CAA66934.1; JOINED.
 DR EMBL; X98290; CAA66934.1; JOINED.
 DR EMBL; X98289; CAA94792.1; -;
 DR EMBL; X98290; CAB94792.1; JOINED.
 DR EMBL; D49549; BAA08497.1; -;
 DR EMBL; D83664; BAA12036.1; -;

DR EMBL; D83657; BAA12030.1; -;
 DR PIR; JC4712; JC4712.
 DR PDB; 1B8A; X-ray; A/B=1-91.
 DR PDB; 1GQM; X-ray; A/B/C/D/E/F/G/H/I/J/K/L=1-91.
 DR PDB; 1ODB; X-ray; A/B/C/D/E/F=1-91.
 DR PDB; 1GMC; X-ray; A/B/C/D/E/F=1-91.
 DR MIM; 603112; -;
 DR GO; GO:0005829; C:cytosol; TAS.
 DR GO; GO:0005626; C:insoluble fraction; TAS.
 DR GO; GO:0005509; F:calcium ion binding; TAS.
 DR GO; GO:0006954; P:inflammatory response; TAS.
 DR InterPro; IPR001751; CAPP_S100.
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR010983; EF_Hand_like.
 DR Pfam; PF00036; efhand; I.
 DR Pfam; PF01023; S_100; I.
 DR ProDom; PD003407; CAPP_S100; I.
 DR PROSITE; PS00018; EF_HAND; FALSE_NEG.
 DR PROSITE; PS00303; S100_CAPP; I.
 KW 3D-structure; Antibiotic; Calcium-binding; Direct protein sequencing;
 KW Fungicide; Metal-binding; Zinc.
 FT INIT MET 0
 FT PEPTIDE 77 91
 FT CA_BIND 18 31
 FT CA_BIND 61 72
 FT HELIX 2 18
 FT TURN 19 19
 FT TURN 24 25
 FT STRAND 26 27
 FT HELIX 29 39
 FT TURN 41 43
 FT TURN 45 48
 FT HELIX 50 60
 FT TURN 62 63
 FT STRAND 58 69
 FT HELIX 70 85
 SQ SEQUENCE 91 AA; 10444 MW; 325685EA8695F6B7 CRC64;
 Alignment Scores:
 Pred. No.: 2,478-84 Length: 91
 Score: 91.00 Matches: 91
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 98.91% Indels: 0
 DB: 1 Gaps: 0
 US-09-910-208B-12 (1-276) x S112_HUMAN (1-91)
 QY 4 ACAAACCTTGAGAGCATCTGGAGGAATTGTCAATATCTTCCACCAATCTCAGTTCCG 63
 Db 1 ThrLysLeuGluGluHisLeuGluGlyIleValAsnIlePheHisGlnTyrSerValArg 20
 QY 64 AAGGGGCATTTGACACCCCTCTCTAAGGGTGGAGCTGAAGCAGCTGCTTACAAAGGAGCTT 123
 Db 21 LysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGluLeu 40
 QY 124 GCAACACACCATCAAGATATCAAGATATAAGCTGTCATTGTGAATAATTTCAAGGCCTG 183
 Db 41 AlaAsnThrLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGlyLeu 60
 QY 184 GATGTAATCAAGATGAACAGCTCGACTTTCAGAAATTCATATCCCTGTAGCCATTGGC 243
 Db 61 AspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIleAla 80
 QY 244 CTGAAGGCTGCCATTACACACCCCAAGAG 276
 Db 81 LeuLysAlaAlaHisTyrHisThrHisLysGlu 91
 RESULT 2
 QSTR16
 ID QSTR16 PRELIMINARY; PRT; 70 AA.
 AC QSTR16;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)

01-MAY-2000 (TRENBLrel. 13, Last sequence update)
01-OCT-2003 (TRENBLrel. 25, Last annotation update)
CORNEA-associated antigen, CO-AG-CALGRANULIN C homolog.
Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
NCBI_TaxID=9913;
[1]
SEQUENCE.
MEDLINE=96181454; PubMed=8603881;
Liu S.H., Gottsch J.D.;
"Amino acid sequence of an immunogenic corneal stromal protein.";
Invest. Ophthalmol. Vis. Sci. 37:944-948(1996).
-!- SIMILARITY: Belongs to the S-100 family.
HSP; P80511; 1E8A.
GO; GO:0005509; F:calcium ion binding; IEA.
InterPro; IPR001751; CaBP_S100.
InterPro; IPR002048; EF-hand.
InterPro; IPR010983; EF_Hand_like.
Pfam; PF01023; S_100; 1.
ProDom; PD003407; CaBP_S100; 1.
SEQUENCE 70 AA; 8134 MW; 7D52BEA97A4D53A5 CRC64;
[1]
Alignment Scores:
Pred. No.: 6.15 Length: 70
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 9.78% Indels: 0
DB: 2 Gaps: 0
US-09-910-208b-12 (1-276) x Q9TR16 (1-70)
QY 37 AATATCTCCCAATACACTCAGTTCGG 63
Db 12 AsnIlePheHisGlnTyrSerValArg 20
RESULT 3
S112_RABIT
ID -S112_RABIT STANDARD; PRT; 81 AA.
AC Q77731;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Calgranulin C (CAGC) (Fragment).
GN Name=S100A12;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
[1]
SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAIN=New Zealand white; TISSUE=Neutrophils;
MEDLINE=96355278; PubMed=8702688; DOI=10.1074/jbc.271.33.19802;
Yang Z., Devere M.J., Gardiner E.E., Devenish R.J., Handley C.J.,
Runderwood J.R., Robinson H.C.;
"Rabbit polymorphonuclear neutrophils form 35S-labeled S-sulfo-
calgranulin C when incubated with inorganic [35S]sulfate.";
J. Biol. Chem. 271:19802-19809(1996).
-!- SIMILARITY: Belongs to the S-100 family.
-!- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
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EMBL; AF091848; AAC61770.1; -;
HSP; P80511; 1E8A.

InterPro; IPR001751; CaBP_S100.
InterPro; IPR002048; EF-hand.
InterPro; IPR010983; EF_Hand_like.
Pfam; PF00036; ehand; 1.
Pfam; PF01023; S_100; 1.
ProDom; PD003407; CaBP_S100; 1.
PROSITE; PS00018; EF_HAND; 1.
PROSITE; PS00303; S100_CaBP; 1.
KW Calcium-binding; Direct protein sequencing.
FT NON_TER 1
FT CA_BIND 8 21 EF-hand 1; low affinity (By similarity).
FT CA_BIND 51 62 EF-hand 2; high affinity (By similarity).
SQ SEQUENCE 81 AA; 9401 MW; 95E67A209180CB66 CRC64;
[1]
Alignment Scores:
Pred. No.: 6.01 Length: 81
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 9.78% Indels: 0
DB: 1 Gaps: 0
US-09-910-208b-12 (1-276) x S112_RABIT (1-81)
QY 37 AATATCTCCCAATACACTCAGTTCGG 63
Db 2 AsnIlePheHisGlnTyrSerValArg 10
RESULT 4
S112_BOVIN
ID -S112_BOVIN STANDARD; PRT; 91 AA.
AC P79105;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Calgranulin C (CAGC) (Calcium-binding protein in amniotic fluid 1)
DE (CAAF1) (RAGE binding protein).
GN Name=S100A12; Synonym=CAAF1;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
[1]
SEQUENCE FROM N.A.
RP TISSUE=Lung;
RC MEDLINE=99325504; PubMed=10399917; DOI=10.1016/S0092-8674(00)80801-6;
Hofmann M.A., Drury S., Fu C., Qu W., Taguchi A., Lu Y., Avila C.,
Kamhan M., Bierhaus A., Nawroth P., Neurath M.F., Slattery T.,
Beach D., McClary J., Nagashima M., Morser J., Stern D., Schmidt A.M.;
"RAGE mediates a novel proinflammatory axis: a central cell surface
receptor for S100/calgranulin polypeptides.";
Cell 97:889-901(1999).
-!- SIMILARITY: Belongs to the S-100 family.
-!- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
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DR EMBL; D49548; BAA08496.1; -.
 DR EMBL; AF011757; AAB65423.1; -.
 DR HSSP; P80511; 1GQM.
 DR InterPro; IPR001751; CaBP S100.
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR010983; EF_Hand_like.
 DR Pfam; PF00036; ehand; 1.
 DR Pfam; PF01023; S_100; 1.
 DR ProDom; PD003407; CaBP S100; 1.
 DR ProSITE; PS00018; EF_HAND; 1.
 DR ProSITE; PS00303; S100_CABP; 1.
 DR Calcium-binding; Metal-binding; Zinc.
 KW INIT_MET 0 By similarity.
 FT CA_BIND 18 31 EF-hand 1; low affinity (By similarity).
 FT CA_BIND 61 72 EF-hand 2; high affinity (By similarity).
 SQ SEQUENCE 91 AA; 10554 MW; 66FBC3C1B0354482 CRC64;

Alignment Scores:
 Pred. No.: 5.9 Length: 91
 Score: 9.00 Matches: 9
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 9.78% Indels: 0
 DB: 1 Gaps: 0

US-09-910-208B-12 (1-276) x S112_BOVIN (1-91)
 QY 37 AATATCTTCCCAATACTCAGTTCGG 63
 DB 12 AsnIlePheHisGlnTyrSerValArg 20
 |||||
 |||||

RESULT 5
 S112_PIG STANDARD; PRT; 91 AA.
 AC P80310;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Calgranulin C (CAGC).
 GN Name=S100A12;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Granulocyte;
 RX MEDLINE=95050708; PubMed=7961855;
 RA Dell'Angelica E.C., Schleicher C.H., Santome J.A.;
 RT "Primary structure and binding properties of calgranulin C, a novel
 RT S100-like calcium-binding protein from pig granulocytes.";
 RL J. Biol. Chem. 269:28929-28936(1994).
 CC -!- TISSUE SPECIFICITY: Found essentially in granulocytes with small
 CC amounts found in lymphocytes.
 CC -!- MISCELLANEOUS: In the absence of zinc binds one calcium ion per
 CC molecule, in the presence of zinc binds two calcium ions per
 CC molecule.
 CC -!- SIMILARITY: Belongs to the S-100 family.
 CC -!- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
 DR PIR; A55406; A55406.
 DR HSSP; P80511; 1E8A.
 DR InterPro; IPR001751; CaBP S100.
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR010983; EF_Hand_like.
 DR Pfam; PF00036; ehand; 1.
 DR Pfam; PF01023; S_100; 1.
 DR ProDom; PD003407; CaBP S100; 1.
 DR ProSITE; PS00018; EF_HAND; FALSE_NEG.
 DR ProSITE; PS00303; S100_CABP; 1.
 KW Calcium-binding; Direct protein sequencing; Metal-binding; Zinc.
 FT CA_BIND 18 31 EF-hand 1; low affinity (By similarity).
 FT CA_BIND 61 72 EF-hand 2; high affinity (By similarity).
 SQ SEQUENCE 91 AA; 10614 MW; B4204461432D7FCE CRC64;

Alignment Scores:
 Pred. No.: 5.9 Length: 91
 Score: 9.00 Matches: 9
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 9.78% Indels: 0
 DB: 1 Gaps: 0

US-09-910-208B-12 (1-276) x S112_PIG (1-91)
 QY 37 AATATCTTCCCAATACTCAGTTCGG 63
 DB 12 AsnIlePheHisGlnTyrSerValArg 20
 |||||
 |||||

RESULT 6
 S109_RABIT STANDARD; PRT; 118 AA.
 ID S109_RABIT
 AC P50117;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Calgranulin B (Migration inhibitory factor-related protein 14) (MRP-14) (Fragment).
 DE 14 (Fragment).
 GN Name=S100A9; Synonyms=MRP-14;
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=New Zealand white; TISSUE=Neutrophils;
 RX MEDLINE=96355278; PubMed=8702688; DOI=10.1074/jbc.271.33.19802;
 RA Yang Z., de Veer M.J., Gardiner E.E., Devenish R.J., Handley C.J.,
 RA Underwood J.R., Robinson H.C.;
 RT "Rabbit polymorphonuclear neutrophils form 35S-labeled S-sulfo-
 RT calgranulin C when incubated with inorganic [35S]sulfate";
 RL J. Biol. Chem. 271:19802-19809(1996).
 RN [2]
 RP SEQUENCE OF 45-82 FROM N.A.
 RC STRAIN=New Zealand white;
 RX MEDLINE=94198229; PubMed=8148323;
 RA Mori S., Goto K., Goto F., Mutakami K., Ohkawara S., Yoshinaga M.;
 RT "Dynamic changes in mRNA expression of neutrophils during the course
 RT of acute inflammation in rabbits.";
 RL Int. Immunol. 6:149-156(1994).
 CC -!- SIMILARITY: Belongs to the S-100 family.
 CC -!- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
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 CC
 CC EMBL; AF091849; AAC61771.1; -.
 CC EMBL; D17404; BAA04227.1; -.
 CC PIR; I46861; I46861.
 CC HSSP; P06702; 1IRJ.
 CC InterPro; IPR001751; CaBP S100.
 CC InterPro; IPR002048; EF-hand.
 CC InterPro; IPR010983; EF_Hand_like.
 CC Pfam; PF00036; ehand; 1.
 CC Pfam; PF01023; S_100; 1.
 CC ProDom; PD003407; CaBP S100; 1.
 CC ProSITE; PS00018; EF_HAND; 1.
 CC ProSITE; PS00303; S100_CABP; 1.
 KW Calcium-binding; Repeat.
 FT NON_TER 1 1
 FT CA_BIND 9 22 EF-hand 1; low affinity (Potential).
 FT CA_BIND 53 64 EF-hand 2; high affinity (Potential).
 FT

RX MEDLINE=99260299; PubMed=10331456;
 RX DOI=10.1002/(SICI)1098-2795(199906)53:2<179::AID-MRD7>3.3.CO;2-G;
 RA Simpson K.S., Adams M.H., Behrendt-Adam C.Y., Baker C.B.,
 RA McDowell K.J.;
 RT "Identification and initial characterization of calyculin and
 RT phospholipase A2 in equine conceptuses";
 RL Mol. Reprod. Dev. 53:179-187(1999).
 CC -!- SUBUNIT: Homodimer, antiparallel. Interacts with SUGT1 (By
 CC similarity).
 CC -!- SIMILARITY: Belongs to the S-100 family.
 CC -!- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
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 CC
 CC EMBL; AF083065; AAC33290.1; -.
 DR HSP; P06703; 1K96.
 DR GO; GO:0005435; C:nuclear membrane; ISS.
 DR GO; GO:0005509; F:calcium ion binding; ISS.
 DR GO; GO:0005515; F:protein binding; ISS.
 DR GO; GO:0007409; P:axonogenesis; ISS.
 DR GO; GO:0048146; P:positive regulation of fibroblast proliferation. .; ISS.
 DR InterPro; IPR001751; CAbp_S100.
 DR InterPro; IPR002048; EF_Hand.
 DR InterPro; IPR010983; EF_Hand_like.
 DR Pfam; PF00036; ehand; 1.
 DR Pfam; PF01023; S_100; 1.
 DR ProDom; PD003407; CAbp_S100; 1.
 DR PROSITE; PS00018; EF_HAND; 1.
 DR PROSITE; PS0303; S100_CABP; 1.
 KW Calcium-binding; Cell cycle; Mitogen.
 FT CA_BIND 20 33
 FT CA_BIND 61 72 EF-hand 1; low affinity (Potential).
 FT CA_BIND 72 EF-hand 2; high affinity (Potential).
 SQ SEQUENCE 92 AA; 10280 MW; 997A2A9E768CE9F3 CRC64;

 Alignment Scores:
 Pred. No.: 62.9 Length: 92
 Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 8.70% Indels: 0
 DB: 1 Gaps: 0

 US-09-910-208B-12 (1-276) x S106_HORSE (1-92)
 QY 79 ACCCTCTCTAAGGCTGAGCTGAAG 102
 Db 28 ThrLeuSerLysGlyGlulLeuLys 35
 |||||
 RESULT 10
 Q6XG62 PRELIMINARY; PRT; 95 AA.
 AC Q6XG62
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Ictacalcin.
 GN Name=icn;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AB; TISSUE=Striated epithelium covering the entire body;
 RA Hsiao C.-D., Tsai H.-J.;
 RL Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.

CC -!- SIMILARITY: Belongs to the S-100 family.
 DR EMBL; AY233453; AAP69564.1; -.
 DR HSP; P35467; 1K2H.
 DR ZFIN; ZDB-GENE-030131-8599; icn.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR InterPro; IPR001751; CAbp_S100.
 DR InterPro; IPR002048; EF_Hand.
 DR InterPro; IPR010983; EF_Hand_like.
 DR Pfam; PF00036; ehand; 1.
 DR Pfam; PF01023; S_100; 1.
 DR ProDom; PD003407; CAbp_S100; 1.
 DR SMART; SM00054; Eph; 1.
 DR PROSITE; PS00018; EF_HAND; UNKNOWN 1.
 DR PROSITE; PS0303; S100_CABP; 1.
 SQ SEQUENCE 95 AA; 10407 MW; FA96C742EA869A73 CRC64;

 Alignment Scores:
 Pred. No.: 62.6 Length: 95
 Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 8.70% Indels: 0
 DB: 2 Gaps: 0

 US-09-910-208B-12 (1-276) x Q6XG62 (1-95)
 QY 79 ACCCTCTCTAAGGCTGAGCTGAAG 102
 Db 29 ThrLeuSerLysGlyGlulLeuLys 36
 |||||
 RESULT 11
 CALB_ASHGO STANDARD; PRT; 175 AA.
 ID CALB_ASHGO
 AC Q75787
 DT 25-OCT-2004 (Rel. 45, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Calcineurin B subunit (protein phosphatase 2B regulatory subunit)
 DE Calcineurin regulatory subunit.
 DE (Calcineurin regulatory subunit).
 GN Name=CNB1; OrderedLocusNames=AER096C;
 OS Ashbya gossypii (Yeast) (Eremothecium gossypii). Saccharomycetes;
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Bremonotheceum.
 OX NCBI_TaxID=33169;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 10895;
 RX PubMed=15001715; DOI=10.1126/science.1095781;
 RX Dietrich F.S., Voegelé S., Brachat S., Lerch A., Gates K., Steiner S.,
 RA Mohr C., Poehlmann R., Luedi P., Choi S., Wing R.A., Flavie A.,
 RA Gaffney T.D., Philippsen P.;
 RT "The Ashbya gossypii genome as a tool for mapping the ancient
 RT Saccharomyces cerevisiae genome.";
 RL Science 304:304-307(2004).
 CC -!- FUNCTION: Regulatory subunit of calcineurin, a calcium-dependent,
 CC calmodulin stimulated protein phosphatase. Confers calcium
 CC sensitivity (By similarity).
 CC -!- SUBUNIT: Composed of a catalytic subunit (A) and a regulatory
 CC subunit (B) (By similarity).
 CC -!- MISCELLANEOUS: This protein has four functional calcium-binding
 CC sites (By similarity).
 CC -!- SIMILARITY: Contains 4 EF-hand calcium-binding domains.
 CC
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 CC
 CC EMBL; AE016896; AAS52780.1; -.
 DR AGD; AER096C; -.

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DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR010983; EF Hand Like.
DR InterPro; IPR008080; Parvalbumin.
DR InterPro; IPR001125; Recoverin.
DR Pfam; PF00036; ehand; 4.
DR PRINTS; PR01697; PARVALBUMIN.
DR PRINTS; PR00450; RECOVERIN.
DR SMART; SM00054; EFh; 4.
DR PROSITE; PS00016; EF_HAND; 4.
DR Calcium-binding; Repeat.
FT CA_BIND 34 45
FT CA_BIND 66 77
FT CA_BIND 103 114
FT CA_BIND 144 155
FT CA_BIND 175 AA; 19743 MW; 583C5422ECD8B3C3 CRC64;
SQ SEQUENCE 175 AA; 19743 MW; 583C5422ECD8B3C3 CRC64;

Alignment Scores:
Pred. No.: 56.8 Length: 175
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 8.70% Indels: 0
DB: 1 Gaps: 0

US-09-910-208B-12 (1-276) x CALB_ASHGO (1-175)

QY 205 GTCGACTTCAAGATTTCATATCC 228
Db 73 ValAspPheGlnGluPheIleSer 80

RESULT 12
QY 205 GTCGACTTCAAGATTTCATATCC 228
Db 73 ValAspPheGlnGluPheIleSer 80

Q9H4U1 PRELIMINARY; PRT; 213 AA.
AC Q9H4U1
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE DJ14N1.2 (Novel S-100/ICaBP type calcium binding domain protein,
DE similar to trichohyalin) (Fragment).
GN Name=dJ14N1.2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Laird G.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the S-100 family.
DR EMBL; ALJ356504; CAC13473.1; -.
DR HSP; P25815; IJ55.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR001751; CaBP S100.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR010983; EF Hand Like.
DR Pfam; PF00036; ehand; 1.
DR PROSITE; PS01023; S100; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN 1.
DR PROSITE; PS00303; S100_CaBP; 1.
FT NON TER 213 213
SQ SEQUENCE 213 AA; 24340 MW; B8C6E0810098E7D2 CRC64;

Alignment Scores:
Pred. No.: 55.1 Length: 213
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 8.70% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-12 (1-276) x Q9H4U1 (1-213)

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```

QY 79 ACCCTCTCTAAGGTGAGCTGAAG 102
Db 27 ThrLeuSerLysGlyGluLeuLys 34

RESULT 13
QY 79 ACCCTCTCTAAGGTGAGCTGAAG 102
Db 27 ThrLeuSerLysGlyGluLeuLys 34

Q87193 PRELIMINARY; PRT; 248 AA.
AC Q87193
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2004 (TRENBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Hypothetical protein VPA0713.
DE OrderedLocNames=VPA0713;
GN Vibrio parahaemolyticus.
OS Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=670;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RIMD 2210633 / Serotype O3:K6;
RX MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;
RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
RA Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
RT distinct from that of V. cholerae.";
RL Lancet 361:743-749 (2003).
DR EMBL; AP005086; BAC62056.1; -.
DR InterPro; IPR001633; EAL.
DR Pfam; PF00563; EAL; 1.
DR SMART; SM00052; DUF2; 1.
DR PROSITE; PS00883; EAL; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 248 AA; 28942 MW; D9BB9097E2E84B6F CRC64;

Alignment Scores:
Pred. No.: 53.7 Length: 248
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 8.79% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-12 (1-276) x Q87193 (1-248)

QY 189 AGCATCCAGCCTTGGAATATTC 166
Db 181 SerileGlnAlaLeuGluTyrPhe 188

RESULT 14
QY 189 AGCATCCAGCCTTGGAATATTC 166
Db 181 SerileGlnAlaLeuGluTyrPhe 188

Q87193 PRELIMINARY; PRT; 254 AA.
AC Q87193
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Protein GltF precursor.
DE Name=gltF; OrderedLocNames=b3214;
GN Escherichia coli.
OS Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=93078627; PubMed=1447980;
RA Castano I., Flores N., Valle F., Covarrubias A.A., Bolivar F.;
RT "gltF, a member of the gltBDF operon of Escherichia coli, is involved
RT in nitrogen-regulated gene expression.";
RL Mol. Microbiol. 6:2733-2741 (1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;

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RX MEDLINE=97426617; PubMed=9278503; DOI=10.1126/science.277.5331.1453;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12."
RL Science 277:1453-1474 (1997).
CC -!- FUNCTION: Involved in induction of the so-called NTR enzymes in
CC response to nitrogen deprivation, as well as in glutamate
CC biosynthesis. May mediate the glutamate-dependent repression of
CC the GLT operon.
CC -!- SIMILARITY: To E.coli yhcF.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M74162; AAA23909.1; -
DR EMBL; U18997; AA58016.1; -
DR EMBL; U00036; AAC76246.1; -
DR PIR; S25281; S25281.
DR EcoBASE; EB1476; -
DR EcoGene; EG11514; gltF.
DR InterPro; IPR010546; DUF1120.
DR Pfam; PF06551; DUF1120; 1.
KW Complete proteome; Signal; Transmembrane.
FT SIGNAL 1 25 Potential.
FT CHAIN 26 254 Protein gltF.
FT TRANSMEM 213 229 Potential.
SQ SEQUENCE 254 AA; 26351 MW; 7424D7D1339A5F27 CRC64;

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Alignment Scores:
Pred. No.: 53.5 Length: 254
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 8.79% Indels: 0
DB: 1 Gaps: 0

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US-09-910-208B-12 (1-276) x GLTF_ECOLI (1-254)

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QY 254 GCAGCCTTCAGCGCAATGCTACC 231
DB 19 AlaAlaPheSerAlaMetAlaThr 26

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RESULT 15

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Q72V46
ID Q72V46 PRELIMINARY; PRT; 264 AA.
AC Q72V46;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=LIC10457;
OS Leptospira interrogans (serogroup Icterohaemorrhagiae / serovar
OC Copenhagen).
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
OX NCBI_TaxID=44275;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Fiocruz LI-130;
RX PubMed=15028702; DOI=10.1128/JB.186.7.2164-2172.2004;
RA Nascimento A.L.T.O., Ko A.I., Martins E.A.L., Monteiro-Vitorello C.B.,
RA Ho P.L., Haake D.A., Verjovski-Almeida S., Hartskeerl R.A.,
RA Marques M.V., Oliveira M.C., Menck C.F.M., Leite L.C.C., Carrer H.,
RA Coutinho L.L., Degrave W.M., Dellagostin O.A., El-Dorry H.,
RA Ferro E.S., Ferro M.I.T., Furlan L.R., Gamberini M., Gigliotti E.A.,
RA Goes-Neto A., Goldman G.H., Goldman M.H.S., Harakava R.,
RA Jeronimo S.M.B., Junqueira-de-Azevedo I.L.M., Kimura E.T.,

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RA Kuramae E.E., Lemos E.G.M., Lemos M.V.F., Marino C.L., Nunes L.R.,
RA de Oliveira R.C., Pereira G.G., Reis M.S., Schriefer A.,
RA Siqueira W.J., Sommer P., Tsai S.M., Simpson A.J.G., Ferro J.A.,
RA Camargo L.E.A., Kitajima J.P., Setubal J.C., Van Sluys M.A.;
RT "Comparative genomics of two Leptospira interrogans serovars reveals
RL novel insights into physiology and pathogenesis."
RL J. Bacteriol. 186:2164-2172 (2004).
KW EMBL; AE017288; AAS69078.1; -.
KW Complete proteome.
SQ SEQUENCE 264 AA; 30901 MW; A28C7BB11C128F79 CRC64;

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Alignment Scores:
Pred. No.: 53.2 Length: 264
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 8.79% Indels: 0
DB: 2 Gaps: 0

```

US-09-910-208B-12 (1-276) x Q72V46 (1-264)

```

QY 184 CCAGGCTTGGGAATATTTTCATCAA 161
DB 139 ProGlyLeuGlyIlePheHisGln 146

```

Search completed: February 23, 2005, 12:38:15
Job time : 133 secs

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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: February 23, 2005, 12:14:04 ; Search time 114 Seconds
(without alignments)
1872.734 Million cell updates/sec

Title: US-09-910-208B-12

Perfect score: 92

Sequence: 1 atgacaaaactgaagacgca.....attaccacacccacaaagag 276

Scoring table: OLIGO
Xgapop 60.0, Xgapext 60.0
Ygapop 60.0, Ygapext 60.0
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 4105692 seqs, 386760381 residues

Word size: 1

Total number of hits satisfying chosen parameters: 3967864

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Command line parameters: -DEV=xlp
-MODEL=frame+ n2p.model -DB=FASTA
-Q=/sgn2_1/USPTO spool_p/HADAD-09-910208B/runat_23022005_102315_15790/app.query.fasta.1
-DB=A_Geneseq_16Dec04 -QFMT=fastan -SURFIX=oligo.rag -MINMATCH=0.1 -LOOPEL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=500 -DALIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000
-USER=HADAD-09-910208B @CGN 1.1.224 @runat_23022005_102315_15790 -NCPU=6
-ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THRAADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DSEXT=7

Database : A_Geneseq_16Dec04:.*
1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	92	100.0	92	2	Aaw03564 Calcium b
2	92	100.0	92	2	Aaw24137 Human che
3	92	100.0	92	3	Aab45542 Human S10
4	92	100.0	92	4	Aab31911 Amino aci
5	92	100.0	92	4	Aab31907 Amino aci
6	92	100.0	92	4	Aab31908 Amino aci
7	92	100.0	92	7	ADA93649 Human cal
8	92	100.0	92	8	ADN04192 Antipsori
9	92	100.0	92	8	ADN19540 Human PRO
10	92	100.0	92	8	ADR14333 Human NF-

11	92	100.0	92	8	ADP23921	Adp23921	PRO polyp
12	92	100.0	92	8	ADS74331	AdS74331	PRO polyp
13	91	98.9	91	4	AA31909	Aa31909	Amino aci
14	74	80.4	95	4	ABG27582	Abg27582	Novel hum
15	46	50.0	46	4	AB43183	Ab43183	Peptide #
16	46	50.0	46	4	AA37021	Aa37021	Peptide #
17	46	50.0	46	4	ABB26281	AbB26281	Protein #
18	46	50.0	46	4	AA676914	Aa676914	Human bon
19	46	50.0	46	4	AA64093	Aa64093	Human bra
20	46	50.0	46	4	ABG58579	Abg58579	Human liv
21	46	50.0	46	5	ABG46027	Abg46027	Human pep
22	22	23.9	363	3	ABG27581	Abg27581	Novel hum
23	9	9.8	90	3	AA90765	Aa90765	Bovine CA
24	9	9.8	90	3	AA90764	Aa90764	Bovine co
25	9	9.8	91	2	AAW01826	AaW01826	Component
26	9	9.8	91	2	AAW93819	AaW93819	Angiotrop
27	9	9.8	92	2	AAW03563	AaW03563	Calcium b
28	8	8.7	8	7	ADB61382	AdB61382	Rheumatoi
29	8	8.7	70	5	ABP34077	AbP34077	Human ORP
30	8	8.7	202	4	ABG22271	Abg22271	Novel hum
31	8	8.7	206	5	ABP51289	AbP51289	Human MDD
32	8	8.7	218	4	AAW25257	AaW25257	Human pro
33	8	8.7	396	2	AAW23327	AaW23327	Meripilus
34	8	8.8	516	5	ABP26046	AbP26046	Streptoco
35	8	8.7	542	8	ADN99439	AdN99439	Novel hum
36	8	8.7	1780	4	ABB71483	AbB71483	Drosophi
37	7	7.7	52	4	AAU61087	AaU61087	Propionib
38	7	7.7	52	6	ABM57606	AbM57606	Propionib
39	7	7.6	59	4	AAW77603	AaW77603	Human col
40	7	7.6	62	6	ADA36111	AdA36111	Acinetoba
41	7	7.7	84	4	AAO05978	AaO05978	Human ova
42	7	7.6	85	5	ABP41678	AbP41678	Human ova
43	7	7.7	86	5	ADK35063	AdK35063	Novel hum
44	7	7.7	90	3	AA91420	Aa91420	Human sec
45	7	7.7	91	4	AAW91115	AaW91115	Human imm
46	7	7.7	93	4	ABG17471	AbG17471	Novel hum
47	7	7.6	93	6	ABU52339	AbU52339	Human GPC
48	7	7.6	93	8	ADL24013	AdL24013	Human NOV
49	7	7.6	99	4	AAW39964	AaW39964	Human pol
50	7	7.6	106	6	ABU05340	AbU05340	Human dia
51	7	7.7	108	4	AAW93932	AaW93932	Human pol
52	7	7.7	108	8	ADL32073	AdL32073	Human pro
53	7	7.6	112	2	AAW05275	AaW05275	N-termina
54	7	7.6	113	2	AAW05274	AaW05274	N-termina
55	7	7.6	113	3	AAW45500	AaW45500	Murine in
56	7	7.6	113	5	ABG94296	AbG94296	Mouse int
57	7	7.6	113	5	ABG80608	AbG80608	Mouse mat
58	7	7.6	113	7	ADK17209	AdK17209	Mouse int
59	7	7.6	114	8	ADL05480	AdL05480	M. catarr
60	7	7.6	115	2	AAW05273	AaW05273	N-termina
61	7	7.6	115	2	AAW72948	AaW72948	Truncated
62	7	7.6	116	3	AAW45502	AaW45502	Modified
63	7	7.6	116	3	AAW45526	AaW45526	Modified
64	7	7.7	117	3	ADP59399	AdP59399	Human pol
65	7	7.6	121	5	ABG94350	AbG94350	Mouse C-I
66	7	7.6	121	5	ABG80662	AbG80662	Mouse IL-
67	7	7.6	121	7	ADK17221	AdK17221	Mouse C-I
68	7	7.6	122	3	AAW45524	AaW45524	Modified
69	7	7.6	122	3	AAW45527	AaW45527	Modified
70	7	7.6	122	3	AAW45503	AaW45503	Modified
71	7	7.6	122	3	AAW45504	AaW45504	Modified
72	7	7.6	122	3	AAW45507	AaW45507	Modified
73	7	7.6	124	3	AAW45523	AaW45523	Modified
74	7	7.6	124	3	AAW45505	AaW45505	Modified
75	7	7.6	124	3	AAW45501	AaW45501	Modified
76	7	7.7	124	4	ABG02537	AbG02537	Novel hum
77	7	7.6	128	3	AAW45529	AaW45529	Modified
78	7	7.6	128	3	AAW45525	AaW45525	Modified
79	7	7.6	128	3	AAW45508	AaW45508	Modified
80	7	7.6	130	3	AAW45506	AaW45506	Modified
81	7	7.6	130	3	AAW45509	AaW45509	Modified
82	7	7.6	130	3	AAW45528	AaW45528	Modified
83	7	7.6	133	1	AAW71064	AaW71064	Murine eo

84	7	7.6	133	1	AAP82969	Ap82969 B cell di	C 157	7	7.7	229	6	ABR99450	Abt99450 Human sec
85	7	7.6	133	1	AAP80280	Ap80280 Murine pl	C 158	7	7.7	229	6	ABR98940	Abt98940 Human sec
86	7	7.6	133	1	AAR96963	Aar96963 T cell re	C 159	7	7.7	229	6	ABO16363	Abt16363 Human sec
87	7	7.6	133	2	AAW72949	Aaw72949 T cell re	C 160	7	7.7	229	6	ABR2263	Abt2263 Human sec
88	7	7.6	133	2	AAW72947	Aaw72947 T cell re	C 161	7	7.7	229	6	ABO18904	Abt18904 Human sec
89	7	7.6	133	4	AAW72618	Aaw72618 Murine in	C 162	7	7.7	229	6	ABR78325	Abt78325 Human sec
90	7	7.6	133	4	ABP78557	Abp78557 N. gonorr	C 163	7	7.7	229	6	ABU71975	Abu71975 Novel hum
91	7	7.6	133	5	ABG94349	Abg94349 Mouse C-I	C 164	7	7.7	229	6	ABU85061	Abu85061 Novel hum
92	7	7.6	134	5	ABG80661	Abg80661 Mouse IL-	C 165	7	7.7	229	6	ABO00200	Abt00200 Novel hum
93	7	7.6	134	5	ADK17220	Adk17220 Mouse C-I	C 166	7	7.7	229	6	ABO11532	Abt11532 Human sec
94	7	7.6	136	5	ABG94348	Abg94348 Mouse C-I	C 167	7	7.7	229	6	ABO02177	Abt02177 Human sec
95	7	7.6	136	5	ABG80660	Abg80660 Mouse IL-	C 168	7	7.7	229	6	ABU88751	Abu88751 Novel hum
96	7	7.6	136	7	ADK17219	Adk17219 Mouse C-I	C 169	7	7.7	229	6	ABU83446	Abu83446 Human sec
97	7	7.6	139	3	AAB45510	Aab45510 Modified	C 170	7	7.7	229	6	ABO06247	Abt06247 Novel hum
98	7	7.6	143	8	ADQ66687	Adq66687 Novel hum	C 171	7	7.7	229	6	ABR59283	Abt59283 Human sec
99	7	7.6	145	3	AAB45530	Aab45530 Modified	C 172	7	7.7	229	6	ABO09345	Abt09345 Human sec
100	7	7.6	149	4	ABG07201	Abg07201 Novel hum	C 173	7	7.7	229	6	ABO119209	Abt119209 Novel hum
101	7	7.6	160	7	ADQ97442	Adq97442 E. faeciu	C 174	7	7.7	229	6	ABO111227	Abt11227 Human sec
102	7	7.7	163	7	AD182689	Ad182689 Murine tr	C 175	7	7.7	229	6	ABR66845	Abt66845 Human sec
103	7	7.6	166	6	ABU41587	Abu41587 Protein e	C 176	7	7.7	229	6	ABO13764	Abt13764 Human sec
104	7	7.6	167	6	ABU41587	Abu41587 Protein e	C 177	7	7.7	229	6	ABU71529	Abu71529 Human sec
105	7	7.6	169	4	ADH88563	Adh88563 Enterococ	C 178	7	7.7	229	6	ABU65667	Abu65667 Human sec
106	7	7.6	171	7	ADH88563	Adh88563 Enterococ	C 179	7	7.7	229	6	ABO07515	Abt07515 Human PRO
107	7	7.6	172	8	ADN46597	Adn46597 Thermococ	C 180	7	7.7	229	6	ABO03702	Abt03702 Human sec
108	7	7.6	175	2	ADN46597	Adn46597 Thermococ	C 181	7	7.7	229	6	ABR67150	Abt67150 Human sec
109	7	7.6	175	8	ADN46597	Adn46597 Thermococ	C 182	7	7.7	229	6	ABO15753	Abt15753 Human sec
110	7	7.7	184	7	ADN46597	Adn46597 Thermococ	C 183	7	7.7	229	6	ABU56034	Abu56034 Human sec
111	7	7.7	188	7	ADD30218	Adi30218 Plant tra	C 184	7	7.7	229	6	ABU72310	Abu72310 Human PRO
112	7	7.7	188	8	AD44051	Adi44051 Plant tra	C 185	7	7.7	229	6	ABU65362	Abu65362 Human PRO
113	7	7.7	194	4	ADH87433	Adh87433 Human gen	C 186	7	7.7	229	6	ABU53307	Abu53307 Novel hum
114	7	7.7	195	7	ABO80098	Abt80098 Pseudomon	C 187	7	7.7	229	6	ABU71210	Abu71210 Human PRO
115	7	7.6	210	8	ADH87433	Adh87433 Human gen	C 188	7	7.7	229	6	ABO07820	Abt07820 Human PRO
116	7	7.6	201	4	AAW41239	Aaw41239 Human pol	C 189	7	7.7	229	6	ABR70061	Abt70061 Human sec
117	7	7.6	210	6	ABP79921	Abp79921 N. gonorr	C 190	7	7.7	229	6	ABR69394	Abt69394 Human PRO
118	7	7.6	210	6	ABP79921	Abp79921 N. gonorr	C 191	7	7.7	229	6	ABO01535	Abt01535 Human PRO
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126	7	7.7	229	6	ABU58498	Abu58498 Human PRO	C 199	7	7.7	229	6	ABU59266	Abu59266 Human sec
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132	7	7.7	229	6	ABU58041	Abu58041 Human PRO	C 205	7	7.7	229	6	ABU90545	Abu90545 Novel hum
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ALIGNMENTS

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ID AAW03564 standard; protein; 92 AA.
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AC AAW03564;
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DT 01-MAY-1997 (first entry)
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XX Calcium binding protein CAAFl.
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KW Calcium binding protein; human; amniotic fluid; S100 protein family;
KW intracellular signal transduction; squamous epithelial cell; neutrophil;
KW macrophage; cancer; cancerous lesion; inflammation; neoplasia; cervix;
KW squamous cell carcinoma; skin; oesophagus; CAAFl; lung; blood disease.
OS Homo sapiens.
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PN EP731166-A2:
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PD 11-SEP-1996:
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XX 04-DEC-1995: 95EP-00119045.
XX
XX 06-MAR-1995: 95JP-00045564.
PR 06-MAR-1995: 95JP-00070468.
XX
XX (TOFU ) TONEN CORP.
PA (HITO/) HITOMI J.
XX
PI Hitomi J, Yamaguchi K, Yamamura T, Kimura T;
XX
XX WPI; 1996-403989/41.
DR N-PSDB; AAT39346.
XX
XX New human or bovine calcium binding protein and related nucleic acid - is
PT a marker for inflammation, neoplasia, skin and blood diseases.
XX
XX Claim 1; Page 24; 36pp; English.
XX
XX This sequence represents the CAAF1 calcium-binding protein isolated from
CC human amniotic fluid. CAAF1 belongs to the S100 protein family, which
CC includes calyculin, MRP8, and MRP14. Intracellular calcium ion
CC concentration is one of the key factors for intracellular signal
CC transduction. The calcium signals are transduced by various calcium-
CC binding proteins, such as this protein. CAAF1 is normally expressed in
CC squamous epithelial cells, neutrophils and macrophages, but atypical
CC epithelial cells are negative for CAAF1 and overexpression is observed in
CC several types of cancer cells and neutrophils/macrophages infiltrating
CC cancerous lesions. Detection of CAAF1 (using antibodies in usual
CC immunoassays) can be used to diagnose (or monitor) inflammation,
CC neoplasia (particularly squamous cell carcinoma of the skin, oesophagus,
CC lung and cervix), and skin and blood diseases
XX
XX Sequence 92 AA;
SQ
Alignment Scores:
Pred. No.: 1.04e-80 Length: 92
Score: 92.00 Matches: 92
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0
US-09-910-208B-12 (1-276) x AAW03564 (1-92)
QY 1 ATGACAAAACCTTGAAGAGCATCTGGAGGGAATTGTCAATATCTTCCACCAATACTCAGTT 60
Db 1 MetThrLysLeuGluGluHisLeuGluGlyIleValAsnIlePheHisGlnTyrSerVal 20
QY 61 CGGAGGGGCATTTTGACACCTCTCTAGGGTGAGCTGAAGCAGCTGCTTCAAGGAG 120
Db 21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGlu 40
QY 121 CTTGCAAAACCATCAAGAAATATCAAGATAAAGCTGTCTATGTAGTAATATTTCCAAGGC 180
Db 41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60
QY 181 CTGGATGCTTAATCAAGATGAACAGGTCGACTTTTCAAGAAATTCATATCCCTGGTAGCCATT 240
Db 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80
QY 241 GCGCTGAAGGCTGCCCATTTACCACACCCCAAGAG 276
Db 81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92
RESULT 2
AAW24137
ID AAW24137 standard; protein; 92 AA.
XX
AC AAW24137;
```

```
XX 28-JAN-1998 (first entry)
XX
XX Human chemotactic cytokine I.
XX
XX chemotactic cytokine; tumour; autoimmune disease; antagonist; agonist.
XX
XX Homo sapiens.
XX
XX WO9723640-A1.
XX
XX 03-JUL-1997.
XX
XX 26-DEC-1995; 95WO-US016871.
XX
XX 26-DEC-1995; 95WO-US016871.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ni J, Yu G, Alfonso P, Gentz R, Su JY;
XX
XX WPI; 1997-351075/32.
XX
XX N-PSDB; AAT85774.
XX
XX DNA encoding chemotactic cytokine I - used to treat, e.g. tumours,
XX chronic infection, leukaemia, etc.
XX
XX Claim 12; Page 48-49; 64pp; English.
XX
XX This is a human chemotactic cytokine I polypeptide. The encoding
XX polynucleotide, along with a vector and a host cell can be used for the
XX recombinant production of the chemotactic cytokine. Cytokine agonists and
XX antagonists can be used for the treatment of a patient requiring a
XX chemotactic cytokine I and for the treatment of a patient requiring the
XX inhibition of a chemotactic cytokine I polypeptide, respectively. The
XX chemotactic cytokine is used to treat tumours, chronic infection,
XX leukaemia and T-cell mediated autoimmune diseases
XX
XX Sequence 92 AA;
SQ
Alignment Scores:
Pred. No.: 1.04e-80 Length: 92
Score: 92.00 Matches: 92
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0
US-09-910-208B-12 (1-276) x AAW24137 (1-92)
QY 1 ATGACAAAACCTTGAAGAGCATCTGGAGGGAATTGTCAATATCTTCCACCAATACTCAGTT 60
Db 1 MetThrLysLeuGluGluHisLeuGluGlyIleValAsnIlePheHisGlnTyrSerVal 20
QY 61 CGGAGGGGCATTTTGACACCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTCAAAAGGAG 120
Db 21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGlu 40
QY 121 CTTGCAAAACCATCAAGAAATATCAAGATAAAGCTGTCTATGTAGTAATATTTCCAAGGC 180
Db 41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60
QY 181 CTGGATGCTTAATCAAGATGAACAGGTCGACTTTTCAAGAAATTCATATCCCTGGTAGCCATT 240
Db 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80
QY 241 GCGCTGAAGGCTGCCCATTTACCACACCCCAAGAG 276
Db 81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92
RESULT 3
AAW45542
ID AAW45542 standard; protein; 92 AA.
```

XX AC AAB45542;
 XX DT 22-FEB-2001 (first entry)
 XX DE Human S100A12 protein.
 XX S100 protein; human; treatment; cardiomyopathy; cardiac insufficiency;
 KW calcium-binding protein; calcium homeostasis; cardiac muscle;
 KW pumping capacity; myocardial cell; systolic calcium ion release;
 KW sarcoplasmic reticulum; cardiac disease; hypertension; rhythm disorder;
 KW valve defect.
 XX OS Homo sapiens.
 XX DE19915485-A1.
 XX PD 19-OCT-2000.
 XX PF 07-APR-1999; 99DE-01015485.
 XX PR 07-APR-1999; 99DE-01015485.
 XX PA (KATU//) KATUS.H.A.
 XX PA (REMP//) REMPPIS.A.
 XX Katus HA, Remppis A;
 XX WPI: 2000-673510/66.
 XX N-PSDB; AAC61812.
 XX Composition containing S100 protein, corresponding nucleic acid or
 PT vector, useful for treating cardiomyopathy and cardiac insufficiency.
 XX Claim 35; Page 20; 36pp; German.
 XX This invention describes a novel composition for treating primary or
 CC secondary cardiomyopathy or cardiac insufficiency contains at least one
 CC S100 protein (I) or nucleic acid (II) encoding (I), or their mutants or
 CC fragments, or a gene transfer vector containing (II), optionally
 CC formulated with auxiliaries and/or carriers. (I) are calcium-binding
 CC proteins involved in calcium homeostasis, so their overexpression in
 CC cardiac muscle will improve pumping capacity (and overall capacity) of
 CC the heart. In cultured myocardial cells they increase the contraction and
 CC relaxation rates associated with increased systolic calcium ion release
 CC from the sarcoplasmic reticulum (SR) and calcium re-uptake by SR. (I) are
 CC used to treat cardiomyopathy (CMP) where inherited or caused by
 CC spontaneous mutations and ischemic CMP caused by arteriosclerosis,
 CC dilative CMP caused by toxic/infectious disease, cardiac disease caused
 CC by pulmonary and/or arterial hypertension, and structural disease caused
 CC by rhythm disorders or valve defects, generally any condition associated
 CC with reduced contractile force. Unlike calmodulin, which is expressed
 CC ubiquitously, (I) show tissue-specific expression and treat the
 CC underlying defect in the sarcoplasmic reticulum (SR) that causes cardiac
 CC disease
 XX SQ Sequence 92 AA;
 Alignment Scores:
 Pred. No.: 1.04e-80 Length: 92
 Score: 92.00 Matches: 92
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 3 Gaps: 0
 US-09-910-208b-12 (1-276) x AAB45542 (1-92)
 QY 1 ATGACAAACTTGAAGAGCATCTGGAGGAATTTGTCATATCTTCCACCAATCTCAGTT 60
 Db 1 MetThrLysLeuGluGluHisLeuGluGlyLeuValAsnIlePheHisGlnTyrSerVal 20
 QY 61 CGGAAGGGGCAATTTTGAACCCCTCTCTAAGGGTGAAGTGAAGCAGCTGCTTACAAAGGAG 120

Db 21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGlu 40
 QY 121 CTTGCAACACCATCAAGATATCAAGATAAAGCTGTGTCATTGATGAATATTCGAAGGC 180
 Db 41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60
 QY 181 CTGGATCTTAATCAAGATGAACAGGTCGACTTTTCAAGAAATTCATATCCCTGGTAGCATT 240
 Db 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80
 QY 241 GCCTGAAGGCTCCCATTCACCAACCCACAAAGAG 276
 Db 81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92
 RESULT 4
 AAB31911
 ID AAB31911 standard; protein; 92 AA.
 XX AC AAB31911;
 XX DT 15-MAY-2001 (first entry)
 XX DE Amino acid sequence of a human protein.
 XX Human; perlecan; retinol-binding plasma protein; calgranulin B; vaccine;
 KW ganglioside GM2 activator; saposin B; degenerative disease; glial cell;
 KW neurological disease; auto-immune disease; multiple sclerosis; toxicity;
 KW Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;
 KW rheumatoid polyarthritis; lupus erythematosus; gene therapy.
 XX OS Homo sapiens.
 XX WO200105422-A2.
 XX PD 25-JAN-2001.
 XX PF 17-JUL-2000; 2000WO-FR002057.
 XX PR 15-JUL-1999; 99FR-00009372.
 XX PA (INNR) BIOMERIEUX STELHYS.
 XX PI Roecklin D, Kolbe H, Charles M, Malcus C, Santoro L, Perron H;
 XX WPI: 2001-159475/16.
 XX Detecting, preventing and treating degenerative, neurological and
 PT autoimmune diseases, particularly multiple sclerosis, using specified
 PT polypeptides or related nucleic acid or ligand.
 XX Claim 1; Page 168; 209pp; French.
 CC The present sequence represents a human protein, which is used in the
 CC method of the invention. The specification describes a method which uses
 CC at least one polypeptide or polynucleotide sequence belonging to the
 CC perlecan, precursor of the retinol-binding plasma protein, precursor of
 CC the ganglioside GM2 activator, calgranulin B or saposin B protein
 CC families. The method is used for detecting, preventing or treating a
 CC degenerative, neurological and/or auto-immune disease. The
 CC polynucleotides and polypeptides are used for diagnosis, prognosis,
 CC prevention and treatment of multiple sclerosis (in its various forms and
 CC phases). They may also be useful in cases of e.g. Alzheimer's and
 CC Parkinson's diseases, amyotrophic lateral sclerosis, rheumatoid
 CC polyarthritis and lupus erythematosus, including use as vaccines and in
 CC gene therapy (expression of sense or antisense sequences). They can also
 CC be used to assess efficacy of potential therapeutic agents, particularly
 CC compounds that reduce or inhibit toxicity towards glial cells

XX Sequence 92 AA;

Alignment Scores:

Pred. No.: 1.04e-80 Length: 92

Score: 92.00 Matches: 92
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-910-208B-12 (1-276) x AAB31911 (1-92)

QY 1 ATGACAAAATTGAAGAGCATCTGGAGGAATTGTCAATATCTTCCACCAATACTCAGTT 60
DB 1 MetThrLysLeuGluGluHisLeuGluGlyIleValAsnIlePheHisGlnTyrSerVal 20

QY 61 CGGAAGGGGCATTTTGACACCCCTCTTAAGGGTGAGCTGAAGCAGCTGCTTCAAAAGGAG 120
DB 21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGlu 40

QY 121 CTTGCAAAACCATCAAGAAATCAAGATTAAGCTGCTCATTCAGTAATATTCACAGGC 180
DB 41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60

QY 181 CTGGATGCTAATCAAGATGAACAGGTCGACTTTTCAAGAAATTCATATCCCTGGTAGCCATT 240
DB 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80

QY 241 GCGCTGAAGCGTCCCATTCACACCCCAAGAG 276
DB 81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92

RESULT 5
AAB31907
ID AAB31907 standard; protein; 92 AA.
AC AAB31907;
XX
XX
DT 15-MAY-2001 (first entry)
XX
DE Amino acid sequence of a human protein.
XX
KW Human; perlecan; retinol-binding plasma protein; calgranulin B; vaccine;
KW ganglioside GM2 activator; saposin B; degenerative disease; glial cell;
KW neurological disease; auto-immune disease; multiple sclerosis; toxicity;
KW Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;
KW rheumatoid polyarthritis; lupus erythematosus; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200105422-A2.
XX
PD 25-JAN-2001.
XX
PF 17-JUL-2000; 2000WO-FR002057.
XX
PR 15-JUL-1999; 99FR-00009372.
XX
XX (INNR) BIOMERIEUX STELHYS.
XX
PI Roeklin D, Kolbe H, Charles M, Malcus C, Santoro L, Perron H;
XX WPI; 2001-159475/16.
XX
DR
XX
PT Detecting, preventing and treating degenerative, neurological and
PT autoimmune diseases, particularly multiple sclerosis, using specified
PT polypeptides or related nucleic acid or ligand.
XX
XX Claim 1; Page 166-167; 209pp; French.
XX
CC The present sequence represents a human protein, which is used in the
CC method of the invention. The specification describes a method which uses
CC at least one polypeptide or polynucleotide sequence belonging to the
CC perlecan, precursor of the retinol-binding plasma protein, precursor of
CC the ganglioside GM2 activator, calgranulin B or saposin B protein
CC families. The method is used for detecting, preventing or treating a
CC degenerative, neurological and/or auto-immune disease. The

CC polynucleotides and polypeptides are used for diagnosis, prognosis,
CC prevention and treatment of multiple sclerosis (in its various forms and
CC phases). They may also be useful in cases of e.g. Alzheimer's and
CC Parkinson's diseases, amyotrophic lateral sclerosis, rheumatoid
CC polyarthritis and lupus erythematosus, including use as vaccines and in
CC gene therapy (expression of sense or antisense sequences). They can also
CC be used to assess efficacy of potential therapeutic agents, particularly
CC compounds that reduce or inhibit toxicity towards glial cells

XX Sequence 92 AA;

Alignment Scores:
Pred. No.: 1.04e-80 Length: 92
Score: 92.00 Matches: 92
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-910-208B-12 (1-276) x AAB31907 (1-92)

QY 1 ATGACAAAATTGAAGAGCATCTGGAGGAATTGTCAATATCTTCCACCAATACTCAGTT 60
DB 1 MetThrLysLeuGluGluHisLeuGluGlyIleValAsnIlePheHisGlnTyrSerVal 20

QY 61 CGGAAGGGGCATTTTGACACCCCTCTTAAGGGTGAGCTGAAGCAGCTGCTTCAAAAGGAG 120
DB 21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGlu 40

QY 121 CTTGCAAAACCATCAAGAAATCAAGATTAAGCTGCTCATTCAGTAATATTCACAGGC 180
DB 41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60

QY 181 CTGGATGCTAATCAAGATGAACAGGTCGACTTTTCAAGAAATTCATATCCCTGGTAGCCATT 240
DB 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80

QY 241 GCGCTGAAGCGTCCCATTCACACCCCAAGAG 276
DB 81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92

RESULT 6
AAB31908
ID AAB31908 standard; protein; 92 AA.
AC AAB31908;
XX
XX
DT 15-MAY-2001 (first entry)
XX
DE Amino acid sequence of a human protein.
XX
KW Human; perlecan; retinol-binding plasma protein; calgranulin B; vaccine;
KW ganglioside GM2 activator; saposin B; degenerative disease; glial cell;
KW neurological disease; auto-immune disease; multiple sclerosis; toxicity;
KW Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;
KW rheumatoid polyarthritis; lupus erythematosus; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200105422-A2.
XX
PD 25-JAN-2001.
XX
PF 17-JUL-2000; 2000WO-FR002057.
XX
PR 15-JUL-1999; 99FR-00009372.
XX
XX (INNR) BIOMERIEUX STELHYS.
XX
PI Roeklin D, Kolbe H, Charles M, Malcus C, Santoro L, Perron H;
XX WPI; 2001-159475/16.
XX
DR
XX

PT Detecting, preventing and treating degenerative, neurological and
PT autoimmune diseases, particularly multiple sclerosis, using specified
PT polypeptides or related nucleic acid or ligand.
XX
PS Claim 1; Page 167; 209pp; French.
XX
CC The present sequence represents a human protein, which is used in the
CC method of the invention. The specification describes a method which uses
CC at least one polypeptide or polynucleotide sequence belonging to the
CC perlecan, precursor of the retinol-binding plasma protein, precursor of
CC the ganglioside GM2 activator, calgranulin B or saposin B protein
CC families. The method is used for detecting, preventing or treating a
CC degenerative, neurological and/or auto-immune disease. The
CC polynucleotides and polypeptides are used for diagnosis, prognosis,
CC prevention and treatment of multiple sclerosis (in its various forms and
CC phases). They may also be useful in cases of e.g. Alzheimer's and
CC Parkinson's diseases, anyotrophic lateral sclerosis, rheumatoid
CC polyarthritis and lupus erythematosus, including use as vaccines and in
CC gene therapy (expression of sense or antisense sequences). They can also
CC be used to assess efficacy of potential therapeutic agents, particularly
CC compounds that reduce or inhibit toxicity towards glial cells
XX
SQ Sequence 92 AA;
XX
Alignment Scores:
Pred. No.: 1.04e-80 Length: 92
Score: 92.00 Matches: 92
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
US-09-910-208B-12 (1-276) x AAB31908 (1-92)
QY 1 ATGACAAAACCTTGAAGAGCATCTGGAGGAATGTCAATATCTTCCACCAATCTCAGTT 60
Db 1 MetThrLysLeuGluHisLeuGluGlyIleValAsnIlePheHisGlnTyrSerVal 20
QY 61 CGGAAGGGGCAATTTGACACCCCTCTTAAGGCTGAGCTCAAGCAGCTGCTTACAAGGAG 120
Db 21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGlu 40
QY 121 CTTCGAAACACCATCAAGATATCAAGATAAAGCTGTCAATGATGAATATTTCAAGGC 180
Db 41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60
QY 181 CTGGATGCTTAATCAAGATGAACAGTTCGACTTTCAAGATTCATATCCCTGGTAGCCATT 240
Db 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80
QY 241 GCCTGAAGCTGCCATTTACCAACCCACCAAGAG 276
Db 81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92
RESULT 7
ADA93649
ID ADA93649 standard; protein; 92 AA.
XX
AC ADA93649;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human calgranulin C protein SEQ ID NO:2.
XX
KW inflammatory disease; calgranulin C; antiinflammatory; gene therapy;
KW vasculitis; Kawasaki disease; cystic fibrosis;
KW chronic inflammatory disease; ulcerative colitis; Crohn's disease;
KW chronic bronchitis; inflammatory arthritis; psoriatic arthritis;
KW rheumatoid arthritis; seronegative arthritis;
KW systemic onset juvenile rheumatoid arthritis; SOJRA; Still's disease;
KW acute inflammation; human.
XX
OS Homo sapiens.

XX WO2003069341-A2.
XX 21-AUG-2003.
XX 17-FEB-2003; 2003WO-EP001575.
XX 15-FEB-2002; 2002US-00077600.
XX (SWIT-) SWITCH BIOTECH AG.
XX (SORG/) SORG C.
XX (ROTH/) ROTH J.
XX Sorg C, Roth J;
XX WPI; 2003-671681/63.
XX N-PSDB; ADA93648.
XX Diagnosing, treating or preventing inflammatory diseases comprises
XX determining the amount and/or concentration of CALGRANULIN C polypeptide
XX and/or nucleic acids encoding the polypeptide present in a biological
XX sample.
XX Claim 7; Page 64; 64pp; English.
XX
CC The present invention describes a method for diagnosing inflammatory
CC diseases, which comprises determining the amount and/or concentration of
CC calgranulin C polypeptide and/or nucleic acids encoding the polypeptide
CC present in the biological sample. Also described are methods for treating
CC or preventing an inflammatory disease in a mammal, and medical treatment
CC of the mammal, where the treatment is based on the stage of the disease
CC to be treated or prevented. Calgranulin C has antiinflammatory activity
CC and can be used in gene therapy. The method is useful for diagnosing,
CC treating or preventing inflammatory diseases, e.g. vasculitis
CC (particularly Kawasaki disease), cystic fibrosis, chronic inflammatory
CC diseases like ulcerative colitis or Crohn's disease, chronic bronchitis,
CC inflammatory arthritis (e.g. psoriatic arthritis, rheumatoid arthritis or
CC seronegative arthritis), systemic onset juvenile rheumatoid arthritis
CC (SOJRA or Still's disease), acute inflammation above the background of a
CC chronic inflammatory disease, an acquired infection on the background of an
CC inflammatory disease, or an exacerbation of an already present disease.
CC The method is also useful for diagnosing specific stages of inflammatory
CC diseases, for determining the risk of relapse, and for discriminating
CC between diseases with similar symptoms. The present sequence represents
CC human calgranulin C, which is used in the exemplification of the present
CC invention.
XX
SQ Sequence 92 AA;
XX
Alignment Scores:
Pred. No.: 1.04e-80 Length: 92
Score: 92.00 Matches: 92
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0
US-09-910-208B-12 (1-276) x ADA93649 (1-92)
QY 1 ATGACAAAACCTTGAAGAGCATCTGGAGGAATGTCAATATCTTCCACCAATCTCAGTT 60
Db 1 MetThrLysLeuGluHisLeuGluGlyIleValAsnIlePheHisGlnTyrSerVal 20
QY 61 CGGAAGGGGCAATTTGACACCCCTCTTAAGGCTGAGCTCAAGCAGCTGCTTACAAGGAG 120
Db 21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGlu 40
QY 121 CTTCGAAACACCATCAAGATATCAAGATAAAGCTGTCAATGATGAATATTTCAAGGC 180
Db 41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60
QY 181 CTGGATGCTTAATCAAGATGAACAGTTCGACTTTCAAGATTCATATCCCTGGTAGCCATT 240

Db 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80
QY 241 GCCTGAAGCTGCCATTACCAACACCCCAAGAG 276
Db 81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92
RESULT 8
ADN04192
ID ADN04192 standard; protein; 92 AA.
XX
AC ADN04192;
XX
DT 01-JUL-2004 (first entry)
XX
DE Antipsoriatic protein sequence #291.
XX
KW antipsoriatic; gene therapy; psoriasis; diagnosis.
XX
OS Homo sapiens.
XX
PN WO2004028479-A2.
XX
PD 08-APR-2004.
XX
PF 25-SEP-2003; 2003WO-US030907.
XX
PR 25-SEP-2002; 2002US-0414006P.
XX
PA (GETH) GENENTECH INC.,
XX
PI Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;
PI Wu TD;
XX
DR WPI; 2004-305105/28.
DR N-PSDB; ADN04191.
XX
XX New PRO nucleic acid or polypeptide, useful for preparing a
PT pharmaceutical composition for diagnosing or treating psoriasis in a
PT mammal.
XX
PS Claim 9; SEQ ID NO 586; 3069pp; English.
XX
CC The invention relates to novel polynucleotide and polypeptides for
CC treating psoriasis or a sequence having at least 80% identity to the
CC above sequences. The nucleic acid is useful for preparing a composition
CC for diagnosing or treating psoriasis in a mammal. This sequence
CC corresponds to one of the polypeptides of the invention.
XX
SQ Sequence 92 AA;
Alignment Scores:
Pred. No.: 1,04e-80 Length: 92
Score: 92.00 Matches: 92
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0
US-09-910-208B-12 (1-276) x ADN04192 (1-92)
QY 1 ATGACAAACTTGAAGACATCTGGAGGAATTGTCAATATCTTCCCAATACTCAGTT 60
Db 1 MetThrLysLeuGluHisLeuGluGlyIleValAsnIlePheHisGlnTyrSerVal 20
QY 61 CGAAGGGCATTTTCACACCTCTCAAGGCTGAGCTGAGCAGCTGCTTCAAGAG 120
Db 21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuThrLysGlu 40
QY 121 CTTGCAAAACACCATCAAGATATCAAGATAAAGCTGTCTTGGATGATATATTTCCAAAGGC 180
Db 41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60
QY 181 CTGGATGCTAATCAAGATGAACAGGTCGACTTTTCAAGAATTTCATATCCCTGGTAGCCATT 240

Db 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80
QY 241 GCGCTGAAGCTGCCATTACCAACACCCCAAGAG 276
Db 81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92
RESULT 9
ADN019540
ID ADN019540 standard; protein; 92 AA.
XX
AC ADN019540;
XX
DT 12-AUG-2004 (first entry)
XX
DE Human PRO polypeptide #235.
XX
KW Human; PRO; immune related disorder; systemic lupus erythematosus;
KW rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis;
KW systemic sclerosis; Sjogren's syndrome; vasculitis; sarcoidosis;
KW autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis;
KW diabetes mellitus; renal disease; demyelinating disease;
KW central nervous system; peripheral nervous system;
KW demyelinating polyneuropathy; Guillain-Barre syndrome;
KW chronic inflammatory demyelinating polyneuropathy.
XX
OS Homo sapiens.
XX
PN WO2004043361-A2.
XX
PD 27-MAY-2004.
XX
PF 06-NOV-2003; 2003WO-US035268.
XX
PR 08-NOV-2002; 2002US-0425235P.
XX
PA (GETH) GENENTECH INC.
XX
PI Fong S, Dennis K, Clark H, Chiu H, Schoenfeld J, Williams PM;
PI Wood WI, Wu TD;
XX
DR WPI; 2004-420067/39.
DR N-PSDB; ADN019539.
XX
XX Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO86388 useful for
PT treating an immune related disorder such as systemic lupus erythematosus,
PT rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or
PT spondyloarthritis.
XX
PS Claim 7; SEQ ID NO 470; 1731pp; English.
XX
CC The invention relates to human PRO polypeptides and the polynucleotides
CC encoding them. The polypeptides and polynucleotides are useful for
CC treating and diagnosing immune related disorders in mammals. The immune
CC related disorders include systemic lupus erythematosus, rheumatoid
CC arthritis, osteoarthritis, juvenile chronic arthritis, systemic
CC sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune
CC haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes
CC mellitus, immune-mediated renal disease, demyelinating diseases of the
CC central or peripheral nervous system, demyelinating polyneuropathy,
CC Guillain-Barre syndrome and chronic inflammatory demyelinating
CC polyneuropathy. This sequence represents a human PRO polypeptide of the
XX invention.
SQ Sequence 92 AA;
Alignment Scores:
Pred. No.: 1,04e-80 Length: 92
Score: 92.00 Matches: 92
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-09-910-208B-12 (1-276) x ADO19540 (1-92)

QY 1 ATGCAAAACTTGAAGACATCTGGAGGAATTCATATCTTCCACCAATACTCAGTT 60
 Db 1 MetThrLysLeuGluGluHisLeuGluGlyLeuValAsnIlePheHisGlnTyrSerVal 20

QY 61 CGGAAGGGGCATTTTGACACCTCTCTAAGGCTGAGCTGAAGCAGCTGCTTACAAAGGAG 120
 Db 21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGlu 40

QY 121 CTTGCAACACCATCAAGAATATCAAGATTAAGCTGTCATGTGATGAATATTCAGAGGC 180
 Db 41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60

QY 181 CTGGATGCTAATCAAGATGAACAGTTCGACTTTCAAGAAATTCATATCCTCGTAGCCATT 240
 Db 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80

QY 241 GCGCTGAAGGCTGCCATTACCACACCCACCAAGAG 276
 Db 81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92

RESULT 10
 ID ADR14333
 AC ADR14333 standard; protein; 92 AA.
 XX ADR14333;
 XX
 DT 21-OCT-2004 (first entry)
 XX

Human NF-kappaB pathway-associated protein SeqID334.

XX NF-kappaB pathway; antiinflammatory; cytostatic; hepatotropic; virucide;
 KW antiarthritic; antirheumatic; gastrointestinal-Gen; antiasthmatic;
 KW antiarteriosclerotic; immunomodulator; cerebroprotective; vasotropic;
 KW immunosuppressive; vulnerable; gene therapy; immune disorder;
 KW inflammatory disorder; NF-kappaB regulation; cancer; aberrant apoptosis;
 KW hepatic disorder; Hodgkin's lymphoma; haematopoietic tumour;
 KW hyper-IGM syndrome; hypohidrotic ectodermal dysplasia;
 KW X-linked anhidrotic ectodermal dysplasia; immunodeficiency;
 KW viral infection; HIV-1; hepatitis B; hepatitis C; EBV; influenza;
 KW viral replication; host cell survival; evasion of immune response;
 KW rheumatoid arthritis; inflammatory bowel disease; colitis; asthma;
 KW atherosclerosis; cachexia; euthyroid sick syndrome; stroke; EAE;
 KW autoimmune disorder; hyper immune activity;
 KW aberrant acute phase response; hypercongenital condition; birth defect;
 KW necrotic lesion; wound; organ transplant rejection;
 KW aberrant signal transduction; proliferating disorder; cancer;
 KW HIV propagation; human.
 XX
 XX Homo sapiens.
 XX
 XX WO2004065577-A2.
 XX
 XX 05-AUG-2004.
 XX
 XX 13-JAN-2004; 2004WO-US000798.
 XX
 XX 14-JAN-2003; 2003US-0440068P.
 XX
 XX 12-MAY-2003; 2003US-0469757P.
 XX
 XX (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX
 XX Nadler SG, Neubauer MG, Feder JN, Carman J;
 XX
 XX WPI; 2004-562168/54.
 XX
 XX N-PSDB; ADR14332.
 XX
 XX New isolated polynucleotides and polypeptides associated with NF-kappaB
 PT pathway, useful for diagnosing, treating, or preventing disorders or
 PT diseases associated with NF-kappaB pathway.
 XX

PS This invention relates to the novel association of protein sequences (and
 XX the genes which encode them) to the NF-kappaB pathway. The invention may
 CC be useful for the production of compounds with an antiinflammatory,
 CC cytostatic, hepatotropic, virucide, antiarthritic, antirheumatic,
 CC gastrointestinal-gen, antiasthmatic, antiarteriosclerotic,
 CC immunomodulator, cerebroprotective, vasotropic, immunosuppressive or
 CC vulnerable activity or for gene therapy. The proteins and nucleotides are
 CC useful for diagnosing, preventing, treating, or ameliorating conditions
 CC or diseases associated with the NF-kappaB pathway. The condition is an
 CC immune disorder, an inflammatory disorder, an inflammatory disorder
 CC related to aberrant NF-kappaB regulation, cancer, aberrant apoptosis,
 CC hepatic disorders, Hodgkin's lymphomas, haematopoietic tumours, hyper-IGM
 CC syndromes, hypohidrotic ectodermal dysplasia, X-linked anhidrotic
 CC ectodermal dysplasia, immunodeficiency, viral infections, HIV-1, HTLV-1,
 CC hepatitis B, hepatitis C, EBV, influenza, viral replication, host cell
 CC survival, evasion of immune responses, rheumatoid arthritis, inflammatory
 CC bowel disease, colitis, asthma, atherosclerosis, cachexia, euthyroid sick
 CC syndrome, stroke, EAE, autoimmune disorders, disorders related to hyper
 CC immune activity, disorders related to aberrant acute phase responses,
 CC hypercongenital conditions, birth defects, necrotic lesions, wounds,
 CC organ transplant rejection, conditions related to organ transplant
 CC rejection, disorders related to aberrant signal transduction,
 CC proliferating disorders, cancers and HIV propagation in cells infected
 CC with other viruses. The present sequence is that of a human protein which
 CC is subject to the novel association with the NF-kappaB pathway of the
 CC invention. Note: This sequence does not appear in the specification but
 CC was obtained by the indexer from Genbank.
 XX
 XX Sequence 92 AA;
 SQ

Alignment Scores:
 Pred. No.: 1.04e-80 Length: 92
 Score: 92.00 Matches: 92
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 8 Gaps: 0

US-09-910-208B-12 (1-276) x ADR14333 (1-92)

QY 1 ATGCAAAACTTGAAGACATCTGGAGGAATTCATATCTTCCACCAATACTCAGTT 60
 Db 1 MetThrLysLeuGluGluHisLeuGluGlyLeuValAsnIlePheHisGlnTyrSerVal 20

QY 61 CGGAAGGGGCATTTTGACACCTCTCTAAGGCTGAGCTGAAGCAGCTGCTTACAAAGGAG 120
 Db 21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGlu 40

QY 121 CTTGCAACACCATCAAGAATATCAAGATTAAGCTGTCATGTGATGAATATTCAGAGGC 180
 Db 41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60

QY 181 CTGGATGCTAATCAAGATGAACAGTTCGACTTTCAAGAAATTCATATCCTCGTAGCCATT 240
 Db 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80

QY 241 GCGCTGAAGGCTGCCATTACCACACCCACCAAGAG 276
 Db 81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92

RESULT 11
 ADP23921
 ID ADP23921 standard; protein; 92 AA.
 XX
 XX ADP23921;
 XX
 XX 18-NOV-2004 (first entry)
 XX
 XX PRO polypeptide SEQ ID NO:1099.
 XX
 XX PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive;
 KW

osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic;
antasthmatic; hepatotropic; respiratory; gene therapy; immune system.
Unidentified.
WO2004041170-A2.
21-MAY-2004.
30-OCT-2003; 2003WO-US034312.
01-NOV-2002; 2002US-0423394P.
(GETH) GENENTECH INC.
Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI;
Wu TD;
WPI; 2004-419628/39.
N-PSDB; ADP23920.
New PRO polypeptides and polynucleotides, useful for treating e.g.
erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated
renal disease, or demyelinating diseases of the central or peripheral
nervous system.
Claim 7; SEQ ID NO 1099; 2940pp; English.
The invention relates to a novel isolated nucleic acid and the PRO
polypeptide encoded by it. A protein of the invention has
antiflammatory, antiarthritic, antirheumatic, immunosuppressive,
osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic,
antasthmatic, hepatotropic, and respiratory activity. A polynucleotide
of the invention may have a use in gene therapy. The PRO polypeptide, its
agonist, antagonist, or antibody that specifically binds to the
polypeptide is useful for treating an immune related disorder such as
systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
disease, a demyelinating disease of the central or peripheral nervous
system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,
a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary
disease, infectious or autoimmune chronic active hepatitis, primary
biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
disease, an autoimmune or immune-mediated skin disease, a bullous skin
disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
disease, atopic rhinitis, atopic dermatitis, food
hypersensitivity, urticaria, an immunologic disease of the lung,
eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
pneumonitis, a transplantation associated disease, graft rejection or
graft-versus-host disease. The present sequence represents a PRO protein
of the invention.
Sequence 92 AA;
Alignment Scores:
Pred. No.: 1.04e-80 Length: 92
Score: 92.00 Matches: 92
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0
US-09-910-208B-12 (1-276) x ADP23921 (1-92)
QY 1 ATGACAAAACCTTGAAGCATCTGGAGGAATTTGTCATATCTTCCACCAATCTCAGTT 60
Db 1 MetThrLysLeuGluGluHisLeuGluGlyIleValAsnIlePheHisGlnIleVal 20
QY 61 CGGAAGGGGCGATTTTGACACCTCTCTTAAGGGTGAGCTGAAGCAGCTGCTTCAAAAGGAG 120

Db 21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGlu 40
QY 121 CTTGCAAAACACCATCAAGAATATCAAGATAAAGCTGTCTATTGATGAAATATTCCAAAGC 180
Db 41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluLeuPheGlnGly 60
QY 181 CTGGATGCTAATCAAGATGAACAGCTCGACTTTTCAAGATTTCATATCCTCGTAGCATT 240
Db 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80
QY 241 GCGCTGAAGGCTGCCCATTTACACACCCACCAAGAG 276
Db 81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92
RESULT 12
ADS74331
ID ADS74331 standard; protein; 92 AA.
XX
AC ADS74331;
XX
DT 16-DEC-2004 (first entry)
XX
DE PRO polypeptide PRO62943, role in immune-related disease.
XX
KW PRO62943; rheumatoid arthritis; psoriasis; antirheumatic; antiarthritic;
KW antipsoriatic; gene therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 4..47
FT /note= "S-100/ICaBP type calcium binding domain"
FT Region 60..65
FT /note= "N-myristoylation site"
XX
PN WO2004081199-A2.
XX
PD 23-SEP-2004.
XX
PF 10-MAR-2004; 2004WO-US007862.
XX
PR 11-MAR-2003; 2003US-0454025P.
XX
PA (GETH) GENENTECH INC.
PI Baldwin D, Bodary S, Clark H, Fong S, Gurney AL, Williams PM;
XX
DR WPI; 2004-668955/65.
DR N-PSDB; ADS74330.
XX
PT New nucleic acid encoding PRO polypeptide, useful for diagnosing and
PT treating psoriasis, Crohn's disease, Ulcerative Colitis, or rheumatoid
PT arthritis.
XX
PS Claim 9; SEQ ID NO 50; 166pp; English.
XX
CC The present sequence is the protein sequence of novel human PRO
CC polypeptide PRO62943. The invention provides newly identified and
CC isolated nucleotide sequences encoding polypeptides referred to as PRO
CC polypeptides that are useful in the diagnosis and treatment of immune-
CC related diseases. Microarray analysis showed that expression of PRO62943
CC is up-regulated 4-fold in lesional skin as compared to non-lesional skin
CC from psoriasis patients and up-regulated 2-fold in white blood cells from
CC rheumatoid arthritis patients as compared to those from healthy donors
CC It is also down-regulated 2-fold upon activation of CD4 T cells with CD28
CC or ICAM, down-regulated 6-fold upon differentiation of monocytes into
CC macrophages after 7 days in differentiation media and up-regulated 4-fold
CC upon activation of monocytes with LPS. PRO62943 can be used in a claimed
CC method of identifying a compound that inhibits expression of the gene
CC encoding it. The candidate compound is especially an antisense nucleic
CC acid. The PRO polypeptide can be obtained by recombinant expression,
CC especially in CHO, Escherichia coli or yeast host cells. The polypeptide,

CC its antagonist or an antibody that binds the polypeptide are used in
CC claimed methods for the alleviation or diagnosis of rheumatoid arthritis
CC and psoriasis.

XX
SQ Sequence 92 AA;

Alignment Scores:
Pred. No.: 1.04e-80 Length: 92
Score: 92.00 Matches: 92
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-09-910-208B-12 (1-276) x ADS74331 (1-92)

QY 1 ATGACAAACCTTGAGAGCATCTGGAGGAATTGTCAATATCTTCCACCAATCTCAGTT 60
DB 1 MetThrLysLeuGluGluHisLeuGluGlyIleValAsnIlePheHisGlnTyrSerVal 20
QY 61 CGGAAGGGGCATTTTACACACCTCTCTAAGGCTGAGTGAAGCAGCTCTTACAAAGAG 120
DB 21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGlu 40
QY 121 CTTGCAACACCATCAAGAATATCAAGATAAAGCTGTCAATGATGAATATTCAGGC 180
DB 41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60
QY 181 CTGATGCTTAATCAAGATGAACAGCTCGACTTTCAGAAATTCATATCCTGTAGCCATT 240
DB 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80
QY 241 GCGCTGAAGCTGCCCATTTACACACCCACAAAGAG 276
DB 81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92

RESULT 13
AAB31909
ID AAB31909 standard; protein; 91 AA.

XX
AC AAB31909;
DT 15-MAY-2001 (first entry)
XX

DE Amino acid sequence of a human protein.

XX Human; perlecan; retinol-binding plasma protein; calgranulin B; vaccine;
KW ganglioside GM2 activator; saposin B; degenerative disease; glial cell;
KW neurological disease; auto-immune disease; multiple sclerosis; toxicity;
KW Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;
KW rheumatoid polyarthritis; lupus erythematosus; gene therapy.

XX Homo sapiens.

XX WO200105422-A2.

XX 25-JAN-2001.

XX 17-JUL-2000; 2000WO-FR002057.

XX 15-JUL-1999; 99FR-00009372.

XX (INMR) BIONERIEUX STELHYS.

XX Roecklin D, Kolbe H, Charles M, Malcus C, Santoro L, Perron H;

XX WPI; 2001-159475/16.

XX Detecting, preventing and treating degenerative, neurological and
PT autoimmune diseases, particularly multiple sclerosis, using specified
PT polypeptides or related nucleic acid or ligand.

XX Claim 1; Page 167; 209pp; French.

XX The present sequence represents a human protein, which is used in the
CC method of the invention. The specification describes a method which uses
CC at least one polypeptide or polynucleotide sequence belonging to the
CC perlecan, precursor of the retinol-binding plasma protein, precursor of
CC the ganglioside GM2 activator, calgranulin B or saposin B protein
CC families. The method is used for detecting, preventing or treating a
CC degenerative, neurological and/or auto-immune disease. The
CC polynucleotides and polypeptides are used for diagnosis, prognosis,
CC prevention and treatment of multiple sclerosis (in its various forms and
CC phases). They may also be useful in cases of e.g. Alzheimer's and
CC Parkinson's diseases, amyotrophic lateral sclerosis, rheumatoid
CC polyarthritis and lupus erythematosus, including use as vaccines and in
CC gene therapy (expression of sense or antisense sequences). They can also
CC be used to assess efficacy of potential therapeutic agents, particularly
CC compounds that reduce or inhibit toxicity towards glial cells

XX Sequence 91 AA;

Alignment Scores:
Pred. No.: 9.86e-80 Length: 91
Score: 91.00 Matches: 91
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.91% Indels: 0
DB: 4 Gaps: 0

US-09-910-208B-12 (1-276) x AAB31909 (1-91)

QY 4 ACAAACTTGAAGAGCATCTGGAGGAATTGTCAATATCTTCCACCAATCTCAGTTCCG 63
DB 1 ThrLysLeuGluGluHisLeuGluGlyIleValAsnIlePheHisGlnTyrSerValArg 20
QY 64 AAGGGCATTTTGACACCTCTCTAAGGCTGAGCTGAAGCAGCTGTACAAAGAGCCTT 123
DB 21 LysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGluLeu 40
QY 124 GCAACACCATCAAGAATATCAAGATAAAGCTGTCTATTGATGAATATTCCAAGGCTG 183
DB 41 AlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGlyLeu 60
QY 184 GATGCTAATCAAGATGAACAGCTGACTTTTCAGAAATTCATATCCCTGGTAGCCATTGCG 243
DB 61 AspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIleAla 80
QY 244 CTGAAGGCTGCCCATTTACCACACCCACAAAGAG 276

DB 81 LeuLysAlaAlaHisTyrHisThrHisLysGlu 91

RESULT 14
AAB31909
ID AAB31909 standard; protein; 95 AA.

XX AC AAB31909;

XX DT 18-FEB-2002 (first entry)

XX DE Novel human diagnostic protein #27573.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;

XX food supplement; medical imaging; diagnostic; genetic disorder.

XX OS Homo sapiens.

XX PN WO200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US008631.

XX PR 31-MAR-2000; 2000US-00540217.

XX PR 23-AUG-2000; 2000US-00649167.

PA (HYSE-) HYSEQ INC.
XX Drmanac RT, Liu C, Tang YT;
XX
XX
XX WPI: 2001-639362/73.
XX N-PSDB; AAS91769.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
XX Claim 20; SEQ ID NO 57941; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 95 AA;
SQ
Alignment Scores:
Pred. No.: 3.67e-63 Length: 74.00 Matches: 74
Score: 74.00
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 80.43% Indels: 0
DB: 4 Gaps: 0
US-09-910-208B-12 (1-276) x ABG27582 (1-95)
QY 55 TCAGTTCGAAGGGGCATTTTGCACACCCCTCTTAAGGGTGAGCTGAAGCAGCTGCTTACA 114
Db 22 SerValArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThr 41
QY 115 AGGAGCTTGCAACACCATCAAGATATCAAGATAAAGCTGTCATTCGATGAATATTC 174
Db 42 LysGluLeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePhe 61
QY 175 CAAGGCTCGATGCTAATCAAGATGAACAGCTCGACTTTCAAGAATTCATATCCCTGGTA 234
Db 62 GlnGlyLeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuVal 81
QY 235 GCCATTGCCTGAAGCTGCCCATTTACCAACCCCAAGAG 276
Db 82 AlaIleAlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 95
RESULT 15
ABB43183
ID ABB43183 standard; peptide; 46 AA.
XX
XX ABB43183;
XX
XX
XX 04-FEB-2002 (first entry)
XX
XX Peptide #10689, encoded by human foetal liver single exon probe.

XX Human; foetal liver; gene expression; single exon nucleic acid probe.
XX Homo sapiens.
OS
XX WO200157277-A2.
PN
XX
XX 09-AUG-2001.
PD
XX
XX 30-JAN-2001; 2001WO-US000669.
PF
XX
XX 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024283.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
PA
XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI
XX WPI; 2001-483447/52.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human fetal liver.
PT
XX
XX Claim 27; SEQ ID NO 35818; 639pp + Sequence Listing; English.
PS
XX
XX The invention relates to a single exon nucleic acid probe for measuring
CC human gene expression in a sample derived from human foetal liver. The
CC single exon nucleic acid probes may be used for predicting, measuring and
CC displaying gene expression in samples derived from human fetal liver. The
CC present sequence is a peptide encoded by a single exon nucleic acid probe
CC of the invention. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 46 AA;
SQ
Alignment Scores:
Pred. No.: 8.14e-36 Length: 46 Matches: 46
Score: 46.00
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 50.00% Indels: 0
DB: 4 Gaps: 0
US-09-910-208B-12 (1-276) x ABB43183 (1-46)
QY 1 ATGACAAACTTGAAGAGCATCTGGAGGGAATTGTCAATATCTCCACCAATACTCAGTT 60
Db 1 MetThrLysLeuGluGluHisLeuGluGlyIleValAsnIlePheHisGlnIleVal 20
QY 61 CGGAAGGGGCATTTTGCACACCCCTCTTAAGGGTGAGCTGAAGCAGCTGCTTACAAGGAG 120
Db 21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuLeuThrLysGlu 40
QY 121 CTTGCAACACCATCAAG 138
Db 41 LeuAlaAsnThrIleLys 46
Search completed: February 23, 2005, 12:34:17
Job time : 130 secs

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OM nucleic - protein search, using frame_plus_n2p model

Run on: February 23, 2005, 12:38:26 ; Search time 88 Seconds
(without alignments)
2052.694 Million cell updates/sec

Title: US-09-910-208B-12

Perfect score: 92

Sequence: 1 atgacaaaacttgaagagca.....attaccacaccacacaaagag 276

Scoring table:

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Xgapop 60.0	Xgapext 60.0
Ygapop 60.0	Ygapext 60.0
Fgapop 6.0	Fgapext 7.0
Delop 6.0	Delext 7.0

Searched: 1380268 seqs, 327241040 residues

Word size: 1

Total number of hits satisfying chosen parameters: 2651796

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

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-MODEL=frame+ n2p model -DB=FASTA
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-DB=Published Applications AA -QFMT=fastan -SUFFIX=oligo.rapb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo
-TRANS=human40.cdi -LIST=500 -DOCALLIGN=200 -THR SCORE=quality -THR MIN=1
-ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0
-MAXLEN=2000000000
-USER=HADDAD-09-910208B @CEN_1_199 @runat_23022005_102318_15872 -NCPU=6
-ICPU=3 -NO_MMAP -LARGESUBQRY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : Published Applications AA:

1:	/cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pcp.*
2:	/cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pcp.*
3:	/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pcp.*
4:	/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pcp.*
5:	/cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pcp.*
6:	/cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pcp.*
7:	/cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pcp.*
8:	/cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pcp.*
9:	/cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pcp.*
10:	/cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pcp.*
11:	/cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pcp.*
12:	/cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pcp.*
13:	/cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pcp.*
14:	/cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pcp.*
15:	/cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pcp.*
16:	/cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pcp.*
17:	/cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pcp.*
18:	/cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pcp.*
19:	/cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pcp.*
20:	/cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	92	100.0	92	14	US-10-077-600-2
2	92	100.0	92	16	US-10-755-889-334
3	46	50.0	46	9	US-09-864-761-41579
4	9	9.8	90	9	US-09-826-589-3
5	9	9.8	90	9	US-09-826-589-3
6	9	9.8	90	9	US-09-872-185B-11
7	9	9.8	90	9	US-09-872-185B-12
8	9	9.8	90	15	US-10-666-513-3
9	9	9.8	90	16	US-10-665-867-3
10	9	9.8	90	16	US-10-665-867-4
11	8	8.7	63	15	US-10-425-114-40894
12	8	8.7	70	11	US-09-864-408A-6100
13	8	8.7	86	15	US-10-424-599-151862
14	8	8.7	206	16	US-10-363-829-311
15	8	8.7	218	15	US-10-236-115-772
16	8	8.7	607	15	US-10-424-599-159714
17	7	7.6	45	15	US-10-424-599-161822
18	7	7.7	53	16	US-10-437-963-165162
19	7	7.6	59	14	US-10-106-698-8379
20	7	7.7	69	15	US-10-424-599-257331
21	7	7.6	75	16	US-10-437-963-159895
22	7	7.7	78	15	US-10-424-599-211482
23	7	7.6	85	15	US-10-264-049-2810
24	7	7.7	90	9	US-09-739-254-141
25	7	7.7	90	9	US-09-904-615-141
26	7	7.7	90	14	US-10-054-888-141
27	7	7.6	93	15	US-10-094-886-58
28	7	7.6	95	16	US-10-767-701-50872
29	7	7.6	106	16	US-10-250-889-112
30	7	7.6	113	14	US-10-289-454-235
31	7	7.6	113	14	US-10-050-902-235
32	7	7.6	113	14	US-10-050-898-235
33	7	7.7	121	15	US-10-424-599-225685
34	7	7.6	121	14	US-10-289-454-334
35	7	7.6	121	14	US-10-050-902-334
36	7	7.6	121	14	US-10-050-898-334
37	7	7.6	134	14	US-10-289-454-333
38	7	7.6	134	14	US-10-050-902-333
39	7	7.6	134	14	US-10-050-898-333
40	7	7.6	136	14	US-10-289-454-332
41	7	7.6	136	14	US-10-050-902-332
42	7	7.6	136	14	US-10-050-898-332
43	7	7.7	157	16	US-10-437-963-197129
44	7	7.7	164	16	US-10-767-701-45310
45	7	7.6	166	15	US-10-282-122A-67980
46	7	7.6	167	15	US-10-282-122A-69511
47	7	7.7	169	16	US-10-437-963-129103
48	7	7.6	175	15	US-10-369-493-22220
49	7	7.6	179	15	US-10-335-977-6637
50	7	7.7	184	15	US-10-425-563-4
51	7	7.7	187	16	US-10-437-963-198666
52	7	7.7	188	15	US-10-225-066A-250
53	7	7.7	188	15	US-10-374-780A-2514
54	7	7.7	194	9	US-09-789-561-174
55	7	7.7	194	17	US-10-883-936-174
56	7	7.6	195	15	US-10-369-493-22782
57	7	7.6	205	15	US-10-424-599-191747
58	7	7.7	227	16	US-10-331-053-36
59	7	7.7	229	9	US-09-989-723-258
60	7	7.7	229	9	US-09-989-723-258
61	7	7.7	229	9	US-09-989-279-258
62	7	7.7	229	9	US-09-989-727-258
63	7	7.7	229	9	US-09-989-731-258
64	7	7.7	229	9	US-09-989-732-258
65	7	7.7	229	9	US-09-991-073-258
66	7	7.7	229	9	US-09-990-442-258
67	7	7.7	229	9	US-09-991-163-258
68	7	7.7	229	9	US-09-993-604-258
69	7	7.7	229	9	US-09-990-456-258
70	7	7.7	229	9	US-09-989-721-258

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C 72	7	7.7	229	9	US-09-989-293A-258	Sequence 258, App	C 145	7	7.7	229	14	US-10-063-513-48	Sequence 48, Appl
C 73	7	7.7	229	9	US-09-989-735-258	Sequence 258, App	C 146	7	7.7	229	14	US-10-063-515-48	Sequence 48, Appl
C 74	7	7.7	229	9	US-09-990-444-258	Sequence 258, App	C 147	7	7.7	229	14	US-10-063-512-48	Sequence 198, App
C 75	7	7.7	229	9	US-09-991-181-258	Sequence 258, App	C 148	7	7.7	229	14	US-10-173-706-198	Sequence 198, App
C 76	7	7.7	229	9	US-09-989-730-258	Sequence 258, App	C 149	7	7.7	229	14	US-10-175-738-198	Sequence 198, App
C 77	7	7.7	229	9	US-09-990-436-258	Sequence 258, App	C 150	7	7.7	229	14	US-10-175-752-198	Sequence 198, App
C 78	7	7.7	229	9	US-09-993-687-258	Sequence 258, App	C 151	7	7.7	229	14	US-10-176-482-198	Sequence 198, App
C 79	7	7.7	229	10	US-09-989-734-258	Sequence 258, App	C 152	7	7.7	229	14	US-10-176-757-198	Sequence 198, App
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C 81	7	7.7	229	10	US-09-989-724-258	Sequence 258, App	C 154	7	7.7	229	14	US-10-180-552-198	Sequence 198, App
C 82	7	7.7	229	10	US-09-989-728-258	Sequence 258, App	C 155	7	7.7	229	14	US-10-180-557-198	Sequence 198, App
C 83	7	7.7	229	10	US-09-990-441-258	Sequence 258, App	C 156	7	7.7	229	14	US-10-063-502-48	Sequence 48, Appl
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C 86	7	7.7	229	10	US-09-997-666-258	Sequence 258, App	C 159	7	7.7	229	14	US-10-174-579-198	Sequence 198, App
C 87	7	7.7	229	10	US-09-990-438-258	Sequence 258, App	C 160	7	7.7	229	14	US-10-174-582-198	Sequence 198, App
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C 92	7	7.7	229	10	US-09-990-437-258	Sequence 258, App	C 165	7	7.7	229	14	US-10-176-747-198	Sequence 198, App
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C 97	7	7.7	229	10	US-09-990-726-258	Sequence 258, App	C 170	7	7.7	229	14	US-10-176-999-198	Sequence 198, App
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C 107	7	7.7	229	10	US-09-997-857-258	Sequence 258, App	C 180	7	7.7	229	14	US-10-176-485-198	Sequence 198, App
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C 114	7	7.7	229	10	US-09-993-583-258	Sequence 258, App	C 187	7	7.7	229	14	US-10-176-978-198	Sequence 198, App
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C 381	7	7.7	229	14	US-10-201-328-198	Sequence 198, App	C 454	7	7.7	229	14	US-10-192-016-198	Sequence 198, App
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C 390	7	7.7	229	14	US-10-205-502-198	Sequence 198, App	C 463	7	7.7	229	14	US-10-195-891-198	Sequence 198, App
C 391	7	7.7	229	14	US-10-205-511-198	Sequence 198, App	C 464	7	7.7	229	14	US-10-196-746-198	Sequence 198, App
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C 393	7	7.7	229	14	US-10-205-902-198	Sequence 198, App	C 466	7	7.7	229	14	US-10-196-753-198	Sequence 198, App
C 394	7	7.7	229	14	US-10-205-907-198	Sequence 198, App	C 467	7	7.7	229	14	US-10-196-761-198	Sequence 198, App
C 395	7	7.7	229	14	US-10-176-484-198	Sequence 198, App	C 468	7	7.7	229	14	US-10-197-692-198	Sequence 198, App
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C 398	7	7.7	229	14	US-10-198-770-198	Sequence 198, App	C 471	7	7.7	229	14	US-10-197-703-198	Sequence 198, App
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C 432	7	7.7	229	14	US-10-207-921-198	Sequence 198, App							
C 433	7	7.7	229	14	US-10-207-922-198	Sequence 198, App							
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ALIGNMENTS

RESULT 1

US-10-077-600-2

; Sequence 2, Application US/10077600

; Publication No. US20030175713A1

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; GENERAL INFORMATION:
; APPLICANT: Switch Biotech AG
; TITLE OF INVENTION: Method for diagnosis of inflammatory diseases using Calgranulin C
; FILE REFERENCE: S30274US
; CURRENT APPLICATION NUMBER: US/10/077,600
; CURRENT FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 92
; TYPE: PRT
; ORGANISM: homo sapiens
; ORGANISM: homo sapiens
US-10-077-600-2

Alignment Scores:
Pred. No.: 6,83e-83 Length: 92
Score: 92.00 Matches: 92
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-09-910-208b-12 (1-276) x US-10-077-600-2 (1-92)

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QY 121 CTTGCAAAACACCATCAAGAAATATCAAGATAAAGCTGTCTCATTCATGAAATATTTCCAAGGC 180
Db 41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60
QY 181 CTGGATGCTAATCAAGATGAACAGCTCGACTTTTCAAGATTTCATATCCCTGGTAGCCATT 240
Db 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80
QY 241 GCGCTGAAGGCTGCCCATTTACCACACCCACCAAGAG 276
Db 81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92

RESULT 3
US-09-864-761-41579
; Sequence 41579, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aesomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203

US-10-755-889-334
; Sequence 334, Application US/10755889
; Publication No. US20040171823A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-KB
; TITLE OF INVENTION: PATHWAY
; FILE REFERENCE: D0284 NP
; CURRENT APPLICATION NUMBER: US/10/755,889
; CURRENT FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: U.S. 60/440,068
; PRIOR FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: U.S. 60/469,757
; PRIOR FILING DATE: 2003-05-12
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 334
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-10-755-889-334

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Score: 92.00 Matches: 92
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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US-09-910-208b-12 (1-276) x US-10-755-889-334 (1-92)

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QY 121 CTTGCAAAACACCATCAAGAAATATCAAGATAAAGCTGTCTCATTCATGAAATATTTCCAAGGC 180
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QY 181 CTGGATGCTAATCAAGATGAACAGCTCGACTTTTCAAGATTTCATATCCCTGGTAGCCATT 240
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QY 241 GCGCTGAAGGCTGCCCATTTACCACACCCACCAAGAG 276
Db 81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92

RESULT 3
US-09-864-761-41579
; Sequence 41579, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aesomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
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12 AsnIlePheHisGlnTyrSerValArg 20

RESULT 5
 US-09-826-589-4
 ; Sequence 4, Application US/09826589
 ; Patent No. US20020106726A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Schmidt, Ann Marie
 ; APPLICANT: Stern, David
 ; TITLE OF INVENTION: EXTRACELLULAR NOVEL RAGE BINDING PROTEIN (EN-RAGE) AND USES THERE
 ; FILE REFERENCE: 0575/55873-B-PCT-US
 ; CURRENT APPLICATION NUMBER: US/09/826,589
 ; CURRENT FILING DATE: 2001-04-05
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 4
 ; LENGTH: 90
 ; TYPE: PRT
 ; ORGANISM: Bovine
 US-09-826-589-4

Alignment Scores:
 Pred. No.: 5.1 Length: 90
 Score: 9.00 Matches: 9
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 9.78% Indels: 0
 DB: Gaps: 0

US-09-910-208B-12 (1-276) x US-09-826-589-4 (1-90)

QY 37 AATATCTCCACCAATCTAGTTCGG 63
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RESULT 6
 US-09-872-185B-11
 ; Sequence 11, Application US/09872185B
 ; Patent No. US20020122799A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Stern, David M.
 ; APPLICANT: Herold, Kevin
 ; APPLICANT: Yan, Shi Du
 ; APPLICANT: Schmidt, Ann Marie
 ; APPLICANT: Lamster, Ira
 ; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATION
 ; FILE REFERENCE: 0575/64080
 ; CURRENT APPLICATION NUMBER: US/09/872,185B
 ; CURRENT FILING DATE: 2001-06-01
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 11
 ; LENGTH: 90
 ; TYPE: PRT
 ; ORGANISM: Bovine
 US-09-872-185B-11

Alignment Scores:
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 Score: 9.00 Matches: 9
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US-09-910-208B-12 (1-276) x US-09-872-185B-11 (1-90)

QY 37 AATATCTCCACCAATCTAGTTCGG 63
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 DB 12 AsnIlePheHisGlnTyrSerValArg 20

RESULT 7
 US-09-872-185B-12

12 AsnIlePheHisGlnTyrSerValArg 20

RESULT 5
 US-09-826-589-4
 ; Sequence 4, Application US/09826589
 ; Patent No. US20020106726A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Schmidt, Ann Marie
 ; APPLICANT: Stern, David
 ; TITLE OF INVENTION: EXTRACELLULAR NOVEL RAGE BINDING PROTEIN (EN-RAGE) AND USES THERE
 ; FILE REFERENCE: 0575/55873-B-PCT-US
 ; CURRENT APPLICATION NUMBER: US/09/826,589
 ; CURRENT FILING DATE: 2001-04-05
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 4
 ; LENGTH: 90
 ; TYPE: PRT
 ; ORGANISM: Bovine
 US-09-826-589-4

Alignment Scores:
 Pred. No.: 5.1 Length: 90
 Score: 9.00 Matches: 9
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
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US-09-910-208B-12 (1-276) x US-09-826-589-4 (1-90)

QY 37 AATATCTCCACCAATCTAGTTCGG 63
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 DB 12 AsnIlePheHisGlnTyrSerValArg 20

RESULT 6
 US-09-872-185B-11
 ; Sequence 11, Application US/09872185B
 ; Patent No. US20020122799A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Stern, David M.
 ; APPLICANT: Herold, Kevin
 ; APPLICANT: Yan, Shi Du
 ; APPLICANT: Schmidt, Ann Marie
 ; APPLICANT: Lamster, Ira
 ; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATION
 ; FILE REFERENCE: 0575/64080
 ; CURRENT APPLICATION NUMBER: US/09/872,185B
 ; CURRENT FILING DATE: 2001-06-01
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 11
 ; LENGTH: 90
 ; TYPE: PRT
 ; ORGANISM: Bovine
 US-09-872-185B-11

Alignment Scores:
 Pred. No.: 5.1 Length: 90
 Score: 9.00 Matches: 9
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 9.78% Indels: 0
 DB: Gaps: 0

US-09-910-208B-12 (1-276) x US-09-872-185B-11 (1-90)

QY 37 AATATCTCCACCAATCTAGTTCGG 63
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 DB 12 AsnIlePheHisGlnTyrSerValArg 20

RESULT 7
 US-09-872-185B-12

; Sequence 12, Application US/09872185B
; Patent No. US20020122799A1
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Herold, Kevan
; APPLICANT: Yan, Shi Du
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Lamster, Ira
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATION
; FILE REFERENCE: 0575/64080
; CURRENT APPLICATION NUMBER: US/09/872,185B
; CURRENT FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; TYPE: PRT
; LENGTH: 90
; ORGANISM: Bovine
US-09-872-185B-12

Alignment Scores:
Pred. No.: 5.1 Length: 90
Score: 9.00 Matches: 9
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US-09-910-208B-12 (1-276) x US-09-872-185B-12 (1-90)

QY 37 AATATCTTCCACCAATACTCAGTTCGG 63
Db 12 AsnIlePheHisGlnTyrSerValArg 20
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RESULT 8
US-10-666-513-3
; Sequence 3, Application US/10666513
; Publication No. US20040043412A1
; GENERAL INFORMATION:
; APPLICANT: Stern, David
; TITLE OF INVENTION: Extracellular No. US20040043412A1el RAGE Binding Protein (EN-RAGE)
; FILE REFERENCE: 0575/55873
; CURRENT APPLICATION NUMBER: US/10/666,513
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/167,705B
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; TYPE: PRT
; LENGTH: 90
; ORGANISM: Human
US-10-666-513-3

Alignment Scores:
Pred. No.: 5.1 Length: 90
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 9.78% Indels: 0
DB: 15 Gaps: 0

US-09-910-208B-12 (1-276) x US-10-666-513-3 (1-90)

QY 37 AATATCTTCCACCAATACTCAGTTCGG 63
Db 12 AsnIlePheHisGlnTyrSerValArg 20
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RESULT 9
US-10-665-867-3
; Sequence 3, Application US/10665867

; Publication No. US20040121372A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Stern, David
; TITLE OF INVENTION: EXTRACELLULAR NOVEL RAGE BINDING PROTEIN (EN-RAGE) AND USES THEREOF
; FILE REFERENCE: 0575/55873-B-PCT-US
; CURRENT APPLICATION NUMBER: US/10/665,867
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US/09/826,589
; PRIOR FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; TYPE: PRT
; LENGTH: 90
; ORGANISM: Bovine
US-10-665-867-3

Alignment Scores:
Pred. No.: 5.1 Length: 90
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 9.78% Indels: 0
DB: 16 Gaps: 0

US-09-910-208B-12 (1-276) x US-10-665-867-3 (1-90)

QY 37 AATATCTTCCACCAATACTCAGTTCGG 63
Db 12 AsnIlePheHisGlnTyrSerValArg 20
|||||

RESULT 10
US-10-665-867-4
; Sequence 4, Application US/10665867
; Publication No. US20040121372A1
; GENERAL INFORMATION:
; APPLICANT: Stern, David
; TITLE OF INVENTION: EXTRACELLULAR NOVEL RAGE BINDING PROTEIN (EN-RAGE) AND USES THEREOF
; FILE REFERENCE: 0575/55873-B-PCT-US
; CURRENT APPLICATION NUMBER: US/10/665,867
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US/09/826,589
; PRIOR FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Bovine
US-10-665-867-4

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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 9.78% Indels: 0
DB: 16 Gaps: 0

US-09-910-208B-12 (1-276) x US-10-665-867-4 (1-90)

QY 37 AATATCTTCCACCAATACTCAGTTCGG 63
Db 12 AsnIlePheHisGlnTyrSerValArg 20
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RESULT 11
US-10-425-114-40894
; Sequence 40894, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong

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; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 40894
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3050-011-F6_FLI.pep
US-10-425-114-40894

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Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 8.70% Indels: 0
DB: 15 Gaps: 0

US-09-910-208B-12 (1-276) x US-10-425-114-40894 (1-63)
QY 134 TCAGATATCAAGATAAGCTG 157
Db 13 SerArgileSerLysileysleu 20

RESULT 12
; Sequence 6100, Application US/09864408A
; Publication No. US20040009474A1
; GENERAL INFORMATION:
; APPLICANT: Leach, Martin D.
; TITLE OF INVENTION: No. US20040009474A1 Human Polynucleotides and Polypeptides Encod
; FILE REFERENCE: 21402-012
; CURRENT APPLICATION NUMBER: US/09/864,408A
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/206,690
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 9068
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 6100
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-864-408A-6100

Alignment Scores:
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 8.79% Indels: 0
DB: 11 Gaps: 0

US-09-910-208B-12 (1-276) x US-09-864-408A-6100 (1-70)
QY 167 TCATCATGACAGCTTATCTTG 144
Db 17 SerSerMetThrAlaLeuSerLeu 24

RESULT 13
US-10-424-599-151862
; Sequence 151862, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 151862
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(86)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_108155C.1.pep
US-10-424-599-151862

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DB: 15 Gaps: 0

US-09-910-208B-12 (1-276) x US-10-424-599-151862 (1-86)
QY 203 AGTTCGACTTTCAGAAATTCATAT 226
Db 30 ArgSerThrPhelysAsnSerTyr 37

RESULT 14
US-10-363-829-311
; Sequence 311, Application US/10363829
; Publication No. US20040142331A1
; GENERAL INFORMATION:
; APPLICANT: Jackson, Stuart E.; Lincoln, Stephen E.;
; APPLICANT: Chalus, Christina M.; Dufour, Gerard E.;
; APPLICANT: Chalup, Michael S.; Jackson, Jennifer L.;
; APPLICANT: Jones, Anissa L.; Yu, Jimmy Y.;
; APPLICANT: Wright, Rachel J.; Gietzen, Darryl;
; APPLICANT: Liu, Tommy F.; Yap, Pierre E.;
; APPLICANT: Dahl, Christopher R.; Momiyama, Monika G.;
; APPLICANT: Bradley, Diana L.; Rohatgi, Sameer D.;
; APPLICANT: Harris, Bernard; Roseberry Lincoln, Ann M.;
; APPLICANT: Gerstin, Jr., Edward H.; Peralta, Careyna H.;
; APPLICANT: David, Marie H.; Panzer, Scott R.;
; APPLICANT: Flores, Vincent Z.; Daffo, Abel;
; APPLICANT: Marwaha, Rakesh; Chen, Alice J.;
; APPLICANT: Chang, Simon C.; Au, Alan P.;
; APPLICANT: Imman, Rebekah R.
; TITLE OF INVENTION: MOLECULES FOR DISEASE DETECTION AND TREATMENT
; FILE REFERENCE: PT-1183 USN
; CURRENT APPLICATION NUMBER: US/10/363,829
; CURRENT FILING DATE: 2003-03-05
; PRIOR APPLICATION NUMBER: PCT/US01/27628
; PRIOR FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 60/229,751
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 60/229,749
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 60/229,750
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 60/229,747
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 60/229,748
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 60/230,583
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; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 60/230,517
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: US 60/230,610
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: US 60/230,597
; PRIOR FILING DATE: 2000-09-06
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PERL Program
; SEQ ID NO 311
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: LG:282729.1.orfl:2000SEP08
US-10-363-829-311

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Pred. No.: 44.6 Length: 206
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Query Match: 8.70% Indels: 0
DB: 16 Gaps: 0

US-09-910-208B-12 (1-276) x US-10-363-829-311 (1-206)

QY 79 ACCCTCTTAAGGTCAGCTGAAG 102

Db 31 ThrLeuSerLysGlyGluLeuLys 38
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RESULT 15

US-10-296-115-772
; Sequence 772, Application US/10296115
; Publication No. US20040053248A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: No. US20040053248A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 784PCT
; CURRENT APPLICATION NUMBER: US/10/296,115
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 1478
; SEQ ID NO 772
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-296-115-772

Alignment Scores:
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Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 8.70% Indels: 0
DB: 15 Gaps: 0

US-09-910-208B-12 (1-276) x US-10-296-115-772 (1-218)

QY 79 ACCCTCTTAAGGTCAGCTGAAG 102

Db 31 ThrLeuSerLysGlyGluLeuLys 38
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Search completed: February 23, 2005, 12:55:36
Job time : 96 secs

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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: February 23, 2005, 12:27:10 ; Search time 29.5 Seconds
(without alignments)
1396.823 Million cell updates/sec

Title: US-09-910-208B-12

Perfect score: 92

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Searched: 513545 seqs, 74649064 residues

Word size: 1

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi
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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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4	9	9.8	51	3	US-09-270-455-2
5	9	9.8	90	4	US-09-263-312-3
6	9	9.8	90	4	US-09-826-589-3
7	9	9.8	90	4	US-09-826-589-4
8	9	9.8	91	3	US-08-794-000-2
9	9	9.8	91	4	US-09-646-651C-1
10	9	9.8	92	2	US-08-568-310D-19
11	9	9.8	92	3	US-09-270-455-19
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14	8	8.7	103	3	US-08-788-622B-5	Sequence 5, Appli
15	8	8.7	103	3	US-08-788-621B-5	Sequence 5, Appli
16	8	8.7	103	4	US-09-270-767-40569	Sequence 40569, A
17	8	8.7	103	4	US-09-270-767-55785	Sequence 55785, A
18	8	8.7	266	4	US-09-902-540-13043	Sequence 13043, A
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22	7	7.6	113	4	US-09-556-818-12	Sequence 12, Appl
23	7	7.6	114	4	US-09-540-236-3166	Sequence 3166, Ap
24	7	7.6	116	4	US-09-556-818-14	Sequence 14, Appl
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26	7	7.6	122	4	US-09-556-818-15	Sequence 15, Appl
27	7	7.6	122	4	US-09-556-818-16	Sequence 16, Appl
28	7	7.6	122	4	US-09-556-818-19	Sequence 19, Appl
29	7	7.6	122	4	US-09-556-818-48	Sequence 48, Appl
30	7	7.6	122	4	US-09-556-818-54	Sequence 54, Appl
31	7	7.6	124	4	US-09-556-818-13	Sequence 13, Appl
32	7	7.6	124	4	US-09-556-818-17	Sequence 17, Appl
33	7	7.6	124	4	US-09-556-818-46	Sequence 46, Appl
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38	7	7.6	130	4	US-09-556-818-21	Sequence 21, Appl
39	7	7.6	130	4	US-09-556-818-56	Sequence 56, Appl
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42	7	7.6	139	4	US-09-556-818-60	Sequence 60, Appl
43	7	7.6	157	1	US-08-328-322-15	Sequence 15, Appl
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46	7	7.6	171	1	US-08-328-322-17	Sequence 17, Appl
47	7	7.7	195	4	US-09-252-991A-28844	Sequence 28844, A
48	7	7.6	262	4	US-09-710-279-366	Sequence 366, App
49	7	7.6	264	4	US-09-107-433-2798	Sequence 2798, Ap
50	c	7.7	265	4	US-09-543-681A-6305	Sequence 6305, Ap
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55	c	7.7	305	4	US-09-599-360B-114	Sequence 114, App
56	7	7.6	310	4	US-09-902-540-13414	Sequence 13414, A
57	7	7.6	335	4	US-09-949-016-6262	Sequence 6262, Ap
58	7	7.6	345	4	US-09-252-991A-28350	Sequence 28350, A
59	7	7.6	359	3	US-09-134-001C-3728	Sequence 3728, Ap
60	c	7.7	383	4	US-09-583-110-3044	Sequence 3044, Ap
61	c	7.7	383	4	US-09-107-433-4404	Sequence 4404, Ap
62	c	7.7	442	2	US-08-821-355A-5	Sequence 5, Appli
63	c	7.7	442	2	US-09-003-687A-5	Sequence 5, Appli
64	c	7.7	442	3	US-09-136-605-5	Sequence 5, Appli
65	7	7.6	447	1	US-07-937-609-29	Sequence 29, Appl
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67	7	7.6	447	3	US-08-029-170-29	Sequence 29, Appl
68	7	7.6	447	4	US-09-443-745-29	Sequence 29, Appl
69	7	7.6	448	1	US-08-570-157-3	Sequence 3, Appli
70	7	7.6	448	3	US-09-076-510-3	Sequence 3, Appli
71	7	7.6	448	4	US-09-004-349-3	Sequence 3, Appli
72	7	7.6	453	1	US-07-937-609-26	Sequence 26, Appl
73	7	7.6	453	1	US-07-937-609-27	Sequence 27, Appl
74	7	7.6	453	1	US-08-570-157-4	Sequence 5, Appli
75	7	7.6	453	1	US-08-029-170-26	Sequence 4, Appli
76	7	7.6	453	3	US-08-029-170-27	Sequence 26, Appl
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83	7	7.6	507	1	US-08-484-494-12	Sequence 12, Appl
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86	7	7.6	507	3	US-09-249-003-12	Sequence 12, Appl	C 159	6	6.6	35	4	US-09-350-641C-234	Sequence 234, App
87	7	7.6	507	4	US-09-685-844-12	Sequence 12, Appl	C 160	6	6.6	35	4	US-09-350-641C-235	Sequence 235, App
88	7	7.6	535	4	US-09-248-796A-18860	Sequence 18860, A	C 161	6	6.6	35	4	US-09-350-641C-236	Sequence 236, App
89	7	7.6	632	4	US-09-250-991A-32280	Sequence 32280, A	C 162	6	6.6	35	4	US-09-350-641C-237	Sequence 237, App
90	7	7.6	659	4	US-09-543-681A-8248	Sequence 8248, Ap	C 163	6	6.6	35	4	US-09-350-641C-238	Sequence 238, App
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92	7	7.7	1054	4	US-09-949-016-9821	Sequence 9821, Ap	C 165	6	6.6	35	4	US-09-350-641C-240	Sequence 240, App
93	7	7.7	1054	4	US-09-949-016-9822	Sequence 9822, Ap	C 166	6	6.6	35	4	US-09-350-641C-241	Sequence 241, App
94	7	7.7	1220	4	US-09-540-236-3011	Sequence 3011, Ap	C 167	6	6.6	35	4	US-09-350-641C-242	Sequence 242, App
95	7	7.7	1262	3	US-09-357-251-33	Sequence 33, Appl	C 168	6	6.6	35	4	US-09-350-641C-243	Sequence 243, App
96	7	7.7	1262	4	US-09-943-016-6182	Sequence 6182, Ap	C 169	6	6.6	35	4	US-09-350-641C-244	Sequence 244, App
97	7	7.7	1262	4	US-09-943-016-6850	Sequence 6850, Ap	C 170	6	6.6	35	4	US-09-350-641C-245	Sequence 245, App
98	7	7.7	1266	1	US-08-468-557-4	Sequence 4, Appl	C 171	6	6.6	35	4	US-09-350-641C-246	Sequence 246, App
99	7	7.7	1266	3	US-09-357-251-32	Sequence 32, Appl	C 172	6	6.6	35	4	US-09-350-641C-247	Sequence 247, App
100	6	6.5	16	3	US-08-492-411A-13	Sequence 13, Appl	C 173	6	6.6	35	4	US-09-350-641C-248	Sequence 248, App
101	6	6.5	16	3	US-08-492-411A-15	Sequence 15, Appl	C 174	6	6.6	35	4	US-09-350-641C-249	Sequence 249, App
102	6	6.5	19	4	US-09-106-568E-124	Sequence 124, App	C 175	6	6.6	35	4	US-09-350-641C-250	Sequence 250, App
103	6	6.6	23	4	US-09-570-921-74	Sequence 74, Appl	C 176	6	6.6	35	4	US-09-350-641C-251	Sequence 251, App
104	6	6.5	25	3	US-09-049-691-58	Sequence 58, Appl	C 177	6	6.6	35	4	US-09-350-641C-252	Sequence 252, App
105	6	6.5	25	3	US-09-049-691-59	Sequence 59, Appl	C 178	6	6.6	35	4	US-09-350-641C-253	Sequence 253, App
106	6	6.5	25	3	US-09-049-691-62	Sequence 62, Appl	C 179	6	6.6	35	4	US-09-350-641C-254	Sequence 254, App
107	6	6.6	28	3	US-09-082-279B-97	Sequence 97, Appl	C 180	6	6.6	35	4	US-09-350-641C-255	Sequence 255, App
108	6	6.6	28	3	US-09-315-304B-97	Sequence 97, Appl	C 181	6	6.6	35	4	US-09-350-641C-256	Sequence 256, App
109	6	6.6	28	4	US-09-834-784-97	Sequence 97, Appl	C 182	6	6.6	35	4	US-09-350-641C-257	Sequence 257, App
110	6	6.6	28	4	US-09-515-965A-97	Sequence 97, Appl	C 183	6	6.6	35	4	US-09-350-641C-258	Sequence 258, App
111	6	6.6	28	4	US-09-350-641C-97	Sequence 97, Appl	C 184	6	6.6	35	4	US-09-350-641C-259	Sequence 259, App
112	6	6.6	28	4	US-09-350-641A-97	Sequence 97, Appl	C 185	6	6.6	35	4	US-09-350-641C-260	Sequence 260, App
113	6	6.5	34	4	US-09-493-795B-258	Sequence 258, App	C 186	6	6.5	48	5	PCT-US93-08528-205	Sequence 58868, A
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c 283	6	6.6	135	4	US-09-543-681A-8052	Sequence 8052, Ap	c 356	6	6.5	202	3	US-08-867-352-2	Sequence 2, Appl
c 284	6	6.5	135	4	US-09-489-039A-12058	Sequence 12058, A	c 357	6	6.5	203	3	US-08-795-430-53	Sequence 53, Appl
c 285	6	6.6	135	4	US-09-401-064-203	Sequence 203, Ap	c 358	6	6.5	204	3	US-08-999-811-5	Sequence 5, Appl
c 286	6	6.5	135	4	US-09-710-279-400	Sequence 400, Ap	c 359	6	6.5	205	2	US-08-778-273-2	Sequence 2, Appl
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c 289	6	6.6	137	4	US-09-270-767-49754	Sequence 49754, A	c 362	6	6.5	208	3	US-08-867-352-2	Sequence 2, Appl
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c 294	6	6.5	139	4	US-09-543-681A-4605	Sequence 4605, Ap	c 367	6	6.5	213	4	US-09-513-775B-2	Sequence 2, Appl
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c 296	6	6.6	140	4	US-09-434-122-23	Sequence 23, Appl	c 369	6	6.5	215	4	US-10-084-488-5	Sequence 5, Appl
c 297	6	6.5	146	3	US-08-914-375C-35	Sequence 35, Appl	c 370	6	6.5	216	4	US-09-534-376A-53	Sequence 53, Appl
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C 381	6	6.6	207	4	US-09-583-110-4418	Sequence 4418, Ap	454	6	6.5	238	4	US-09-615-765B-65	Sequence 65, Appl
C 382	6	6.6	209	4	US-09-259-991A-23141	Sequence 23141, A	455	6	6.5	238	4	US-09-626-580C-65	Sequence 65, Appl
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C 385	6	6.5	211	4	US-09-214-982-30	Sequence 30, Appl	458	6	6.5	240	3	US-09-302-540-13362	Sequence 13362, A
C 386	6	6.5	211	5	PCT-US91-02766-22	Sequence 22, Appl	459	6	6.5	241	4	US-08-178-257-19	Sequence 19, Appl
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C 390	6	6.5	211	6	5194596-13	Patent No. 5194596	463	6	6.6	245	4	US-09-248-796A-13065	Sequence 13065, A
C 391	6	6.5	211	6	5219739-13	Patent No. 5219739	464	6	6.5	248	4	US-09-438-185A-787	Sequence 787, App
C 392	6	6.5	211	6	5219759-2	Patent No. 5219759	465	6	6.6	248	4	US-09-270-767-38186	Sequence 38186, A
C 393	6	6.5	212	3	US-08-861-774E-42	Sequence 42, Appl	466	6	6.6	249	4	US-09-270-767-53403	Sequence 53403, A
C 394	6	6.5	213	3	US-08-971-158-4	Sequence 4, Appl	467	6	6.5	250	4	US-09-134-000C-4273	Sequence 4273, Ap
C 395	6	6.5	213	4	US-09-416-488-4	Sequence 4, Appl	468	6	6.6	252	4	US-09-270-767-43707	Sequence 43707, A
C 396	6	6.6	214	3	US-08-914-375C-27	Sequence 27, Appl	469	6	6.6	252	4	US-09-270-767-57384	Sequence 57384, A
C 397	6	6.5	214	3	US-09-134-001C-4093	Sequence 4093, Ap	470	6	6.6	254	3	US-09-128-450-26	Sequence 26, Appl
C 398	6	6.6	215	4	US-09-830-433A-48	Sequence 48, Appl	471	6	6.6	254	3	US-09-823-494-26	Sequence 26, Appl
C 399	6	6.6	216	4	US-09-907-794A-59	Sequence 59, Appl	472	6	6.5	255	4	US-09-252-991A-22593	Sequence 22593, A
C 400	6	6.6	216	4	US-09-905-135A-59	Sequence 59, Appl	473	6	6.5	255	4	US-09-173-300-33	Sequence 33, Appl
C 401	6	6.6	216	4	US-09-902-775A-59	Sequence 10, Appl	474	6	6.5	255	4	US-10-027-450-33	Sequence 33, Appl
C 402	6	6.6	216	4	US-09-715-805-10	Sequence 59, Appl	475	6	6.5	258	3	US-09-336-643A-12	Sequence 12, Appl
C 403	6	6.6	216	4	US-09-908-700-59	Sequence 59, Appl	476	6	6.5	258	4	US-09-684-938-181	Sequence 181, App
C 404	6	6.6	216	4	US-09-903-603A-59	Sequence 59, Appl	477	6	6.5	258	4	US-09-308-825A-181	Sequence 261, App
C 405	6	6.6	216	4	US-09-904-920A-59	Sequence 59, Appl	478	6	6.5	258	4	US-09-940-244-261	Sequence 3714, Ap
C 406	6	6.6	216	4	US-09-909-064-59	Sequence 59, Appl	479	6	6.5	259	4	US-09-134-001C-3714	Sequence 16738, A
C 407	6	6.6	216	4	US-09-905-381A-59	Sequence 59, Appl	480	6	6.6	259	4	US-09-252-991A-16738	Sequence 430, App
C 408	6	6.6	216	4	US-09-906-618-59	Sequence 8206, Ap	481	6	6.6	259	4	US-09-198-452A-430	Sequence 5472, Ap
C 409	6	6.6	216	4	US-09-489-039A-12229	Sequence 12229, A	482	6	6.6	259	4	US-09-107-532A-5472	Sequence 11024, A
C 410	6	6.6	219	3	US-08-871-572B-12	Sequence 12, Appl	483	6	6.5	259	4	US-09-489-039A-11024	Sequence 59221, A
C 411	6	6.6	221	3	US-09-382-155-17	Sequence 17, Appl	484	6	6.6	260	4	US-09-270-767-59221	Sequence 7490, Ap
C 412	6	6.6	221	3	US-09-074-044A-17	Sequence 17, Appl	485	6	6.6	260	4	US-09-489-039A-7490	Sequence 7220, Ap
C 413	6	6.6	221	4	US-09-543-681A-6365	Sequence 6365, Ap	486	6	6.5	263	6	Patent No. 5229279	Patent No. 5229279
C 414	6	6.6	223	4	US-09-583-110-5133	Sequence 30403, A	487	6	6.5	263	6	Sequence 26214, A	Sequence 26214, A
C 415	6	6.5	223	4	US-09-252-991A-10403	Sequence 17223, A	488	6	6.5	264	4	Sequence 1122, Ap	Sequence 1122, Ap
C 416	6	6.5	227	4	US-09-248-796A-17223	Sequence 17223, A	489	6	6.5	264	4	Sequence 5132, Ap	Sequence 5132, Ap
C 417	6	6.6	228	1	US-08-447-591-2	Sequence 2, Appl	490	6	6.6	267	4	Sequence 3025, Ap	Sequence 3025, Ap
C 418	6	6.6	228	1	US-08-447-591-3	Sequence 3, Appl	491	6	6.6	267	4	Sequence 15326, A	Sequence 15326, A
C 419	6	6.6	228	1	US-08-447-591-4	Sequence 4, Appl	492	6	6.6	267	4	Sequence 3601, Ap	Sequence 3601, Ap
C 420	6	6.6	228	1	US-08-447-591-5	Sequence 5, Appl	493	6	6.6	268	4	Sequence 9, Appl	Sequence 9, Appl
C 421	6	6.6	228	1	US-08-450-943-2	Sequence 2, Appl	494	6	6.6	268	4	Sequence 1048, Ap	Sequence 1048, Ap
C 422	6	6.6	228	1	US-08-450-943-3	Sequence 3, Appl	495	6	6.6	269	4	Sequence 18363, A	Sequence 18363, A
C 423	6	6.6	228	1	US-08-450-943-4	Sequence 4, Appl	496	6	6.6	270	4	Sequence 12630, A	Sequence 12630, A
C 424	6	6.6	228	1	US-08-450-943-5	Sequence 5, Appl	497	6	6.6	272	4	Sequence 413, App	Sequence 413, App
C 425	6	6.6	228	1	US-08-059-031-2	Sequence 2, Appl	498	6	6.5	272	4	Sequence 7231, Ap	Sequence 7231, Ap
C 426	6	6.6	228	1	US-08-059-031-3	Sequence 3, Appl	499	6	6.6	273	4		
C 427	6	6.6	228	2	US-08-450-942-2	Sequence 2, Appl	500	6	6.5				
C 428	6	6.6	228	2	US-08-450-942-3	Sequence 3, Appl							
C 429	6	6.6	228	2	US-08-450-942-4	Sequence 4, Appl							
C 430	6	6.6	228	5	PCT-US94-05090-2	Sequence 2, Appl							
C 431	6	6.6	228	5	PCT-US94-05090-3	Sequence 3, Appl							
C 432	6	6.6	228	5	PCT-US94-05090-4	Sequence 4, Appl							
C 433	6	6.6	229	3	US-09-134-001C-5029	Sequence 5029, Ap							
C 434	6	6.6	229	4	US-09-252-991A-28931	Sequence 28931, A							
C 435	6	6.5	229	4	US-09-270-767-31836	Sequence 31836, A							
C 436	6	6.5	230	4	US-09-270-767-45900	Sequence 45900, A							
C 437	6	6.6	232	1	US-07-990-300A-4	Sequence 4, Appl							
C 438	6	6.6	232	3	US-08-944-483-45	Sequence 45, Appl							
C 439	6	6.5	232	4	US-09-198-452A-834	Sequence 834, App							
C 440	6	6.6	232	4	US-09-302-540-16266	Sequence 16266, A							
C 441	6	6.6	233	1	US-08-221-750A-7	Sequence 7, Appl							
C 442	6	6.5	233	4	US-09-711-164-304	Sequence 304, App							
C 443	6	6.6	233	4	US-09-489-039A-7432	Sequence 7432, Ap							
C 444	6	6.6	233	4	US-09-492-709A-386	Sequence 386, App							
C 445	6	6.6	233	4	US-09-248-796A-20191	Sequence 20191, A							
C 446	6	6.6	234	4	US-09-270-767-46602	Sequence 46602, A							
C 447	6	6.6	234	4	US-09-949-016-11566	Sequence 11566, A							
C 448	6	6.5	235	4	US-09-270-767-43504	Sequence 43504, A							
C 449	6	6.6	235	4	US-09-107-433-2959	Sequence 2959, Ap							
C 450	6	6.5	237	4	US-09-640-211A-2212	Sequence 2212, Ap							

ALIGNMENTS

RESULT 1
US-08-568-310D-20
; Sequence 20, Application US/08568310D
; Patent No. 5976832
; GENERAL INFORMATION:
; APPLICANT: HITOMI, JIRO
; APPLICANT: YAMAGUCHI, KEN
; APPLICANT: YAMAMURA, TOKUJIRO
; APPLICANT: KIMURA, TATSUJI
; TITLE OF INVENTION: NOVEL CALCIUM-BINDING PROTEINS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WYATT GERBER, MELLER & O'ROURKE
; STREET: 99 PARK AVENUE
; CITY: NEW YORK CITY
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016

COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH, 720 KB
MEDIUM TYPE: STORAGE
COMPUTER: IBM-PC COMPATIBLE
OPERATING SYSTEM: PC-DOS 6.2
SOFTWARE: WORDPERFECT 6.1
CURRENT APPLICATION DATA:
FILING DATE: DECEMBER 6, 1995
APPLICATION NUMBER: US/08/568,310D
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 7-70468 and 7-45564 (both Japan)
FILING DATE: 3/6/95 and 3/6/95, respectively
ATTORNEY/AGENT INFORMATION:
NAME: KLEIN, MILTON
REGISTRATION NUMBER: 27101
REFERENCE/DOCKET NUMBER: 3316
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)953-3350
TELEFAX: (212)953-3352
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 92
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: CDNA
PUBLICATION INFORMATION:
RELEVANT RESIDUES IN SEQ ID NO: 20:
RELEVANT RESIDUES IN SEQ ID NO: FROM 1 TO 92
US-08-568-310D-20

Alignment Scores:
Pred. No.: 8 41e-84 Length: 92
Score: 92.00 Matches: 92
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-12 (1-276) x US-08-568-310D-20 (1-92)

QY 1 ATGACAAAACCTGAAGAGCATCTGGAGGAATTGTCAATATCTTCCACCAATCTCAGTT 60
Db 1 MetThrLysLeuGluGluHisLeuGluGlyIleValAsnIlePheHisGlnTyrSerVal 20
QY 61 CGGAGGGGCATTTTGCACACCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTCAAGAGG 120
Db 21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuThrLysGlu 40
QY 121 CTTCGAAACACCATCAAGAAATATCAAGATAAAGCTGTCATTGATGAATATTTCCAAGGC 180
Db 41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60
QY 181 CTGGATGCTTAATCAAGATGAACAGGTCGACTTTTCAAGAAATTCATATCCCTGGTAGCCATT 240
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QY 241 GCGCTGAAGGTCGCCCATTCACACACCCCAAGAG 276
Db 81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92

RESULT 2

US-09-270-455-20
Sequence 20, Application US/09270455
Patent No. 6313267
GENERAL INFORMATION:
APPLICANT: HITOMI, JIRO
APPLICANT: YAMAGUCHI, KEN
APPLICANT: YAMAMURA, TOKUJIRO
APPLICANT: KIMURA, TATSUJI
TITLE OF INVENTION: NOVEL CALCIUM-BINDING PROTEINS
NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:
ADDRESSEE: WYATT, GERBER, MELLER & O'ROURKE
STREET: 99 PARK AVENUE
STREET: 6th FLOOR
CITY: NEW YORK CITY
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH, 720 KB
MEDIUM TYPE: STORAGE
COMPUTER: IBM-PC COMPATIBLE
OPERATING SYSTEM: PC-DOS 6.2
SOFTWARE: WORDPERFECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/270,455
FILING DATE:
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/568,310
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: KLEIN, MILTON
REGISTRATION NUMBER: 27101
REFERENCE/DOCKET NUMBER: 3316
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)953-3350
TELEFAX: (212)953-3352
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 92
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: CDNA
PUBLICATION INFORMATION:
RELEVANT RESIDUES IN SEQ ID NO: 20:
RELEVANT RESIDUES IN SEQ ID NO: FROM 1 TO 92
US-09-270-455-20

Alignment Scores:
Pred. No.: 8 41e-84 Length: 92
Score: 92.00 Matches: 92
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-09-910-208B-12 (1-276) x US-09-270-455-20 (1-92)

QY 1 ATGACAAAACCTGAAGAGCATCTGGAGGAATTGTCAATATCTTCCACCAATCTCAGTT 60
Db 1 MetThrLysLeuGluGluHisLeuGluGlyIleValAsnIlePheHisGlnTyrSerVal 20
QY 61 CGGAGGGGCATTTTGCACACCTCTCTAAGGGTGAGCTGAAGCAGCTGCTTCAAGAGG 120
Db 21 ArgLysGlyHisPheAspThrLeuSerLysGlyGluLeuLysGlnLeuThrLysGlu 40
QY 121 CTTCGAAACACCATCAAGAAATATCAAGATAAAGCTGTCATTGATGAATATTTCCAAGGC 180
Db 41 LeuAlaAsnThrIleLysAsnIleLysAspLysAlaValIleAspGluIlePheGlnGly 60
QY 181 CTGGATGCTTAATCAAGATGAACAGGTCGACTTTTCAAGAAATTCATATCCCTGGTAGCCATT 240
Db 61 LeuAspAlaAsnGlnAspGluGlnValAspPheGlnGluPheIleSerLeuValAlaIle 80
QY 241 GCGCTGAAGGTCGCCCATTCACACACCCCAAGAG 276
Db 81 AlaLeuLysAlaAlaHisTyrHisThrHisLysGlu 92

RESULT 3

US-08-568-310D-2
Sequence 2, Application US/08568310D
Patent No. 5976832

```

; GENERAL INFORMATION:
; APPLICANT: HITOMI, JIRO
; APPLICANT: YAMAGUCHI, KEN
; APPLICANT: YAMAMURA, TOKUJIRO
; APPLICANT: KIMURA, TATSUJI
; TITLE OF INVENTION: NOVEL CALCIUM-BINDING PROTEINS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WYATT, GERBER, MELLER & O'ROURKE
; STREET: 99 PARK AVENUE
; CITY: 6th FLOOR
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH, 720 KB
; MEDIUM TYPE: STORAGE
; COMPUTER: IBM-PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS 6.2
; SOFTWARE: WORDPERFECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/568,310D
; FILING DATE: DECEMBER 6, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 7-70468 and 7-45564 (both Japan)
; FILING DATE: 3/6/95 and 3/6/95, respectively
; ATTORNEY/AGENT INFORMATION:
; NAME: KLEIN, MILTON
; REGISTRATION NUMBER: 27101
; REFERENCE/DOCKET NUMBER: 3316
; TELEPHONE: (212)953-3350
; TELEFAX: (212)953-3352
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 51
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; PUBLICATION INFORMATION:
; RELEVANT RESIDUES IN SEQ ID NO: 2:
; RELEVANT RESIDUES IN SEQ ID NO: FROM 1 TO 51
US-08-568-310D-2

Alignment Scores:
Pred. No.: 1.12 Length: 51
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 9.78% Indels: 0
DB: 2 Gaps: 0

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Db 12 AsnIlePheHisGlnTyrSerValArg 20

RESULT 4
US-09-270-455-2
; Sequence 2, Application US/09270455
; Patent No. 6313267
; GENERAL INFORMATION:
; APPLICANT: HITOMI, JIRO
; APPLICANT: YAMAGUCHI, KEN
; APPLICANT: YAMAMURA, TOKUJIRO
; APPLICANT: KIMURA, TATSUJI
; TITLE OF INVENTION: NOVEL CALCIUM-BINDING PROTEINS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WYATT, GERBER, MELLER & O'ROURKE

```

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; STREET: 99 PARK AVENUE
; STREET: 6th FLOOR
; CITY: NEW YORK CITY
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH, 720 KB
; MEDIUM TYPE: STORAGE
; COMPUTER: IBM-PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS 6.2
; SOFTWARE: WORDPERFECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/270,455
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/568,310
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: KLEIN, MILTON
; REGISTRATION NUMBER: 27101
; REFERENCE/DOCKET NUMBER: 3316
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)953-3350
; TELEFAX: (212)953-3352
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 51
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; PUBLICATION INFORMATION:
; RELEVANT RESIDUES IN SEQ ID NO: 2: FROM 1 TO 51
US-09-270-455-2

Alignment Scores:
Pred. No.: 1.12 Length: 51
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 9.78% Indels: 0
DB: 3 Gaps: 0

US-09-910-208B-12 (1-276) x US-09-270-455-2 (1-51)
QY 37 AATATCTCCACCAATACCTAGTTCGG 63
Db 12 AsnIlePheHisGlnTyrSerValArg 20

RESULT 5
US-09-263-312-3
; Sequence 3, Application US/09263312
; Patent No. 655340
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Stern, David
; TITLE OF INVENTION: Extracellular No. 655340el RAGE Binding Protein (EN-RAGE) and
; FILE REFERENCE: 0575/55873-A
; CURRENT APPLICATION NUMBER: US/09/263,312
; CURRENT FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Human
US-09-263-312-3

Alignment Scores:
Pred. No.: 1.05 Length: 90
Score: 9.00 Matches: 9

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Percent Similarity: 100.00% Conservative: 0
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US-09-910-208B-12 (1-276) x US-09-263-312-3 (1-90)

QY 37 AATATCTTCCACCAATACTCAGTTGG 63
 Db 12 AsnIlePheHisGlnTyrSerValArg 20

RESULT 6

US-09-826-589-3

; Sequence 3, Application US/09826589

; Patent No. 6670136

; GENERAL INFORMATION:

; APPLICANT: Schmidt, Ann Marie

; APPLICANT: Stern, David

; TITLE OF INVENTION: EXTRACELLULAR NOVEL RAGE BINDING PROTEIN (EN-RAGE) AND USES THERE

; FILE REFERENCE: 0575/55873-B-PCT-US

; CURRENT APPLICATION NUMBER: US/09/826,589

; CURRENT FILING DATE: 2001-04-05

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: Patentin version 3.1

; SEQ ID NO 3

; LENGTH: 90

; TYPE: PRT

; ORGANISM: Bovine

US-09-826-589-3

Alignment Scores:

Pred. No.:

Score: 1.05 Length: 90

Percent Similarity: 9.00 Matches: 9

Best Local Similarity: 100.00% Conservative: 0

Mismatches: 0

Query Match: 9.78% Indels: 0

DB: 4 Gaps: 0

US-09-910-208B-12 (1-276) x US-09-826-589-3 (1-90)

QY 37 AATATCTTCCACCAATACTCAGTTGG 63
 Db 12 AsnIlePheHisGlnTyrSerValArg 20

RESULT 7

US-09-826-589-4

; Sequence 4, Application US/09826589

; Patent No. 6670136

; GENERAL INFORMATION:

; APPLICANT: Schmidt, Ann Marie

; APPLICANT: Stern, David

; TITLE OF INVENTION: EXTRACELLULAR NOVEL RAGE BINDING PROTEIN (EN-RAGE) AND USES THERE

; FILE REFERENCE: 0575/55873-B-PCT-US

; CURRENT APPLICATION NUMBER: US/09/826,589

; CURRENT FILING DATE: 2001-04-05

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: Patentin version 3.1

; SEQ ID NO 4

; LENGTH: 90

; TYPE: PRT

; ORGANISM: Bovine

US-09-826-589-4

Alignment Scores:

Pred. No.:

Score: 1.05 Length: 90

Percent Similarity: 9.00 Matches: 9

Best Local Similarity: 100.00% Conservative: 0

Mismatches: 0

Query Match: 9.78% Indels: 0

DB: 4 Gaps: 0

US-09-910-208B-12 (1-276) x US-09-826-589-4 (1-90)

QY 37 AATATCTTCCACCAATACTCAGTTGG 63
 Db 12 AsnIlePheHisGlnTyrSerValArg 20

RESULT 8

US-08-794-000-2

; Sequence 2, Application US/08794000

; Patent No. 6087123

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: Metal-Containing Ribonucleotide Polypeptides

; NUMBER OF SEQUENCES: 4

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/794,000

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/DE96/01337

; FILING DATE: 17-JUL-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: DE 195 25 992.0

; FILING DATE: 17-JUL-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: DE 195 30 500.0

; FILING DATE: 18-AUG-1995

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 91 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-794-000-2

Alignment Scores:

Pred. No.:

Score: 1.05 Length: 91

Percent Similarity: 9.00 Matches: 9

Best Local Similarity: 100.00% Conservative: 0

Query Match: 9.78% Mismatches: 0

DB: 3 Indels: 0

Gaps: 0

US-09-910-208B-12 (1-276) x US-08-794-000-2 (1-91)

QY 37 AATATCTTCCACCAATACTCAGTTGG 63
 Db 12 AsnIlePheHisGlnTyrSerValArg 20

RESULT 9

US-09-646-651C-1

; Sequence 1, Application US/09646651C

; Patent No. 6770455

; GENERAL INFORMATION:

; APPLICANT: Klessewetter, Stefan

; APPLICANT: Kuhn, Eckehard

; APPLICANT: Koch-Pelster, Brigitte

; APPLICANT: Brunner, Herwig

; TITLE OF INVENTION: METAL-CONTAINING RIBONUCLEOTIDE POLYPEPTIDES

; FILE REFERENCE: 206579

; CURRENT APPLICATION NUMBER: US/09/646,651C

; CURRENT FILING DATE: 2001-01-16

; PRIOR APPLICATION NUMBER: PCT/EP98/07722

; PRIOR FILING DATE: 1998-11-30

; PRIOR APPLICATION NUMBER: DE 198 11 047.2

; PRIOR FILING DATE: 1998-03-13

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: Patentin version 3.0

; SEQ ID NO 1

; LENGTH: 91

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Alignment Scores:
Pred. No.: 1.05 Length: 92
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 9.78% Indels: 0
DB: 2 Gaps: 0

US-09-910-208B-12 (1-276) x US-08-568-310D-19 (1-92)

QY 37 AATATCTTCACCAATACTCAGTTCG 63
DB 13 ASnllpHeHglnTySrValArg 21

RESULT 11
US-09-270-455-19
; Sequence 19, Application US/09270455
; Patent No. 6313267
; GENERAL INFORMATION:
; APPLICANT: HITOMI, JIRO
; APPLICANT: YAMAGUCHI, KEN
; APPLICANT: YAMAMURA, TOKUJIRO
; APPLICANT: KIMURA, TATSUJI
; TITLE OF INVENTION: NOVEL CALCIUM-BINDING PROTEINS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WYATT, GERBER, MELLER & O'ROURKE
; STREET: 99 PARK AVENUE
; STREET: 6th FLOOR
; CITY: NEW YORK CITY
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH, 720 Kb
; MEDIUM TYPE: STORAGE
; COMPUTER: IBM-PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS 6.2
; SOFTWARE: WORDPERFECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/270,455
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/568,310
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: KLEIN, MILTON
; REGISTRATION NUMBER: 27101
; REFERENCE/DOCKET NUMBER: 3316
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)953-3350
; TELEFAX: (212)953-3352
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 92
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; PUBLICATION INFORMATION:
; RELEVANT RESIDUES IN SEQ ID NO: 19: FROM 1 TO 92
US-09-270-455-19

Alignment Scores:
Pred. No.: 1.05 Length: 92
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 9.78% Indels: 0
DB: 3 Gaps: 0

US-09-910-208B-12 (1-276) x US-09-270-455-19 (1-92)

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Qy	37	AAATATCTCCACCAATACACTTCATTCGG	63
Db	13	ASnllpHeHieGlnTyrSerValarg	21
RESULT 12			
US-08-585-585A-5			
; Sequence 5, Application US/08585585A			
; Patent No. 5874308			
; GENERAL INFORMATION:			
; APPLICANT: Kilburn, Douglas G.			
; APPLICANT: Humphries, Keith R.			
; APPLICANT: Doherty, James G.			
; APPLICANT: Jervis, Eric			
; APPLICANT: Alimonti, Judie			
; TITLE OF INVENTION: Compositions and methods for modulating			
; cell proliferation using growth factor-polysaccharide			
; TITLE OF INVENTION: binding fusion proteins			
; NUMBER OF SEQUENCES: 14			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: Rae-Venter Law Group			
; STREET: Box 60039			
; CITY: Palo Alto			
; STATE: CA			
; COUNTRY: U.S.			
; ZIP: 94306			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: PatentIn Release #1.0, Version #1.30			
; CURRENT APPLICATION DATA:			
; FILING DATE: 16-JAN-1996			
; CLASSIFICATION: 435			
; ATTORNEY/AGENT INFORMATION:			
; NAME: Kung, Viola T.			
; REGISTRATION NUMBER: 41,131			
; REFERENCE/DOCKET NUMBER: CBPT.016.000US			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: (650)328-4400			
; TELEFAX: (650)328-4477			
; INFORMATION FOR SEQ ID NO: 5:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 103 amino acids			
; TYPE: amino acid			
; STRANDEDNESS: not relevant			
; TOPOLOGY: not relevant			
; MOLECULE TYPE: peptide			
US-08-585-585A-5			
Alignment Scores:			
Pred. No.: 10.4 Length: 103			
Score: 8.00 Matches: 8			
Percent Similarity: 100.00% Conservative: 0			
Best Local Similarity: 100.00% Mismatches: 0			
Query Match: 8.70% Indels: 0			
DB: 2 Gaps: 0			
US-09-910-208B-12 (1-276) x US-08-585-585A-5 (1-103)			
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Db	2	AlaSerGlyGlyAsnCysGlnTyr	9
RESULT 13			
US-08-249-037C-5			
; Sequence 5, Application US/08249037C			
; Patent No. 5928917			
; GENERAL INFORMATION:			
; APPLICANT: Kilburn, Douglas G.			
; APPLICANT: Miller, Robert C.			
; APPLICANT: Warren, Richard A.J.			
; TITLE OF INVENTION: Polysaccharide binding fusion proteins			
; TITLE OF INVENTION: and conjugates			
; NUMBER OF SEQUENCES: 21			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: Rae-Venter Law Group, P.C.			

Qy	37	AAATATCTCCACCAATACACTTCAGG 63																								
Db	13	ASnllephEieGlnTyrSerValarg 21																								
<p>RESULT 12</p> <p>US-08-585-585A-5</p> <p>Sequence 5, Application US/08585585A</p> <p>Patent No. 5874308</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: Kilburn, Douglas G.</p> <p>APPLICANT: Humphries, Keith R.</p> <p>APPLICANT: Doherty, James G.</p> <p>APPLICANT: Jervis, Eric</p> <p>APPLICANT: Alimonti, Judie</p> <p>TITLE OF INVENTION: Compositions and methods for modulating cell proliferation using growth factor-polysaccharide binding fusion proteins</p> <p>TITLE OF INVENTION: cell proliferation using growth factor-polysaccharide binding fusion proteins</p> <p>NUMBER OF SEQUENCES: 14</p> <p>CORRESPONDENCE ADDRESS:</p> <p>ADDRESSEE: Rae-Venter Law Group</p> <p>STREET: Box 60039</p> <p>CITY: Palo Alto</p> <p>STATE: CA</p> <p>COUNTRY: U.S.</p> <p>ZIP: 94306</p> <p>COMPUTER READABLE FORM:</p> <p>MEDIUM TYPE: Floppy disk</p> <p>COMPUTER: IBM PC compatible</p> <p>OPERATING SYSTEM: PC-DOS/MS-DOS</p> <p>SOFTWARE: PatentIn Release #1.0, Version #1.30</p> <p>CURRENT APPLICATION DATA:</p> <p>APPLICATION NUMBER: US/08/585,585A</p> <p>FILING DATE: 16-JAN-1996</p> <p>CLASSIFICATION: 435</p> <p>ATTORNEY/AGENT INFORMATION:</p> <p>NAME: Kung, Viola T.</p> <p>REGISTRATION NUMBER: 41,131</p> <p>REFERENCE/DOCKET NUMBER: CBPT.016.000US</p> <p>TELECOMMUNICATION INFORMATION:</p> <p>TELEPHONE: (650)328-4400</p> <p>TELEFAX: (650)328-4477</p> <p>INFORMATION FOR SEQ ID NO: 5:</p> <p>SEQUENCE CHARACTERISTICS:</p> <p>LENGTH: 103 amino acids</p> <p>TYPE: amino acid</p> <p>STRANDEDNESS: not relevant</p> <p>TOPOLOGY: not relevant</p> <p>MOLECULE TYPE: peptide</p> <p>US-08-585-585A-5</p> <p>Alignment Scores:</p> <table border="1"> <tr> <td>Pred. No.:</td><td>10.4</td><td>Length:</td><td>103</td></tr> <tr> <td>Score:</td><td>8.00</td><td>Matches:</td><td>8</td></tr> <tr> <td>Percent Similarity:</td><td>100.00%</td><td>Conservative:</td><td>0</td></tr> <tr> <td>Best Local Similarity:</td><td>100.00%</td><td>Mismatches:</td><td>0</td></tr> <tr> <td>Query Match:</td><td>8.70%</td><td>Indels:</td><td>0</td></tr> <tr> <td>DB:</td><td>2</td><td>Gaps:</td><td>0</td></tr> </table> <p>US-09-910-208B-12 (1-276) x US-08-585-585A-5 (1-103)</p> <p>Qy 18 GCATCTGGAGGAATTGTCAATAT 41</p> <p>Db 2 AlaserGlyGlyAsnCysGlnTyr 9</p> <p>RESULT 13</p> <p>US-08-249-037C-5</p> <p>Sequence 5, Application US/08249037C</p> <p>Patent No. 5928917</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: Kilburn, Douglas G.</p> <p>APPLICANT: Miller, Robert C.</p> <p>APPLICANT: Warren, Richard A.J.</p>			Pred. No.:	10.4	Length:	103	Score:	8.00	Matches:	8	Percent Similarity:	100.00%	Conservative:	0	Best Local Similarity:	100.00%	Mismatches:	0	Query Match:	8.70%	Indels:	0	DB:	2	Gaps:	0
Pred. No.:	10.4	Length:	103																							
Score:	8.00	Matches:	8																							
Percent Similarity:	100.00%	Conservative:	0																							
Best Local Similarity:	100.00%	Mismatches:	0																							
Query Match:	8.70%	Indels:	0																							
DB:	2	Gaps:	0																							

STREET: P.O.Box 60039
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/788,621B
FILING DATE: January 23, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/249,037
FILING DATE: 24-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/865,095
FILING DATE: 08-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,987
FILING DATE: 25-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/216,794
FILING DATE: 08-JUL-1988
ATTORNEY/AGENT INFORMATION:
NAME: Kung, Viola T.
REGISTRATION NUMBER: 41,131
REFERENCE/DOCKET NUMBER: CBDT.002.05US
TELEPHONE: (650)328-4400
TELEFAX: (650)328-4477
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 103 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-788-621B-5
Alignment Scores:
Pred No.: 10.4 Length: 103
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 8.70% Indels: 0
DB: 3 Gaps: 0
US-09-910-208B-12 (1-276) x US-08-788-621B-5 (1-103)
QY 18 GCATCTGGAGGGAATTGTCATAT 41
Db 2 AlaSerGlyGlyAsnCysGlnTyr 9

Search completed: February 23, 2005, 12:40:09
Job time : 35.5 secs

STREET: P.O.Box 60039
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/788,622B
FILING DATE: January 23, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/249,037
FILING DATE: 24-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/865,095
FILING DATE: 08-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,987
FILING DATE: 25-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/216,794
FILING DATE: 08-JUL-1988
ATTORNEY/AGENT INFORMATION:
NAME: Kung, Viola T.
REGISTRATION NUMBER: 41,131
REFERENCE/DOCKET NUMBER: CBDT.002.06US
TELEPHONE: (650)328-4400
TELEFAX: (650)328-4477
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 103 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-788-622B-5
Alignment Scores:
Pred No.: 10.4 Length: 103
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 8.70% Indels: 0
DB: 2 Gaps: 0
US-09-910-208B-12 (1-276) x US-08-788-622B-5 (1-103)
QY 18 GCATCTGGAGGGAATTGTCATAT 41
Db 2 AlaSerGlyGlyAsnCysGlnTyr 9
RESULT 15
US-08-788-621B-5
Sequence 5, Application US/08/788621B
Patent No. 6124117
GENERAL INFORMATION:
APPLICANT: Kilburn, Douglas G.
APPLICANT: Miller, Robert C.
APPLICANT: Warren, Richard A.J.
APPLICANT: Gilkes, Neil R.
TITLE OF INVENTION: Polysaccharide binding fusion proteins
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rae-Venter Law Group, P.C.
STREET: P.O.Box 60039
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.